



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 105281

TO: Vanessa L Ford
Location: CM-1/8A16/8E12
Art Unit: 1645
Monday, October 06, 2003

Case Serial Number: 09/771382

From: David Schreiber
Location: Biotech-Chem Library
CM1-6A03
Phone: 308-4292

david.schreiber@uspto.gov

Search Notes

STIC-Biotech/ChemLib

105281

From: Pak, Michael
Sent: Friday, October 03, 2003 10:39 AM
T : STIC-Biotech/ChemLib
Cc: Ford, Vanessa
Subject: RE: IN Re: 09771382 Sequence search

Dear STIC,

Please search the multiple sequence search request set forth below. The search is necessary for the examination of the application.

thanks,

Mike Pak

-----Original Message-----

Fr m: Chan, Christina
Sent: Friday, October 03, 2003 10:24 AM
To: Ford, Vanessa; Pak, Michael; STIC-Biotech/ChemLib
Subject: RE: IN Re: 09771382 Sequence search

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

-----Original Message-----

From: Ford, Vanessa
Sent: Thursday, October 02, 2003 6:46 PM
To: Chan, Christina
Subject: IN Re: 09771382 Sequence search

Please search SEQ ID NOs: 23-27 and 33-39. Please include interference searches. Please rush.

Vanessa L. Ford
Biotechnology Patent Examiner
Office: CM1 8A16
Mailbox: CM1 8E12
Phone: 703.308.4735
Art Unit: 1645

Searcher: D. Schneider
Phone: 308-427
Location: CM1 6A03
Date Picked Up: _____
Date Completed: 10/6
Searcher Prep/Review: 22
Clerical: _____
Online time: 8

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: 12
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: Compugene
WWW/Internet: _____
Other (specify): _____

48 56

4 7

10 21



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact*:

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 - Circ. Desk



091824206

09724512

09824588

10210296

PA (UYOU) UNIV QUEENSLAND.
XX
XX PI Peak IRA, Jennings MP;
XX
XX WPI: 2001-488774/53.
DR N-PSDB; AAS09172.
XX
XX New Nhba surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX
PS Claim 12; Fig 5; 91pp: English.
XX
XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhba
CC (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence represents N. meningitidis strain PMC21 surface
CC antigen Nhba deletion mutant #1.
XX
SQ Sequence 512 AA:

Query Match 100.0%; Score 2350; DB 22; Length 512;
Best Local Similarity 100.0%; Pred. No. 7.6e-142;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NNETDLTSVGTKEKLSFSANGKRVNITSDTKGLNFAKETAGTNGDTYVHLNGIGSTLTDTL 60
DB 52 NNETDLTSVGTKEKLSFSANGKRVNITSDTKGLNFAKETAGTNGDTYVHLNGIGSTLTDTL 111
OY 61 LMTGATTNTNDNVTDDEKKRAASYKDVYNAGMNIKGVPGTASDNDVFRTYDVEFL 120
DB 112 LMTGATTNTNDNVTDDEKKRAASYKDVYNAGMNIKGVPGTASDNDVFRTYDVEFL 171
OY 121 SADTKTTTVNVSCKNGKTEYKIGAKTSVIEKDKGLVTGDKGENSSSTDEGEGLVTA 180
DB 172 SADTKTTTVNVSCKNGKTEYKIGAKTSVIEKDKGLVTGDKGENSSSTDEGEGLVTA 231
OY 181 KEVIDAVNKGARMKTTTANGOTGOADKFEYVTSCTNTVTFASGKTATVSKDDGNTIV 240
DB 232 KEVIDAVNKGARMKTTTANGOTGOADKFEYVTSCTNTVTFASGKTATVSKDDGNTIV 291
OY 241 MTDVNVGDLANNOLONGSMNIDSKAVAGSSGKVISGNVSPSKGKMDFTVINAGNNIEI 300
DB 292 MTDVNVGDLANNOLONGSMNIDSKAVAGSSGKVISGNVSPSKGKMDFTVINAGNNIEI 351
OY 301 TTRNGKNIDATSMTPOFFSSVSLGAGADAPTLISVDGDALNVGSKDNKPVRITNVAPGVE 360
DB 352 TTRNGKNIDATSMTPOFFSSVSLGAGADAPTLISVDGDALNVGSKDNKPVRITNVAPGVE 411
OY 361 GDTVNVAAQLKGVAQNLLNNRIDVNDGNARAGIAQAATATAGLVQAYLPGKSMMAIGGTYRG 420
DB 412 GDTVNVAAQLKGVAQNLLNNRIDVNDGNARAGIAQAATATAGLVQAYLPGKSMMAIGGTYRG 471
OY 421 EAGYAIGYSSISDGGNMIITKTASGNSRGHFGASASVGYOW 461
DB 472 EAGYAIGYSSISDGGNMIITKTASGNSRGHFGASASVGYOW 512

DE Amino acid sequence of N. meningitidis protein ORF40-1.
XX
XX Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;
KW bacterial infection; treatment.
XX
XX Neisseria meningitidis.
OS WO9936544-A2.
XX
XX
PN 22-JUL-1999.
XX
XX
PD 14-JAN-1999; 99WO-1B00103.
XX
XX
PF 09-OCT-1998; 98GB-0022143.
XX
XX PR 14-JAN-1998; 98GB-0000760.
PR 01-SEP-1998; 98GB-0019015.
XX
XX (CHTR-) CHIRON SPA.
PA Grandi G, Massignani V, Piazza M, Rappuoli R, Scarlato V;
XX
XX WPI: 1999-444400/37.
DR N-PSDB; AAX99124.
XX
XX New protein and its nucleotide sequence, useful in vaccines or
PT diagnostic compositions for treating and/or preventing Neisseria
PT meningitidis infections
XX
XX
PS Claim 1; Page 62; 123pp: English.
XX
XX The invention provides proteins (AAV27201-245) from Neisseria
CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)
CC encoding the proteins. Compositions comprising the protein, nucleic acid
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a
CC vaccine composition or a diagnostic composition. The composition is also
CC useful for treating or preventing an infection due to Neisseria
CC bacteria, especially Neisseria meningitidis.
XX
SQ Sequence 591 AA:

Query Match 99.3%; Score 2333; DB 20; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.1e-140;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TDLTSVGTKEKLSFSANGKRVNITSDTKGLNFAKETAGTNGDTYVHLNGIGSTLTDTLMT 63
DB 134 TDLTSVGTKEKLSFSANGKRVNITSDTKGLNFAKETAGTNGDTYVHLNGIGSTLTDTLMT 193
OY 64 GATTNTVNDNVTDDEKKRAASYKDVYNAGMNIKGVPGTASDNDVFRTYDVEFLSD 123
DB 194 GATTNTVNDNVTDDEKKRAASYKDVYNAGMNIKGVPGTASDNDVFRTYDVEFLSD 253
OY 124 TKTTVNVNVSCKNGKTEYKIGAKTSVIEKDKGLVTGDKGENSSSTDEGEGLVTAKEV 183
DB 254 TKTTVNVNVSCKNGKTEYKIGAKTSVIEKDKGLVTGDKGENSSSTDEGEGLVTAKEV 313
OY 184 IDAVNKGARMKTTTANGOTGOADKFEYVTSCTNTVTFASGKTATVSKDDGNTIVMD 243
DB 314 IDAVNKGARMKTTTANGOTGOADKFEYVTSCTNTVTFASGKTATVSKDDGNTIVMD 373
OY 244 VNVGDLANNOLONGSMNIDSKAVAGSSGKVISGNVSPSKGKMDFTVINAGNNIEITRN 303
DB 374 VNVGDLANNOLONGSMNIDSKAVAGSSGKVISGNVSPSKGKMDFTVINAGNNIEITRN 433
OY 304 GKNIDATSMTPOFFSSVSLGAGADAPTLISVDGDALNVGSKDNKPVRITNVAPGVEGPD 363
DB 434 GKNIDATSMTPOFFSSVSLGAGADAPTLISVDGDALNVGSKDNKPVRITNVAPGVEGPD 493
OY 364 TTVAAQLKGVAQNLLNNRIDVNDGNARAGIAQAATATAGLVQAYLPGKSMMAIGGTYRGEAG 423
DB 494 TTVAAQLKGVAQNLLNNRIDVNDGNARAGIAQAATATAGLVQAYLPGKSMMAIGGTYRGEAG 553
OY 424 VAIIGYSSISDGGNMIITKTASGNSRGHFGASASVGYOW 461

Db 554 YAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 591

RESULT 3

AAV23741
ID AAV23741 standard; Protein: 591 AA.

AC AAV23741;

XX 08-SEP-1999 (first entry)

DE A surface protein of Neisseria meningitidis.

XX Surface protein: surface glycoprotein; infection; vaccine;

KM immunoreactive peptide.

XX Neisseria meningitidis.

OS WO931132-A1.

XX 24-JUN-1999.

PE 14-DEC-1998; 98WO-AU01031.

PR 12-DEC-1997; 97GB-0026398.

PA (ISIS-) ISIS INNOVATION LTD.

XX (UYOU) UNIV QUEENSLAND.

PI Jennings MP, Moxon ER, Peak IRA;

XX WPI: 1999-418754/35.

DR N-PSDB; AAX85793.

PT Neisseria meningitidis surface proteins useful for treating N.

XX meningitidis infections

PS Claim 1; Page 104-106; 132pp; English.

XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.

XX Sequence 591 AA;

Query Match 99.3%; Score 2333; DB 20; Length 591;

Best Local Similarity 100.0%; Pred. No. 1.1e-140;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDLTSVTEKLSFSAANGKVNITSPTKGLNFAKETAGTNGDTVYHLNGISLTLDPLTNT 63

Db 134 TDLTSVTEKLSFSAANGKVNITSPTKGLNFAKETAGTNGDTVYHLNGISLTLDPLTNT 193

QY 64 GATTNVNDVNTDDEKKRAASVSRKDVNLNAGNINIKGVKPGTASDVNDFVRTDYVEFLSAD 123

Db 194 GATTNVNDVNTDDEKKRAASVSRKDVNLNAGNINIKGVKPGTASDVNDFVRTDYVEFLSAD 253

QY 124 TKTTTVNVEKDKGKTEVKIGAKTSYIKKDGKLVYGRKKGESSTDEGELVTAKEV 183

Db 254 TKTTTVNVEKDKGKTEVKIGAKTSYIKKDGKLVYGRKKGESSTDEGELVTAKEV 313

QY 184 IDAVNRKGRMKTTTANGOTGOADKFEVTSGTNVFAASGATTATYSKDDOGITVYMD 243

Db 314 IDAVNRKGRMKTTTANGOTGOADKFEVTSGTNVFAASGATTATYSKDDOGITVYMD 373

QY 244 VNVGDALNVNQLNSGWNILDSKAVAGSSGRVYISGNVSPSKMDETVNINAGNIEITRN 303

Db 374 VNVGDALNVNQLNSGWNILDSKAVAGSSGRVYISGNVSPSKMDETVNINAGNIEITRN 433

QY 304 GKNDIDTSMTPORSSVSLGAGADAPTLISVDGALNANGSKDKNPVITTVAPGVKGGDV 363

Db 434 GKNDIDTSMTPORSSVSLGAGADAPTLISVDGALNANGSKDKNPVITTVAPGVKGGDV 493

QY 364 TTNVAOLKGVANONLNRRIDNVNAGNARAGIQAIAFAGLVQAYLPKSMMAIGGGTYRGEAG 423

Db 494 TTNVAOLKGVANONLNRRIDNVNAGNARAGIQAIAFAGLVQAYLPKSMMAIGGGTYRGEAG 553

QY 424 YAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 461

Db 554 YAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 591

RESULT 4
AAV23746
ID AAV23746 standard; Protein: 591 AA.

AC AAV23746;

XX 08-SEP-1999 (first entry)

DE A surface protein of Neisseria meningitidis.

XX Surface protein: surface glycoprotein; infection; vaccine;

KM immunoreactive peptide.

XX Neisseria meningitidis.

OS WO931132-A1.

XX 24-JUN-1999.

PE 14-DEC-1998; 98WO-AU01031.

PR 12-DEC-1997; 97GB-0026398.

PA (ISIS-) ISIS INNOVATION LTD.

XX (UYOU) UNIV QUEENSLAND.

PI Jennings MP, Moxon ER, Peak IRA;

XX WPI: 1999-418754/35.

DR N-PSDB; AAX85798.

PT Neisseria meningitidis surface proteins useful for treating N.

XX meningitidis infections

PS Claim 1; Page 127-128; 132pp; English.

XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.

XX Sequence 591 AA;

Query Match 99.3%; Score 2333; DB 20; Length 591;

Best Local Similarity 100.0%; Pred. No. 1.1e-140;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDLTSVTEKLSFSAANGKVNITSPTKGLNFAKETAGTNGDTVYHLNGISLTLDPLTNT 63

Db 134 TDLTSVTEKLSFSAANGKVNITSPTKGLNFAKETAGTNGDTVYHLNGISLTLDPLTNT 193

QY 64 GATTNVNDVNTDDEKKRAASVSRKDVNLNAGNINIKGVKPGTASDVNDFVRTDYVEFLSAD 123

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Db      194 GATTIVNTDNDVTDDEKRRASVYKVDLNLGWNINIKGVKPGTTASDNDVFVHTDYVEFLSAD 253
OY      124 TKTITVNVESKDNKGKTEVKIGAKTSVYKEKDKGLVTGKDKGENSSSTDEGEGLVTAKEY 183
Db      254 TKTITVNVESKDNKGKTEVKIGAKTSVYKEKDKGLVTGKDKGENSSSTDEGEGLVTAKEY 313
OY      184 IDAVNKAGRMKTTTANGOTGADKFEYVTSCTNTVTFASGKGTATVSKDDOGNTVMD 243
Db      314 IDAVNKAGRMKTTTANGOTGADKFEYVTSCTNTVTFASGKGTATVSKDDOGNTVMD 373
OY      244 VAVGDLNVNOLONGSGWMLDSKAVAGSSGKVISGNVSPSKGMDFTVINAGNNIEITRN 303
Db      374 VAVGDLNVNOLONGSGWMLDSKAVAGSSGKVISGNVSPSKGMDFTVINAGNNIEITRN 433
OY      304 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDGDALNVGSKKDNKPVRTITNVAPEGKEDV 363
Db      434 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDGDALNVGSKKDNKPVRTITNVAPEGKEDV 493
OY      364 TNVAOLKGVAAQNLNRRIDNVGDNARAGIAQAIAATAGLVQAVLPGKSMAIIGGTYRGEAG 423
Db      494 TNVAOLKGVAAQNLNRRIDNVGDNARAGIAQAIAATAGLVQAVLPGKSMAIIGGTYRGEAG 553
OY      424 VAIGYSISDGGNNIITKGTASGNSRGRFGASASVGYQW 461
Db      554 VAIGYSISDGGNNIITKGTASGNSRGRFGASASVGYQW 591

RESULT 5
AAU06171
ID      AAU06171 standard. Protein: 591 AA.
XX      AAU06171;
AC      24-OCT-2001 (first entry)
XX      24-OCT-2001 (first entry)
DI      N. meningitidis PMC21 surface antigen Nhha polypeptide sequence.
XX      N. meningitidis PMC21 surface antigen Nhha polypeptide sequence.
KW      Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX      Surface antigen Nhha; meningococcal disease; meningitis vaccine.
OS      Neisseria meningitidis strain PMC21.
XX      Neisseria meningitidis strain PMC21.
FH      Key
FT      Peptide
FT      1..51
FT      /label= Signal_peptide
FT      1..50
FT      /label= C1
FT      /note= "Conserved region 1"
FT      51..108
FT      /label= V1
FT      /note= "Variable region 1"
FT      52..591
FT      /label= Mature_Nhha
FT      /note= "Predicted mature protein, specifically
FT      109..120
FT      /label= C2
FT      /note= "Conserved region 2"
FT      121..124
FT      /label= V2
FT      /note= "Variable region 2"
FT      125..188
FT      /label= C3
FT      /note= "Conserved region 3"
FT      189..210
FT      /label= V3
FT      /note= "Variable region 3"
FT      211..229
FT      /label= C4
FT      /note= "Conserved region 4"
FT      230..236
FT      /label= V4
FT      /note= "Variable region 4"
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FT      Region      237..591
FT      /label= C5
FT      /note= "Conserved region 5"
PN      WO20015182-A1.
XX      02-AUG-2001.
XX      25-JAN-2001; 2001WO-AU00069.
XX      25-JAN-2000; 2000US-0177917.
XX      (UYOU ) UNITV QUEENSLAND.
XX      Peak IRA, Jennings MP;
XX      WPI: 2001-488774/53.
XX      N-PSDB; AAS09161.
XX      New Nhha surface antigen polypeptides and polynucleotides from
XX      Neisseria meningitidis, useful in producing vaccines for treating or
XX      preventing broad spectrum of Neisseria meningitidis -
XX      Claim 9; Fig 1; 91pp; English.
XX      The present invention relates to the isolation of novel Neisseria
XX      meningitidis mutant polypeptides of the surface antigen Nhha
XX      (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
XX      characterised by deletions of non-conserved amino acids, particularly
XX      the deletion of variable regions. The deletion mutants are useful in
XX      diagnostics, therapeutic and prophylactic vaccines against a broader
XX      spectrum of N. meningitidis, and in designing and/or screening of
XX      immunise agents. The mutant proteins when used as a vaccine can effectively
XX      immunise against a broader spectrum of N. meningitidis strains than
XX      would be expected from a corresponding wild-type surface antigen.
XX      The present sequence representing the wild type surface antigen Nhha
XX      from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences
XX      (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX      the present invention.
SQ      Sequence      591 AA:
Query Match      99.3%; Score 2333; DB 22; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.le-140;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      4 TDLTSGTEKLSFSANGKVNITSDTKGINFPAKKTAGTNGOTVVLNIGSTLPTLNT 63
Db      134 TDLTSGTEKLSFSANGKVNITSDTKGINFPAKKTAGTNGOTVVLNIGSTLPTLNT 193
OY      64 GATTIVNTDNDVTDDEKRRASVYKVDLNLGWNINIKGVKPGTTASDNDVFVHTDYVEFLSAD 123
Db      194 GATTIVNTDNDVTDDEKRRASVYKVDLNLGWNINIKGVKPGTTASDNDVFVHTDYVEFLSAD 253
OY      124 TKTITVNVESKDNKGKTEVKIGAKTSVYKEKDKGLVTGKDKGENSSSTDEGEGLVTAKEY 183
Db      254 TKTITVNVESKDNKGKTEVKIGAKTSVYKEKDKGLVTGKDKGENSSSTDEGEGLVTAKEY 313
OY      184 IDAVNKAGRMKTTTANGOTGADKFEYVTSCTNTVTFASGKGTATVSKDDOGNTVMD 243
Db      314 IDAVNKAGRMKTTTANGOTGADKFEYVTSCTNTVTFASGKGTATVSKDDOGNTVMD 373
OY      244 VAVGDLNVNOLONGSGWMLDSKAVAGSSGKVISGNVSPSKGMDFTVINAGNNIEITRN 303
Db      374 VAVGDLNVNOLONGSGWMLDSKAVAGSSGKVISGNVSPSKGMDFTVINAGNNIEITRN 433
OY      304 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDGDALNVGSKKDNKPVRTITNVAPEGKEDV 363
Db      434 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDGDALNVGSKKDNKPVRTITNVAPEGKEDV 493
OY      364 TNVAOLKGVAAQNLNRRIDNVGDNARAGIAQAIAATAGLVQAVLPGKSMAIIGGTYRGEAG 423
Db      494 TNVAOLKGVAAQNLNRRIDNVGDNARAGIAQAIAATAGLVQAVLPGKSMAIIGGTYRGEAG 553
```


YY	424	YAIGYSSISDGGNNIINGTASGNSRGHGASASGYOW	461
Db	554	YAIGYSSISDGGNNIINGTASGNSRGHGASASGYOW	591
RESULT	6		
AAU06175			
ID	AAU06175	standard; Protein: 591 AA.	
XX	AAU06175;		
XX	AC		
XX	DT	24-OCT-2001 (first entry)	
XX	DE	N. meningitidis EG329 surface antigen Nhbha polypeptide sequence.	
XX	KW	Surface antigen Nhbha; meningococcal disease; meningitis vaccine.	
XX	OS	Neisseria meningitidis strain EG329.	
XX	Key	Location/Qualifiers	
FT	Region	1..50	
FT		/label= C1	
FT		/note= "Conserved region 1"	
FT	Region	51..108	
FT		/label= V1	
FT		/note= "Variable region 1"	
FT	Region	109..120	
FT		/label= C2	
FT		/note= "Conserved region 2"	
FT	Region	121..124	
FT		/label= V2	
FT		/note= "Variable region 2"	
FT	Region	125..188	
FT		/label= C3	
FT		/note= "Conserved region 3"	
FT	Region	189..210	
FT		/label= V3	
FT		/note= "Variable region 3"	
FT	Region	211..229	
FT		/label= C4	
FT		/note= "Conserved region 4"	
FT	Region	230..236	
FT		/label= V4	
FT		/note= "Variable region 4"	
FT	Region	237..591	
FT		/label= C5	
FT		/note= "Conserved region 5"	
XX	PN	MO200155182-A1.	
XX	PD	02-AUG-2001.	
XX	PF	25-JAN-2001; 2001WO-AU00069.	
XX	PR	25-JAN-2000; 2000US-0177917.	
XX	PA	(UYOU) UNIV QUEENSLAND.	
XX	P1	Peak IRA, Jennings MP;	
XX	XX	WPI; 2001-488774/53.	
XX	DR	N-PSDB; AAS09165.	
PT	XX	New Nhbha surface antigen polypeptides and polynucleotides from	
PT	XX	Neisseria meningitidis, useful in producing vaccines for treating or	
PT	XX	preventing broad spectrum of Neisseria meningitidis -	
XX	PS	Claim 9; Fig 1; 91pp; English.	
CC	CC	The present invention relates to the isolation of novel Neisseria	
CC	CC	meningitidis mutant polypeptides of the surface antigen Nhbha	
CC	CC	(AAU06182-AAU06186). The modified or mutant Nhbha polypeptides are	

CC	characterised by deletions of non-conserved amino acids, particularly
CC	the deletion of variable regions. The deletion mutants are useful in
CC	diagnostics, therapeutic and prophylactic vaccines against a broader
CC	spectrum of <i>N. meningitidis</i> , and in designing and/or screening of
CC	medicaments. The mutant proteins when used as a vaccine can effectively
CC	immunise against a broader spectrum of <i>N. meningitidis</i> strains than
CC	would be expected from a corresponding wild-type surface antigen.
CC	The present sequence representing the wild type surface antigen NnhA
CC	from <i>N. meningitidis</i> strain E6329 is 1 of 10 NnhA polypeptide sequences
CC	(AA006171-AA006180) from 10 different <i>N. meningitidis</i> strains given in
CC	the present invention.
XX	
XX	Sequence 591 AA;
50	
	Query Match 99.3%; Score 2333; DB 22; Length 591;
	Best Local Similarity 100.0%; Pident. No. 1,1e-140;
	Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	4 TDLTSVGTKEKSEFANGKRVITSDTGLNPAKFACTAGTNGDTTYHLNGIGSTLTDLTLNT 63
DB	134 TDLTSVGTKEKSEFANGKRVITSDTGLNPAKFACTAGTNGDTTYHLNGIGSTLTDLTLNT 193
OY	64 GATTNNVNDVNTDDEKKRAASVKVYLVNAGNVIKVKFGTTPASDNDVDFRTYDVEFLSAD 123
DB	194 GATTNNVNDVNTDDEKKRAASVKVYLVNAGNVIKVKFGTTPASDNDVDFRTYDVEFLSAD 253
OY	124 TKTITTVNESKDKNCKTEVKIGAKTSYIKERDGLVITGDKGSEGSTDEGEGLVTAKEV 183
DB	254 TKTITTVNESKDKNCKTEVKIGAKTSYIKERDGLVITGDKGSEGSTDEGEGLVTAKEV 313
OY	184 IDAVNKGAWRKKTITTAANGQTGADRFETVTISGTVTFASGKGTATYVSKDDGNIITYMYD 243
DB	314 IDAVNKGAWRKKTITTAANGQTGADRFETVTISGTVTFASGKGTATYVSKDDGNIITYMYD 373
OY	244 VNVGDALNVNOLONGNWLDSKAAVSGSGKVIKSGNVSPSKKMDETVINAGNNIETTRN 303
DB	374 VNVGDALNVNOLONGNWLDSKAAVSGSGKVIKSGNVSPSKKMDETVINAGNNIETTRN 433
OY	304 GKNIDIAISMTPORFSSVSLGAGADAPTLSDVDGALNNGSKKDKNKPVRITTVNAPGVKKEGDV 363
DB	434 GKNIDIAISMTPORFSSVSLGAGADAPTLSDVDGALNNGSKKDKNKPVRITTVNAPGVKKEGDV 493
OY	364 TNVAQLKGVAONLNNRIDNVGDNARAGIAQAIAATAGLVQAVLPEKSMMAIGGTYRGEAG 423
DB	494 TNVAQLKGVAONLNNRIDNVGDNARAGIAQAIAATAGLVQAVLPEKSMMAIGGTYRGEAG 553
OY	424 YAIQYSSISDGGNWIIGTASGNSRGRFGASASVGYOM 461
DB	554 YAIQYSSISDGGNWIIGTASGNSRGRFGASASVGYOM 591
RESULT 7	
AAI57045	
ID	AAI57045 standard; Protein: 591 AA.
XX	
AC	AAI57045;
XX	
XX	21-FEB-2000 (first entry)
DE	BASB029 amino acid sequence from <i>N. meningitidis</i> strain H44/76.
XX	
XX	BASB029; <i>Neisseria meningitidis</i> ; surface fibril protein; HSF; diagnosis;
KW	Infection; treatment; prevent; antibacterial drug.
XX	
OS	<i>Neisseria meningitidis</i> .
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 90
FT	/note= "Encoded by AAT"
FT	Misc-difference 92
FT	/note= "Encoded by GAT"
FT	Misc-difference 98
FT	/note= "Encoded by AAC"

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FT Misc-difference 108 /note= "Encoded by AATC"
FT Misc-difference 123 /note= "Encoded by ACA"
FT Misc-difference 269 /note= "Encoded by AAA"
FT Misc-difference 389 /note= "Encoded by CGT"
FT WO9558683-A2.
PN
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WO-EP03255.
XX
PR 13-MAY-1998; 98GB-0010276.
XX
PA (SMIK ) SMITHKLINE BECHAM BIOLOGICALS.
XX
PI Ruelle J;
XX
DR WPI: 2000-053103/04.
DR N-PSDB; AAX39865.
XX
PT New polypeptide from neisseria meningitidis useful for diagnosis,
PT treatment or prevention of bacterial infections in mammal
XX
PS Claim 4; Fig 2; 74pp; English.
XX
CC This is the Neisseria meningitidis BASB029 amino acid sequence from
CC serogroup B strain H44/76. The BASB029 protein is homologous to the
CC Haemophilus influenzae surface fliPril (HSF) protein. The invention
CC relates to BASB029 polynucleotide sequences (AAX39864-239865) and
CC polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments.
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria
CC meningitidis infection in a mammal. Compositions containing BASB029
CC polynucleotides and polypeptides are useful for generating an immune
CC response in an animal. A therapeutic composition comprising an antibody
CC directed against BASB029 is useful in treating humans with Neisseria
CC meningitidis disease. The polynucleotide is useful in the diagnosis of
CC the stage of infection, type of infection, susceptibility to an
CC infection which results from increased or decreased expression of the
CC polynucleotide, and for therapeutic or prophylactic purposes,
CC particularly genetic immunisation. Antibodies against BASB029
CC polynucleotides and polypeptides are also useful for treating infections
CC particularly bacterial infections. The protein is useful in the
CC screening and development of antibacterial drugs. Fused recombinant
CC protein is useful for the stimulation of the immune system of an organism
CC receiving the protein.
XX
SQ Sequence 591 AA:
Query Match 99.1%; Score 2330; DB 21; Length 591;
Best Local Similarity 99.8%; Pred. No. 1.7e-140;
Matches 457; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 TDLTSGTEKLSFSANGKVNITSDTKGLNFAKETAGTNGDTVHLNGIGSTLTDTLLNT 63
DB 134 TDLTSGTEKLSFSANGKVNITSDTKGLNFAKETAGTNGDTVHLNGIGSTLTDTLLNT 193
QY 64 GATTNVTNDNTVDDEKRRASVKDYLNAGWNKGVKPGTTASDNDVFRITDTVEFLSAD 123
DB 194 GATTNVTNDNTVDDEKRRASVKDYLNAGWNKGVKPGTTASDNDVFRITDTVEFLSAD 253
QY 124 TTTTNNVESKNGKRTVEKIGAKTSVIEKDKGLVTGDKGKNGSSSTDEGGLVTAKEV 183
DB 254 TTTTNNVESKNGKRTVEKIGAKTSVIEKDKGLVTGDKGKNGSSSTDEGGLVTAKEV 313
QY 184 IDAVNKAQKRMKTTTANGQTGADKFEETVTSCTNTVFAAGKGTATVSKDDOGNTTVMYD 243
DB 314 IDAVNKAQKRMKTTTANGQTGADKFEETVTSCTNTVFAAGKGTATVSKDDOGNTTVMYD 373
QY 244 VAVGALNVLNOLONGSGWNLDSKAVAGSSGKVIISGNVSPSKGMDFTVNIAGNNIEITRN 303
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DB 374 VAVGALNVLNOLONGSGWNLDSKAVAGSSGKVIISGNVSPSKGMDFTVNIAGNNIEITRN 433
QY 304 GKNIDIATSMTPQFSSVSLGAGADAPTLSDDDALNVGSKKNKPVRITNVAPKVEGDY 363
DB 434 GKNIDIATSMTPQFSSVSLGAGADAPTLSDDDALNVGSKKNKPVRITNVAPKVEGDY 493
QY 364 TNVAOLKGYAQNLRNIDNVGNARAGIAQAIAATAGLVQAYLPGKSMATGGGTYRGEAG 423
DB 494 TNVAOLKGYAQNLRNIDNVGNARAGIAQAIAATAGLVQAYLPGKSMATGGGTYRGEAG 553
QY 424 VAIGYSSTSDGGMWITIKGTASGNSRGHCASASVGYOW 461
DB 554 VAIGYSSTSDGGMWITIKGTASGNSRGHCASASVGYOW 591
RESULT 8
AAY23737
ID AAY23737 standard; Protein; 592 AA.
XX
AC AAY23737;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UYU) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX
DR WPI: 1999-418754/35.
DR N-PSDB; AAX85788.
XX
PT Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
PS Claim 1; Page 86-87; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 592 AA:
Query Match 99.1%; Score 2329; DB 20; Length 592;
Best Local Similarity 99.8%; Pred. No. 2e-140;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 TDLTSGTEKLSFSANGKVNITSDTKGLNFAKETAGTNGDTVHLNGIGSTLTDTLLNT 63
DB 135 TDLTSGTEKLSFSANGKVNITSDTKGLNFAKETAGTNGDTVHLNGIGSTLTDTLLNT 194
QY 64 GATTNVTNDNTVDDEKRRASVKDYLNAGWNKGVKPGTTASDNDVFRITDTVEFLSAD 123
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Db      195 GATTNTNDVTDDEKRRASVVDVLAAGNNIKGVKPGTTASDNVDFVRTYDVEFLSAD 254
QY      124 TKTITVVESEKDKNGKTEVIGAKTSYIKERKDLVYGRKNGEGSSTDGEGLVYTAKEV 183
Db      255 TKTITVVESEKDKNGKTEVIGAKTSYIKERKDLVYGRKNGEGSSTDGEGLVYTAKEV 314
QY      184 IDAVNRKAGWRMKTTTANGOTGOADKFEYVTSIGTNTVFASGKGTATVSKDDGNTIYMYD 243
Db      315 IDAVNRKAGWRMKTTTANGOTGOADKFEYVTSIGTNTVFASGKGTATVSKDDGNTIYMYD 374
QY      244 VNVGDALNVNQLONGSGNNLDSKAVAGSSGKVISGNVSPSKGKDETVNINAGNNIETRN 303
Db      375 VNVGDALNVNQLONGSGNNLDSKAVAGSSGKVISGNVSPSKGKDETVNINAGNNIETRN 434
QY      304 GKNDIATSMTPQFSSVSLGAGADAPPLSYDGDALNYSKDKPKPRITNVAPGVKEGDV 363
Db      435 GKNDIATSMTPQFSSVSLGAGADAPPLSYDGDALNYSKDKPKPRITNVAPGVKEGDV 494
QY      364 TTVNVAOLKGYAQNINNRIDNVNAGNARAGIAQAIATAGLVQAYLPGKSMMAIGGTYRGEAG 423
Db      495 TTVNVAOLKGYAQNINNRIDNVNAGNARAGIAQAIATAGLVQAYLPGKSMMAIGGTYRGEAG 554
QY      424 YAIQYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 461
Db      555 YAIQYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 592
```

RESULT 9

AAV23740
ID AAV23740 standard; Protein; 594 AA.

XX AAV23740;

DT 08-SEP-1999 (first entry)

XX A surface protein of *Neisseria meningitidis*.

KW Surface protein; surface glycoprotein; infection; vaccine;
immunoreactive peptide.

OS *Neisseria meningitidis*.

XX WO9931132-A1.

XX 24-JUN-1999.

XX 14-DEC-1998; 98WO-AU01031.

XX 12-DEC-1997; 97GB-0026398.

XX (ISIS-) ISIS INNOVATION LTD.

XX (UYOU) UNIV QUEENSLAND.

XX Jennings MP, Moxon ER, Peak IRA;

XX WPI; 1999-418754/35.

XX N-PSDB; AAX85792.

XX *Neisseria meningitidis* surface proteins useful for treating *N.*

XX *meningitidis* infections

XX Claim 1; Page 100-101; 132pp; English.

XX The present sequence represents a surface protein of *Neisseria*
XX *meningitidis* which is approximately 62 kDa. The *N. meningitidis*
XX surface glycoproteins, nucleic acids, the primers and optionally
XX a thermostable polymerase, or antibodies are useful in a kit for
XX the detection or diagnosis of *N. meningitidis* infection in humans.
XX The *N. meningitidis* surface glycoproteins can also be used to
XX prevent or treat *N. meningitidis* infection in humans, especially
XX in the form of vaccines. The proteins and antibodies can also
XX be used to identify immunoreactive peptides.

```

XX      SQ      Sequence      594 AA;
QY      4 TDLTSVTEKLSFSAANGKNNITSDPTGKLNFAKFTAGTNDPTVHLNGISSTLTDTLLNT 63
Db      136 TDLTSVTEKLSFSAANGKNNITSDPTGKLNFAKFTAGTNDPTVHLNGISSTLTDTLLNT 195
QY      64 GATTNTNDVTDDEKRRASVVDVLAAGNNIKGVKPGTTASDNVDFVRTYDVEFLSAD 123
Db      196 GATTNTNDVTDDEKRRASVVDVLAAGNNIKGVKPGTTASDNVDFVRTYDVEFLSAD 255
QY      124 TKTITVVESEKDKNGKTEVIGAKTSYIKERKDLVYGRKNGEGSSTDGEGLVYTAKEV 183
Db      256 TKTITVVESEKDKNGKTEVIGAKTSYIKERKDLVYGRKNGEGSSTDGEGLVYTAKEV 315
QY      184 IDAVNRKAGWRMKTTTANGOTGOADKFEYVTSIGTNTVFASGKGTATVSKDDGNTIYMYD 243
Db      316 IDAVNRKAGWRMKTTTANGOTGOADKFEYVTSIGTNTVFASGKGTATVSKDDGNTIYMYD 375
QY      244 VNVGDALNVNQLONGSGNNLDSKAVAGSSGKVISGNVSPSKGKDETVNINAGNNIETRN 303
Db      376 VNVGDALNVNQLONGSGNNLDSKAVAGSSGKVISGNVSPSKGKDETVNINAGNNIETRN 435
QY      304 GKNDIATSMTPQFSSVSLGAGADAPPLSYDGD-ALNVGSKDKPKPRITNVAPGVKEGD 362
Db      436 GKNDIATSMTPQFSSVSLGAGADAPPLSYDDEGALNYSKDKPKPRITNVAPGVKEGD 495
QY      363 VTVNVAOLKGYAQNINNRIDNVNAGNARAGIAQAIATAGLVQAYLPGKSMMAIGGTYRGEA 422
Db      496 VTVNVAOLKGYAQNINNRIDNVNAGNARAGIAQAIATAGLVQAYLPGKSMMAIGGTYRGEA 555
QY      423 GYAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 461
Db      556 GYAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 594
```

RESULT 10

AAV57044
ID AAV57044 standard; Protein; 594 AA.

XX AAV57044;

DT 21-FEB-2000 (first entry)

XX BASB029 amino acid sequence from *N. meningitidis* strain ATCC13090.

KW BASB029; *Neisseria meningitidis*; surface fibrin protein; HSF; diagnosis;

XX infection; treatment; prevent; antibacterial drug.

XX *Neisseria meningitidis*.

XX OS *Neisseria meningitidis*.

XX Key Location/Qualifiers

XX W0958683-A2.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-EP03255.

XX 13-MAY-1998; 98GB-0010276.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX Ruelle J;

XX WPI; 2000-053103/04.

XX N-PSDB; AAZ39864.

XX New polypeptide from neisseria meningitidis useful for diagnosis,
 PT treatment or prevention of bacterial infections in mammal
 XX
 XX
 PS Claim 4; Fig 2; 74pp; English.

CC This is the Neisseria meningitidis BASB029 amino acid sequence from
 CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the
 CC Haemophilus influenzae surface fibril (HSF) protein. The invention
 CC relates to BASB029 polynucleotide sequences (AA339864-239865) and
 CC polypeptide sequences (AA57044-Y57045) and their immunogenic fragments.
 CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria
 CC meningitidis infection in a mammal. Compositions containing BASB029
 CC polynucleotides and polypeptides are useful for generating an immune
 CC response in an animal. A therapeutic composition comprising an antibody
 CC directed against BASB029 is useful in treating humans with Neisseria
 CC meningitidis disease. The polynucleotide is useful in the diagnosis of
 CC the stage of infection, type of infection, susceptibility to an
 CC infection which results from increased or decreased expression of the
 CC polynucleotide, and for therapeutic or prophylactic purposes,
 CC particularly genetic immunisation. Antibodies against BASB029
 CC polynucleotides and polypeptides are also useful for treating infections
 CC particularly bacterial infections. The protein is useful in the
 CC screening and development of antibacterial drugs. Fused recombinant
 CC protein is useful for the stimulation of the immune system of an organism
 CC receiving the protein.

XX Sequence 594 AA:

Query Match 96.2%; Score 2260.5; DB 21; Length 594;
 Best Local Similarity 97.4%; Pred. No. 4.6e-136;
 Matches 447; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 4 TDLTSGTEKLSFSSANGKNGKNTSDTKGLNFAKTAGTGDPTVHLNGISTLTDLT 63
 DB 136 TDLTSGTEKLSFSSANGKNGKNTSDTKGLNFAKTAGTGDPTVHLNGISTLTDLT 195
 QY 64 GATTVNTDNTVDDEKRRASVVDVLMAGWNIGKVGPGTTASDNDVFRYDTVEFLSAD 123
 DB 196 GATTVNTDNTVDDEKRRASVVDVLMAGWNIGKVGPGTTASDNDVFRYDTVEFLSAD 255
 QY 124 TKTTVNVNKKNGKNGKTEVKGAKTSYKREKDKGLVTKGDKKENGSSDTBEGGLVYAKEV 183
 DB 256 TKTTVNVNKKNGKNGKTEVKGAKTSYKREKDKGLVTKGDKKENGSSDTBEGGLVYAKEV 315
 QY 184 IDAVKAGKGRMKTATTANGQTQADKFEYVTSCTNTFFASGKTATVSKDDGNTTAMD 243
 DB 316 IDAVKAGKGRMKTATTANGQTQADKFEYVTSCTNTFFASGKTATVSKDDGNTTAMD 375
 QY 244 VAVGDALNVNOLQNSGWNLDKRAVAGSSGKVISGNVSPSKGMDFTVINAGNNIETRN 303
 DB 376 VAVGDALNVNOLQNSGWNLDKRAVAGSSGKVISGNVSPSKGMDFTVINAGNNIETRN 435
 QY 304 GNNDIATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKDKNRPVRTTNAFVKEGD 362
 DB 436 GNNDIATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKDKNRPVRTTNAFVKEGD 495
 QY 363 VTNVAVQLKGVNOLNRRIDNVGNARAGIAQATATAGLQVAILPGKSMVAGGTYRGA 422
 DB 496 VTNVAVQLKGVNOLNRRIDNVGNARAGIAQATATAGLQVAILPGKSMVAGGTYRGA 555
 QY 423 GVAIGYSSISDGGNNIIRKGTASGNSRGHFGASASVGYOW 461
 DB 556 GVAIGYSSISDGGNNIIRKGTASGNSRGHFGASASVGYOW 594

RESULT 11
 AAU06174
 ID AAU06174 standard; Protein; 594 AA.
 AC AAU06174;
 XX
 DT 24-OCT-2001 (first entry)

XX N. meningitidis EG327 surface antigen Noha polypeptide sequence.
 DE
 XX Surface antigen Noha; meningococcal disease; meningitis vaccine.
 KW
 XX
 OS Neisseria meningitidis strain EG327.

XX Key Location/Qualifiers
 FH 1..50
 FT Region /label= C1
 FT /note= "Conserved region 1"
 FT 51..104
 FT Region /label= V1
 FT /note= "Variable region 1"
 FT 105..116
 FT Region /label= C2
 FT /note= "Conserved region 2"
 FT 117..126
 FT Region /label= V2
 FT /note= "Variable region 2"
 FT 127..190
 FT Region /label= C3
 FT /note= "Conserved region 3"
 FT 191..212
 FT Region /label= V3
 FT /note= "Variable region 3"
 FT 213..231
 FT Region /label= C4
 FT /note= "Conserved region 4"
 FT 232..238
 FT Region /label= V4
 FT /note= "Variable region 4"
 FT 239..594
 FT Region /label= C5
 FT /note= "Conserved region 5"

PN WO20015182-A1.

PD 02-AUG-2001.

PE 25-JAN-2001; 2001WO-AU00069.

PR 25-JAN-2000; 2000US-0177917.

PA (UYOU) UNITV QUEENSLAND.

PI Peak IRA, Jennings MP;

XX WPI: 2001-488774/53.

DR N-PSDB; AAS09164.

PT New Noha surface antigen polypeptides and polynucleotides from
 PT Neisseria meningitidis, useful in producing vaccines for treating or
 PT preventing broad spectrum of Neisseria meningitidis -

PS Claim 9; Fig 1; 91pp; English.

XX The present invention relates to the isolation of novel Neisseria
 CC meningitidis mutant polypeptides of the surface antigen Noha
 CC (AAU06182-AAU06186). The modified or mutant Noha polypeptides are
 CC characterised by deletions of non-conserved amino acids, particularly
 CC the deletion of variable regions. The deletion mutants are useful in
 CC diagnostics, therapeutic and prophylactic vaccines against a broader
 CC spectrum of N. meningitidis, and in designing and/or screening of
 CC medicaments. The mutant proteins when used as a vaccine can effectively
 CC immunise against a broader spectrum of N. meningitidis strains than
 CC would be expected from a corresponding wild-type surface antigen.
 CC The present sequence representing the wild type surface antigen Noha
 CC from N. meningitidis strain EG327 is 1 of 10 Noha polypeptide sequences
 CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
 CC the present invention.

XX Sequence 594 AA:

Query Match 96.2%; Score 2260.5; DB 22; Length 594;
Best Local Similarity 97.4%; Pred. No. 4.6e-136;
Matches 447; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 4 TDLTSTVTEKLSFGANGKVNITSDPKGLNFAKETAGTNGDTTVHLNGISSTLTDLTLLNT 63
DB TDLTSTVTEKLSFGANGKVNITSDPKGLNFAKETAGTNGDTTVHLNGISSTLTDLTLLNT 135
QY 64 GATTNTVNDVTDDEKRRASVVDVNLAGNINIGVYKPGTTASDNDVDFVHTDYVEFLSAD 123
DB GATTNTVNDVTDDEKRRASVVDVNLAGNINIGVYKPGTTASDNDVDFVHTDYVEFLSAD 255
QY 124 TKTITVNESKDKNGKTEVIGAKTSYIKERDKLVTKGDKGNGSSTDEGEGLVTAKEV 183
DB TKTITVNESKDKNGKTEVIGAKTSYIKERDKLVTKGDKGNGSSTDEGEGLVTAKEV 315
QY 184 IDAVNKGWBMKTTTANGOTGOADKEFTVTSNTVFASGKGTATVSKDQGNITVMYD 243
DB IDAVNKGWBMKTTTANGOTGOADKEFTVTSNTVFASGKGTATVSKDQGNITVMYD 375
QY 244 VNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGKDETVNINAGNIIETRN 303
DB VNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGKDETVNINAGNIIETRN 435
QY 304 GKNIDIATSMTPPFSSVSLGAGADAPTLISVDG-ALNVGSKDNKPVRIITNVA PGYEGD 362
DB GKNIDIATSMTPPFSSVSLGAGADAPTLISVDGALNVGSKDNKPVRIITNVA PGYEGD 495
QY 363 VTNVAOLKGYAONLNNRIDVNGNARAGIAQAIAATAGLVQAYLPKGSMAIGGTYRGEA 422
DB VTNVAOLKGYAONLNNRIDVNGNARAGIAQAIAATAGLVQAYLPKGSMAIGGTYRGEA 555
QY 423 GYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 461
DB GYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 594

RESULT 12
ID AAY23743 standard; Protein; 599 AA.

XX AAY23743;
XX 08-SEP-1999 (first entry)
XX A surface protein of Neisseria meningitidis.
XX Surface protein; surface glycoprotein; infection; vaccine;
XX Immunoreactive peptide.
XX Neisseria meningitidis.
XX WO931132-A1.
XX 24-JUN-1999.
XX 14-DEC-1998; 98MO-AU01031.
XX 12-DEC-1997; 97GB-0026398.
XX (ISIS-) ISIS INNOVATION LTD.
XX (UYOU) UNIV QUEENSLAND.
XX
XX Jennings MP, Moxon ER, Peak IRA;
XX WPI; 1999-418754/35.
XX N-PSDB; AAX85795.
XX
XX Neisseria meningitidis surface proteins useful for treating N.
XX meningitidis infections
XX
XX Claim 1; Page 114-115; 132pp; English.

XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.

Query Match 96.1%; Score 2257.5; DB 20; Length 599;
Best Local Similarity 97.4%; Pred. No. 7.2e-136;
Matches 447; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 4 TDLTSTVTEKLSFGANGKVNITSDPKGLNFAKETAGTNGDTTVHLNGISSTLTDLTLLNT 63
DB TDLTSTVTEKLSFGANGKVNITSDPKGLNFAKETAGTNGDTTVHLNGISSTLTDLTLLNT 200
QY 64 GATTNTVNDVTDDEKRRASVVDVNLAGNINIGVYKPGTTASDNDVDFVHTDYVEFLSAD 123
DB GATTNTVNDVTDDEKRRASVVDVNLAGNINIGVYKPGTTASDNDVDFVHTDYVEFLSAD 260
QY 124 TKTITVNESKDKNGKTEVIGAKTSYIKERDKLVTKGDKGNGSSTDEGEGLVTAKEV 183
DB TKTITVNESKDKNGKTEVIGAKTSYIKERDKLVTKGDKGNGSSTDEGEGLVTAKEV 320
QY 184 IDAVNKGWBMKTTTANGOTGOADKEFTVTSNTVFASGKGTATVSKDQGNITVMYD 243
DB IDAVNKGWBMKTTTANGOTGOADKEFTVTSNTVFASGKGTATVSKDQGNITVMYD 380
QY 321 IDAVNKGWBMKTTTANGOTGOADKEFTVTSNTVFASGKGTATVSKDQGNITVMYD 380
DB IDAVNKGWBMKTTTANGOTGOADKEFTVTSNTVFASGKGTATVSKDQGNITVMYD 440
QY 244 VNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGKDETVNINAGNIIETRN 303
DB VNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGKDETVNINAGNIIETRN 440
QY 381 VNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGKDETVNINAGNIIETRN 440
DB VNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGKDETVNINAGNIIETRN 500
QY 441 GKNIDIATSMTPPFSSVSLGAGADAPTLISVDGALNVGSKDNKPVRIITNVA PGYEGD 500
DB GKNIDIATSMTPPFSSVSLGAGADAPTLISVDGALNVGSKDNKPVRIITNVA PGYEGD 560
QY 363 VTNVAOLKGYAONLNNRIDVNGNARAGIAQAIAATAGLVQAYLPKGSMAIGGTYRGEA 422
DB VTNVAOLKGYAONLNNRIDVNGNARAGIAQAIAATAGLVQAYLPKGSMAIGGTYRGEA 560
QY 501 VTNVAOLKGYAONLNNRIDVNGNARAGIAQAIAATAGLVQAYLPKGSMAIGGTYRGEA 560
DB GYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 599

RESULT 13
ID AAU06176 standard; Protein; 599 AA.

XX AAU06176;
XX 24-OCT-2001 (first entry)
XX N. meningitidis H38 surface antigen Nhha polypeptide sequence.
XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX Neisseria meningitidis strain H38.
XX
XX Key Location/Qualifiers
XX FH 1..50
XX FT /label= C1
XX FT /note= "Conserved region 1"
XX FT 51..105
XX FT /label= V1
XX FT /note= "Variable region 1"
XX FT 106..117
XX FT /label= C2
XX Region

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FT      /note= "Conserved region 2"
FT      118..131
FT      /label= V2
FT      /note= "Variable region 2"
FT      132..195
FT      /label= C3
FT      /note= "Conserved region 3"
FT      196..217
FT      /label= V3
FT      /note= "Variable region 3"
FT      218..236
FT      /label= C4
FT      /note= "Conserved region 4"
FT      237..243
FT      /label= V4
FT      /note= "Variable region 4"
FT      244..599
FT      /label= C5
FT      /note= "Conserved region 5"

WO20015182-A1.
XX      02-AUG-2001.
XX      25-JAN-2001; 2001WO-AU00069.
XX      25-JAN-2000; 2000US-0177917.
XX      (UYOU ) UNIV QUEENSLAND.
XX      PA
XX      PI Peak IRA, Jennings MP;
XX      DR WPI; 2001-488774/53.
XX      DR N-PSDB; AAS09166.

PT      New Nhba surface antigen polypeptides and polynucleotides from
PT      Neisseria meningitidis, useful in producing vaccines for treating or
PT      preventing broad spectrum of Neisseria meningitidis .
XX      PT
XX      PS Claim 9; Fig 1; 91pp; English.
XX      CC
XX      CC The present invention relates to the isolation of novel Neisseria
XX      CC meningitidis mutant polypeptides of the surface antigen Nhba
XX      CC (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are
XX      CC characterised by deletions of non-conserved amino acids, particularly
XX      CC the deletion of variable regions. The deletion mutants are useful in
XX      CC diagnostics, therapeutic and prophylactic vaccines against a broader
XX      CC spectrum of N. meningitidis, and in designing and/or screening of
XX      CC medicaments. The mutant proteins when used as a vaccine can effectively
XX      CC immunise against a broader spectrum of N. meningitidis strains than
XX      CC would be expected from a corresponding wild-type surface antigen.
XX      CC The present sequence representing the wild type surface antigen Nhba
XX      CC from N. meningitidis strain H38 is 1 of 10 Nhba polypeptide sequences
XX      CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX      CC the present invention.
XX      SQ
XX      SQ Sequence 599 AA:

Query Match          96.1%; Score 2257.5; DB 22; Length 599;
Best Local Similarity 97.4%; Pred. No. 7.2e-136;
Matches 447; Conservative 2; Mismatches 9; Indels 1; Gaps 1;
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QY      304 GKNIDIATSMTPQFSFVSISLGAGADAPTLSDVC -DALANTGSKDNKPVRTITVAPGVKRGD 362
DB      441 GKNIDIATSMTPQFSFVSISLGAGADAPTLSDVC -DALANTGSKDNKPVRTITVAPGVKRGD 500
QY      363 VTNVAQLKGAQNLNMRIDNVGNARAGIAQAIATAGLVQAYLPCKSMATIGCGTYRGEA 422
DB      501 VTNVAQLKGAQNLNMRIDNVGNARAGIAQAIATAGLVQAYLPCKSMATIGCGTYRGEA 560
QY      423 GYATGYSSISDGGNMTITGTASGNSRGHFGASASVGYOM 461
DB      561 GYATGYSSISDGGNMTITGTASGNSRGHFGASASVGYOM 599

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ID      AAV23739 standard; Protein; 594 AA.
XX      AC
XX      AAV23739;
XX      DT 08-SEP-1999 (first entry)
XX      DE A surface protein of Neisseria meningitidis.
XX      KW Surface protein; surface glycoprotein; infection; vaccine;
XX      KW immunoreactive peptide.
XX      OS Neisseria meningitidis.
XX      PN WO9931132-A1.
XX      PD 24-JUN-1999.
XX      PF 14-DEC-1998; 98WO-AU01031.
XX      PR 12-DEC-1997; 97GB-0026398.
XX      PA (ISIS-) ISIS INNOVATION LTD;
XX      PA (UYOU ) UNIV QUEENSLAND.
XX      PI Jennings MP, Moxon ER, Peak IRA;
XX      DR WPI; 1999-418754/35.
XX      DR N-PSDB; AAX85791.
XX      PT Neisseria meningitidis surface proteins useful for treating N.
XX      PT meningitidis infections
XX      PS Claim 1; Page 95-97; 132pp; English.
XX      CC
XX      CC The present sequence represents a surface protein of Neisseria
XX      CC meningitidis which is approximately 62 kDa. The N. meningitidis
XX      CC surface glycoproteins, nucleic acids, the primers and optionally
XX      CC a thermostable polymerase, or antibodies are useful in a kit for
XX      CC the detection or diagnosis of N. meningitidis infection in humans.
XX      CC The N. meningitidis surface glycoproteins can also be used to
XX      CC prevent or treat N. meningitidis infection in humans, especially
XX      CC in the form of vaccines. The proteins and antibodies can also
XX      CC be used to identify immunoreactive peptides.
XX      SQ
XX      SQ Sequence 594 AA:

Query Match          95.7%; Score 2248.5; DB 20; Length 594;
Best Local Similarity 97.2%; Pred. No. 2.7e-135;
Matches 446; Conservative 1; Mismatches 11; Indels 1; Gaps 1;
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DB 256 TKTTVNVESKDKNGKTEVKGAKTSYIKKDKLVTGKDKGENGSTDEGEGLVTAKEV 315
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DB 436 GKNIDIATSMAPQFSSVSLGAGADAPTLSDVDGALNVGSKDNKPKVRIITNVA-PGYKEGD 495
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DB 496 VTNVAOLKGYAQNILNRRIDVNDGNARAGIAQAIAATAGLVAYLPGKSMALGGTTYRGEA 555
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RESULT 15

AAU06179 standard; Protein; 594 AA.

AAU06179;

24-OCT-2001 (first entry)

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XX XX N. meningitidis B2198 surface antigen Nhha polypeptide sequence.
DE XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.
KM XX
XX OS Neisseria meningitidis strain B2198.
FH XX
FH XX Key Location/Qualifiers
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FT XX 51..104
FT XX /note= "Conserved region 1"
FT XX /label= V1
FT XX /note= "Variable region 1"
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FT XX /label= C2
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FT XX 117..126
FT XX /label= V2
FT XX /note= "Variable region 2"
FT XX 127..190
FT XX /label= C3
FT XX /note= "Conserved region 3"
FT XX 191..212
FT XX /label= V3
FT XX /note= "Variable region 3"
FT XX 213..231
FT XX /label= C4
FT XX /note= "Conserved region 4"
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FT XX /label= V4
FT XX /note= "Variable region 4"
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PN W0200155182-A1.
PD 02-AUG-2001.
PE 25-JAN-2001; 2001W0-AU00069.
PR 25-JAN-2000; 2000US-0177917.
XX (UYQU) UNIV QUEENSLAND.
PA
XX Peak IRA, Jennings MP;
PI WPI: 2001-488774/53.
XX N-PSDB: AAS09169.
DR
XX New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
PS Claim 9; Fig 1; 91pp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain B2198 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
XX Sequence 594 AA:
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Query Match 95.7%; Score 2248.5; DB 22; Length 594;
Best Local Similarity 97.2%; Pred. No. 2.7e-135;
Matches 446; Conservative 1; Mismatches 11; Indels 1; Gaps 1;
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OY 423 GYAIGYSSISDGGNWIIGKTASGNSRGHFGASASYGYOW 461
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DB 556 GYAIGYSSISDGGNWIIGKTASGNSRGHFGASASYGYOW 594
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Job time : 41.5887 secs

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:14:45 : Search time 12.3281 Seconds
(without alignments)
1582.188 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2333	99.3	591	3	US-09-377-155-21 Sequence 21, Appl
3	2333	99.3	591	4	US-09-669-974-11 Sequence 11, Appl
4	2333	99.3	591	4	US-09-669-974-21 Sequence 21, Appl
5	2339	99.1	592	4	US-09-377-155-2 Sequence 2, Appl
6	2339	99.1	592	4	US-09-669-974-2 Sequence 2, Appl
7	2260.5	96.2	594	4	US-09-377-155-9 Sequence 9, Appl
8	2260.5	96.2	594	4	US-09-669-974-9 Sequence 9, Appl
9	2257.5	96.1	599	3	US-09-377-155-15 Sequence 15, Appl
10	2257.5	96.1	599	4	US-09-669-974-15 Sequence 15, Appl
11	2248.5	95.7	594	4	US-09-377-155-7 Sequence 7, Appl
12	2248.5	95.7	594	4	US-09-669-974-7 Sequence 7, Appl
13	2235.5	95.1	598	3	US-09-377-155-5 Sequence 5, Appl
14	2235.5	95.1	598	3	US-09-377-155-13 Sequence 13, Appl
15	2235.5	95.1	598	4	US-09-669-974-5 Sequence 5, Appl
16	2235.5	95.1	598	4	US-09-669-974-13 Sequence 13, Appl
17	2207.5	93.9	592	4	US-09-377-155-17 Sequence 17, Appl
18	2207.5	93.9	592	4	US-09-669-974-17 Sequence 17, Appl
19	2069.5	88.1	589	4	US-09-377-155-19 Sequence 19, Appl
20	2069.5	88.1	589	4	US-09-669-974-19 Sequence 19, Appl
21	901.5	38.4	2353	3	US-09-377-155-33 Sequence 33, Appl
22	901.5	38.4	2353	3	US-08-913-942-4 Sequence 4, Appl
23	901.5	38.4	2353	4	US-09-669-974-33 Sequence 33, Appl
24	901.5	38.4	2411	4	US-09-268-347-36 Sequence 36, Appl
25	895	38.1	2354	4	US-09-268-347-47 Sequence 47, Appl
26	889.5	37.9	1094	4	US-09-268-347-32 Sequence 32, Appl
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28	875.5	37.3	1912	3	US-08-685-467-4 Sequence 4, Appl
29	874	37.2	1098	1	US-08-409-995-2 Sequence 2, Appl
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31	874	37.2	1098	3	US-09-377-155-32 Sequence 32, Appl
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33	874	37.2	1098	4	US-09-669-974-32 Sequence 32, Appl
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41	652.5	27.8	679	4	US-08-685-467-15 Sequence 15, Appl
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43	564.5	24.0	1004	4	US-09-268-347-30 Sequence 30, Appl
44	560	23.8	1002	4	US-09-268-347-24 Sequence 24, Appl
45	525	22.3	1104	4	US-09-268-347-28 Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-377-155-11
; Sequence 11, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377, 155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; US-09-377-155-11

Query Match 99.3%; Score 2333; DB 3; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.5e-180;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	184	ITAVKAGRMRTTTTANGTGADRFETVTSNTYFASGKGTATVNSDDGNTVMD	243
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QY	244	VWVGDLANVNOGNSGMNDSKAVAGSSGKTVISGNVSPSKGMDDETIVNAGNIEITRN	303
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QY 424 YAIQSSISDGGNMIKGTASGNSRGHFGASASVGYOW 461
Db 554 YAIQSSISDGGNMIKGTASGNSRGHFGASASVGYOW 591

RESULT 2

US-09-377-155-21
; Sequence 21, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-21

Query Match 99.3%; Score 2333; DB 3; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.5e-180;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 194 GATTNVTNDVNTDDEKKRAASVKDVLNAGWNKGVKPGTTASDNVDFVRYTDVEEFLSAD 253
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RESULT 3

US-09-669-974-11
; Sequence 11, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-11

Query Match 99.3%; Score 2333; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.5e-180;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDLTSVGTGKLSFSANGKKNVITSDTKGLNFAKETAGTNGDTYVHLNGISGTLTDTLNT 63
Db 134 TDLTSVGTGKLSFSANGKKNVITSDTKGLNFAKETAGTNGDTYVHLNGISGTLTDTLNT 193
QY 64 GATTNVTNDVNTDDEKKRAASVKDVLNAGWNKGVKPGTTASDNVDFVRYTDVEEFLSAD 123
Db 194 GATTNVTNDVNTDDEKKRAASVKDVLNAGWNKGVKPGTTASDNVDFVRYTDVEEFLSAD 253
QY 124 TKTTTVNVESKDNKKTVEKIGARTSVYKEKDGKLVYTKDKGNGSSSTDEBEGVLTAKEV 183
Db 254 TKTTTVNVESKDNKKTVEKIGARTSVYKEKDGKLVYTKDKGNGSSSTDEBEGVLTAKEV 313
QY 184 IDAVNKAQWRKKTITTAQNGTQADKFEFVTSNTVFASGKTATVASKDOGNITWAYD 243
Db 314 IDAVNKAQWRKKTITTAQNGTQADKFEFVTSNTVFASGKTATVASKDOGNITWAYD 373
QY 244 VNVGDALNVNOLQNSGMNLDKKAAYAGSSGVYISGNVSPSKGMDETVNIAGNNIETRN 303
Db 374 VNVGDALNVNOLQNSGMNLDKKAAYAGSSGVYISGNVSPSKGMDETVNIAGNNIETRN 433
QY 304 GKNIDIATSMTPQSSVSLGAGADAPTLISVDGALNVGSKDKNRPVRTITNVAPEGVEGDV 363
Db 434 GKNIDIATSMTPQSSVSLGAGADAPTLISVDGALNVGSKDKNRPVRTITNVAPEGVEGDV 493
QY 364 TNVAOLKGAONLNRRIDNVGNARAGIAQAIATAGVQAVLPGKSMMAIGGTYRGAG 423
Db 494 TNVAOLKGAONLNRRIDNVGNARAGIAQAIATAGVQAVLPGKSMMAIGGTYRGAG 553
QY 424 YAIQSSISDGGNMIKGTASGNSRGHFGASASVGYOW 461
Db 554 YAIQSSISDGGNMIKGTASGNSRGHFGASASVGYOW 591

RESULT 4

US-09-669-974-21
; Sequence 21, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974

Query Match 99.3%; Score 2333; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.5e-180;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

;; CURRENT FILING DATE: 2000-09-26
;; PRIOR APPLICATION NUMBER: US 09/377,155
;; PRIOR FILING DATE: 1999-08-19
;; PRIOR APPLICATION NUMBER: PCT/AU98/01031
;; PRIOR FILING DATE: 1998-12-14
;; PRIOR APPLICATION NUMBER: GB 9726398.2
;; PRIOR FILING DATE: 1997-12-12
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: Patentl Ver. 2.0
;; SEQ ID NO 21
;; LENGTH: 591
;; TYPE: PRT
;; ORGANISM: Neisseria meningitidis
US-09-669-974-21

Query Match 99.3%; Score 2333; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 1,5e-180;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDLTSVTEKLSFSGANGKNVITSDTKGLNFAKETAAGTNGDTYVHLNGISGTLTDLTLLNT 63
Db TDLTSVTEKLSFSGANGKNVITSDTKGLNFAKETAAGTNGDTYVHLNGISGTLTDLTLLNT 193
QY 64 GATTNVTNDVNTDDEKRAASVKDVLNAGWNKVGKPGTTASDNVDFVRYDYVEFLSAD 123
Db GATTNVTNDVNTDDEKRAASVKDVLNAGWNKVGKPGTTASDNVDFVRYDYVEFLSAD 253
QY 124 TKTTTAVESKDNCKKTEVKIGATSVYIKEDGKLVYKDKGKNGSSSTDEBEGVLTAKEV 183
Db TKTTTAVESKDNCKKTEVKIGATSVYIKEDGKLVYKDKGKNGSSSTDEBEGVLTAKEV 313
QY 184 IDAVNKAQWRKKTATTANGQTGOADKFEVTSGTNTVFASGKGTATVSKDOGNITWYD 243
Db IDAVNKAQWRKKTATTANGQTGOADKFEVTSGTNTVFASGKGTATVSKDOGNITWYD 373
QY 314 IDAVNKAQWRKKTATTANGQTGOADKFEVTSGTNTVFASGKGTATVSKDOGNITWYD 373
Db IDAVNKAQWRKKTATTANGQTGOADKFEVTSGTNTVFASGKGTATVSKDOGNITWYD 373
QY 244 VNVGDALNVNOLQNSGWNLDKSKAVAGSSGKVIISGNVSPSKGKMDETVINAGNIEITRN 303
Db VNVGDALNVNOLQNSGWNLDKSKAVAGSSGKVIISGNVSPSKGKMDETVINAGNIEITRN 433
QY 304 GKNDIDATSMTPPOSSVSLGAGADAPTLISVDGDLNNGSKKDNKPVRTTNAAPGVKEDV 363
Db GKNDIDATSMTPPOSSVSLGAGADAPTLISVDGDLNNGSKKDNKPVRTTNAAPGVKEDV 493
QY 364 TNVAQLKGVAQNLRIDNVGNARAGIAQAIAATAGLVQAVLPKSMMAIGGTYRGEAG 423
Db TNVAQLKGVAQNLRIDNVGNARAGIAQAIAATAGLVQAVLPKSMMAIGGTYRGEAG 553
QY 494 TNVAQLKGVAQNLRIDNVGNARAGIAQAIAATAGLVQAVLPKSMMAIGGTYRGEAG 553
Db 424 YAIYSSISDGNMIIRKGTASGNSRGHFGASASVGYOW 461
Db 554 YAIYSSISDGNMIIRKGTASGNSRGHFGASASVGYOW 591

RESULT 5

US-09-377-155-2
;; Sequence 2, Application US/09377155
;; Patent No. 6197312
;; GENERAL INFORMATION:
;; APPLICANT: PEAK, Ian Richard Anselm
;; APPLICANT: JENNINGS, Michael Paul
;; APPLICANT: MOXON, E. Richard
;; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
;; FILE REFERENCE: 065064/0128
;; CURRENT APPLICATION NUMBER: US/09/377,155
;; CURRENT FILING DATE: 1999-08-19
;; PRIOR APPLICATION NUMBER: PCT/AU98/01031
;; PRIOR FILING DATE: 1998-12-14
;; PRIOR APPLICATION NUMBER: GB 9726398.2
;; PRIOR FILING DATE: 1997-12-12
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: Patentl Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 592
;; TYPE: PRT

;; ORGANISM: Neisseria meningitidis
US-09-377-155-2

Query Match 99.1%; Score 2329; DB 3; Length 592;
Best Local Similarity 99.8%; Pred. No. 3,1e-180;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TDLTSVTEKLSFSGANGKNVITSDTKGLNFAKETAAGTNGDTYVHLNGISGTLTDLTLLNT 63
Db TDLTSVTEKLSFSGANGKNVITSDTKGLNFAKETAAGTNGDTYVHLNGISGTLTDLTLLNT 194
QY 135 TDLTSVTEKLSFSGANGKNVITSDTKGLNFAKETAAGTNGDTYVHLNGISGTLTDLTLLNT 194
Db TDLTSVTEKLSFSGANGKNVITSDTKGLNFAKETAAGTNGDTYVHLNGISGTLTDLTLLNT 194
QY 64 GATTNVTNDVNTDDEKRAASVKDVLNAGWNKVGKPGTTASDNVDFVRYDYVEFLSAD 123
Db GATTNVTNDVNTDDEKRAASVKDVLNAGWNKVGKPGTTASDNVDFVRYDYVEFLSAD 254
QY 195 GATTNVTNDVNTDDEKRAASVKDVLNAGWNKVGKPGTTASDNVDFVRYDYVEFLSAD 254
Db GATTNVTNDVNTDDEKRAASVKDVLNAGWNKVGKPGTTASDNVDFVRYDYVEFLSAD 254
QY 124 TKTTTAVESKDNCKKTEVKIGATSVYIKEDGKLVYKDKGKNGSSSTDEBEGVLTAKEV 183
Db TKTTTAVESKDNCKKTEVKIGATSVYIKEDGKLVYKDKGKNGSSSTDEBEGVLTAKEV 314
QY 255 TKTTTAVESKDNCKKTEVKIGATSVYIKEDGKLVYKDKGKNGSSSTDEBEGVLTAKEV 314
Db TKTTTAVESKDNCKKTEVKIGATSVYIKEDGKLVYKDKGKNGSSSTDEBEGVLTAKEV 314
QY 184 IDAVNKAQWRKKTATTANGQTGOADKFEVTSGTNTVFASGKGTATVSKDOGNITWYD 243
Db IDAVNKAQWRKKTATTANGQTGOADKFEVTSGTNTVFASGKGTATVSKDOGNITWYD 374
QY 315 IDAVNKAQWRKKTATTANGQTGOADKFEVTSGTNTVFASGKGTATVSKDOGNITWYD 374
Db IDAVNKAQWRKKTATTANGQTGOADKFEVTSGTNTVFASGKGTATVSKDOGNITWYD 374
QY 244 VNVGDALNVNOLQNSGWNLDKSKAVAGSSGKVIISGNVSPSKGKMDETVINAGNIEITRN 303
Db VNVGDALNVNOLQNSGWNLDKSKAVAGSSGKVIISGNVSPSKGKMDETVINAGNIEITRN 434
QY 375 VNVGDALNVNOLQNSGWNLDKSKAVAGSSGKVIISGNVSPSKGKMDETVINAGNIEITRN 434
Db VNVGDALNVNOLQNSGWNLDKSKAVAGSSGKVIISGNVSPSKGKMDETVINAGNIEITRN 434
QY 304 GKNDIDATSMTPPOSSVSLGAGADAPTLISVDGDLNNGSKKDNKPVRTTNAAPGVKEDV 363
Db GKNDIDATSMTPPOSSVSLGAGADAPTLISVDGDLNNGSKKDNKPVRTTNAAPGVKEDV 494
QY 435 GKNDIDATSMTPPOSSVSLGAGADAPTLISVDGDLNNGSKKDNKPVRTTNAAPGVKEDV 494
Db GKNDIDATSMTPPOSSVSLGAGADAPTLISVDGDLNNGSKKDNKPVRTTNAAPGVKEDV 494
QY 364 TNVAQLKGVAQNLRIDNVGNARAGIAQAIAATAGLVQAVLPKSMMAIGGTYRGEAG 423
Db TNVAQLKGVAQNLRIDNVGNARAGIAQAIAATAGLVQAVLPKSMMAIGGTYRGEAG 554
QY 495 TNVAQLKGVAQNLRIDNVGNARAGIAQAIAATAGLVQAVLPKSMMAIGGTYRGEAG 554
Db 424 YAIYSSISDGNMIIRKGTASGNSRGHFGASASVGYOW 461
Db 555 YAIYSSISDGNMIIRKGTASGNSRGHFGASASVGYOW 592

RESULT 6

US-09-669-974-2
;; Sequence 2, Application US/09669974
;; Patent No. 6333173
;; GENERAL INFORMATION:
;; APPLICANT: PEAK, Ian Richard Anselm
;; APPLICANT: JENNINGS, Michael Paul
;; APPLICANT: MOXON, E. Richard
;; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
;; FILE REFERENCE: 065064/0128
;; CURRENT APPLICATION NUMBER: US/09/669,974
;; CURRENT FILING DATE: 2000-09-26
;; PRIOR APPLICATION NUMBER: US 09/377,155
;; PRIOR FILING DATE: 1999-08-19
;; PRIOR APPLICATION NUMBER: PCT/AU98/01031
;; PRIOR FILING DATE: 1998-12-14
;; PRIOR APPLICATION NUMBER: GB 9726398.2
;; PRIOR FILING DATE: 1997-12-12
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: Patentl Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 592
;; TYPE: PRT
;; ORGANISM: Neisseria meningitidis
US-09-669-974-2

Query Match 99.1%; Score 2329; DB 4; Length 592;
Best Local Similarity 99.8%; Pred. No. 3,1e-180;
Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TDLTSVTEKLSFSGANGKNVITSDTKGLNFAKETAAGTNGDTYVHLNGISGTLTDLTLLNT 63
Db TDLTSVTEKLSFSGANGKNVITSDTKGLNFAKETAAGTNGDTYVHLNGISGTLTDLTLLNT 194

Db 496 VTNAOLKGVANLNNDVNDGNARAGIAQAIATAGLVQAYLPKGSMAAIGGTYRGEA 555
Qy 423 GYALGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 461
Db 556 GYALGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 594

RESULT 9

US-09-377-155-15
; Sequence 15, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRF
; ORGANISM: Neisseria meningitidis
US-09-377-155-15

Query Match 96.1%; Score 2257.5; DB 3; Length 599;
Best Local Similarity 97.4%; Pred. No. 1.9e-174;

Matches 447; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

Qy 4 TDLTSVGTETKLSFGANGKVNITSDTKGLNFAKETAGTNGDTTVHLNGISGLTLDTLTNT 63
Db 141 TDLTSVETETKLSFGANGKVNITSDTKGLNFAKETAGTNGDTTVHLNGISGLTLDTLTNT 200
Qy 64 GATTNVTNDNVTDEDEKRAASVKDVLNAGNMIKGVKPGTASDNDVFRYDVEFLSAD 123
Db 201 GATTNVTNDNVTDDKKRAASVKDVLNAGNMIKGVKPGTASDNDVFRYDVEFLSAD 260
Qy 124 TKTTTVNESKDNCKRTEVKIGAKTSVIEKEDGLVYTGKDGKENGSSSTDEEGELVTAKEV 183
Db 261 TKTTTVNESKDNCKRTEVKIGAKTSVIEKEDGLVYTGKDGKENGSSSTDEEGELVTAKEV 320
Qy 184 IDAVNKAQWRKKTITANGOTQADKFEVTVSGTNVTFASGKTATVASKDOGNITVYWD 243
Db 321 IDAVNKAQWRKKTITANGOTQADKFEVTVSGTNVTFASGKTATVASKDOGNITVYWD 380
Qy 244 VNVDALNVNOLNSGMNLDKAVAGSSGKVIISGNVSPSKKMDETVINAGNNIETRN 303
Db 381 VNVDALNVNOLNSGMNLDKAVAGSSGKVIISGNVSPSKKMDETVINAGNNIETRN 440
Qy 304 GKNIDIAVTSMTPOFSSVSLGAGADAPTLISVDG-DALNVGSKDKNKPVRITVAVPGVKEGD 362
Db 441 GKNIDIAVTSMTPOFSSVSLGAGADAPTLISVDG-DALNVGSKDKNKPVRITVAVPGVKEGD 500
Qy 363 VTNAOLKGVANLNNDVNDGNARAGIAQAIATAGLVQAYLPKGSMAAIGGTYRGEA 422
Db 501 VTNAOLKGVANLNNDVNDGNARAGIAQAIATAGLVQAYLPKGSMAAIGGTYRGEA 560
Qy 423 GYALGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 461
Db 561 GYALGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 599

RESULT 10
US-09-669-974-15
; Sequence 15, Application US/09669974
; Patent No. 6333173

; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRF
; ORGANISM: Neisseria meningitidis
US-09-669-974-15

Query Match 96.1%; Score 2257.5; DB 4; Length 599;
Best Local Similarity 97.4%; Pred. No. 1.9e-174;
Matches 447; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

Qy 4 TDLTSVGTETKLSFGANGKVNITSDTKGLNFAKETAGTNGDTTVHLNGISGLTLDTLTNT 63
Db 141 TDLTSVETETKLSFGANGKVNITSDTKGLNFAKETAGTNGDTTVHLNGISGLTLDTLTNT 200
Qy 64 GATTNVTNDNVTDEDEKRAASVKDVLNAGNMIKGVKPGTASDNDVFRYDVEFLSAD 123
Db 201 GATTNVTNDNVTDDKKRAASVKDVLNAGNMIKGVKPGTASDNDVFRYDVEFLSAD 260
Qy 124 TKTTTVNESKDNCKRTEVKIGAKTSVIEKEDGLVYTGKDGKENGSSSTDEEGELVTAKEV 183
Db 261 TKTTTVNESKDNCKRTEVKIGAKTSVIEKEDGLVYTGKDGKENGSSSTDEEGELVTAKEV 320
Qy 184 IDAVNKAQWRKKTITANGOTQADKFEVTVSGTNVTFASGKTATVASKDOGNITVYWD 243
Db 321 IDAVNKAQWRKKTITANGOTQADKFEVTVSGTNVTFASGKTATVASKDOGNITVYWD 380
Qy 244 VNVDALNVNOLNSGMNLDKAVAGSSGKVIISGNVSPSKKMDETVINAGNNIETRN 303
Db 381 VNVDALNVNOLNSGMNLDKAVAGSSGKVIISGNVSPSKKMDETVINAGNNIETRN 440
Qy 304 GKNIDIAVTSMTPOFSSVSLGAGADAPTLISVDG-DALNVGSKDKNKPVRITVAVPGVKEGD 362
Db 441 GKNIDIAVTSMTPOFSSVSLGAGADAPTLISVDG-DALNVGSKDKNKPVRITVAVPGVKEGD 500
Qy 363 VTNAOLKGVANLNNDVNDGNARAGIAQAIATAGLVQAYLPKGSMAAIGGTYRGEA 422
Db 501 VTNAOLKGVANLNNDVNDGNARAGIAQAIATAGLVQAYLPKGSMAAIGGTYRGEA 560
Qy 423 GYALGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 461
Db 561 GYALGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 599

RESULT 11
US-09-377-155-7
; Sequence 7, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14

: PRIOR APPLICATION NUMBER: GB 9726398.2
 : PRIOR FILING DATE: 1997-12-12
 : NUMBER OF SEQ ID NOS: 33
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 7
 : LENGTH: 594
 : TYPE: PR1
 : ORGANISM: Neisseria meningitidis
 : US-09-377-155-7

Query Match	95.7%	Score 2248.5	DB 3	Length 594
Best Local Similarity	97.2%	Pred. No. 1e-173		
Matches 446; Conservative	1;	Mismatches 11;	Indels 1;	Gaps 1.

QY	4	TDLTSTGTEKLEFSFSAANGKVNITTSPTKCLINFAKEIAGINBGDTYHNLNGISITLDTPLNT	63
Dp	136	TDLTSTVEIEKLEFSFSAANGKVNITTSPTKCLINFAKEIAGINBGDTYHNLNGISITLDTPLNT	195
QY	64	GATTNTVNDNTVDDEKKRAAAYKVDLNAAGNMIKGVPGTTASDNDVFRTDYVEFLSAD	123
Dp	196	GATTNTVNDNTVDDEKKRAAAYKVDLNAAGNMIKGVPGTTASDNDVFRTDYVEFLSAD	255
QY	124	TKTTTYNVSCKNGKKTVEYIGAKTSYIKERDGLKYNKDKGEMSSSTDEEGEGLTAKEV	183
Dp	256	TKTTTYNVSCKNGKKTVEYIGAKTSYIKERDGLKYNKDKGEMSSSTDEEGEGLTAKEV	315
QY	184	IDAVNKAGRMKTTTANGQTGQDAFEFTVTSGTNVTFAASKGTATYASKDOGNITVMD	243
Dp	316	IDAVNKAGRMKTTTANGQTGQDAFEFTVTSGTNVTFAASKGTATYASKDOGNITVMD	375
QY	244	VNVGDLANNOLONSGWNDSKAAYVGSSGKATYSGNVSPSKSKMDETYNINAGNIEITRN	303
Dp	376	VNVGDLANNOLONSGWNDSKAAYVGSSGKATYSGNVSPSKSKMDETYNINAGNIEITRN	435
QY	304	GKNIDATSMTPQFSSVSLGACADAPTLTYSVGD-ALNTGSKDKDKPRITNVAPGVKED	362
Dp	436	GKNIDATSMTPQFSSVSLGACADAPTLTYSVGDALNTGSKDKDKPRITNVAPGVKED	495
QY	363	VTVNAOLKVAONLNNRIDNVDGNARAGIAQAIATAGIYQAYLTPGKSMAIGGGTYGCEA	422
Dp	496	VTVNAOLKVAONLNNRIDNVDGNARAGIAQAIATAGIYQAYLTPGKSMAIGGGTYGCEA	555
QY	423	GVAIGYSSISDGGNWTIKGTASGNSRGHFAGASASVGYQW	461
Dp	556	GVAIGYSSISDGGNWTIKGTASGNSRGHFAGASASVGYQW	594

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RESULT 12
US-09-669-974-7
Sequence 7, Application US/09669974
Patent No. 633173
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
PRIORITY FILING DATE: 2000-09-26
PRIORITY APPLICATION NUMBER: US 09/377,155
PRIORITY FILING DATE: 1999-08-19
PRIORITY APPLICATION NUMBER: PCT/AU98/01031
PRIORITY FILING DATE: 1998-12-14
PRIORITY APPLICATION NUMBER: GB 9726398.2
PRIORITY FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 594
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-669-974-7

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Query Match	95.7%;	Score 2248.5;	DB 4;	Length 594;
Best Local Similarity	97.2%;	Pred. No. 1e-173;		
Matches 446;	Conservative	1;	Mismatches 11;	Indels 1;
			Gaps	1;

QY	4	TDLTSVGTSEKLSFSPAGNKVNITTSPTKGINFAKPEAGTGGDTTHLNGISSTLDTLT	63
Db	136	TDLTSVETSEKLSFSGANKNVITTSPTKGINFAKPEAGTGGDTTHLNGISSTLDTLT	195
QY	64	GATTNTVNDNVITDDEKKRAASVYKDYLVNAGMNIKGVPPTNASDNDVFRDYVEFLSAD	123
Db	196	GATTNTVNDNVITDDEKKRAASVYKDYLVNAGMNIKGVPPTNASDNDVFRDYVEFLSAD	255
QY	124	TKTTTVNVESSKONGKKTVEYIGAKTSVYIKENDGKLVYKXDKDGENSSSTDGEGJYNAKEY	183
Db	256	TKTTTVNVESSKONGKKTVEYIGAKTSVYIKENDGKLVYKXDKDGENSSSTDGEGJYNAKEY	315
QY	184	IDAVNRKAGRMKTTTANGOTGQADFFETVTSQTNVTFASCKGTATVYSKXDOGNITVMD	243
Db	316	IDAVNRKAGRMKTTTANGOTGQADFFETVTSQTNVTFASCKGTATVYSKXDOGNITVMD	375
QY	244	VNVGDLANTNOLNONGMINDSKAVAGSSGKVIISGVNPSKSKMDETVNNINAGNIEITRN	303
Db	376	VNVGDLANTNOLNONGMINDSKAVAGSSGKVIISGVNPSKSKMDETVNNINAGNIEITRN	435
QY	304	GKIIDATSMTPQFSSVSLGAGADAPTLTSLVDDEGALNVGSQDKTKPRLITINAVPYKEGD	362
Db	436	GKIIDATSMAPFSSVSLGAGADAPTLTSLVDDEGALNVGSQDKTKPRLITINAVPYKEGD	495
QY	363	VTVNAOLKVAONLNNRIDNVGNA RAGIAQAIATAGLVQAYLVPKSGMMAIGGGTVRGEA	422
Db	496	VTVNAOLKVAONLNNRIDNVGNA RAGIAQAIATAGLVQAYLVPKSGMMAIGGGTVRGEA	555
QY	423	GVAIGYSSISDGGNMWIKGTASGNRGHFPGASASVGYOM	461
Db	556	GVAIGYSSISDGGNMWIKGTASGNRGHFPGASASVGYOM	594

RESULT 13
 US-09-377-155-5
 Sequence 5, Application US/093771155
 Patent No. 6197312
 GENERAL INFORMATION:
 APPLICANT: PEAK, Ian Richard Anselm
 APPLICANT: JENNINGS, Michael Paul
 APPLICANT: MONON, E. Richard
 TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
 FILE REFERENCE: 065064/0128
 CURRENT APPLICATION NUMBER: US/09/377,155
 CURRENT FILING DATE: 1999-08-19
 PRIOR APPLICATION NUMBER: PCT/AU99/01031
 PRIOR FILING DATE: 1998-12-14
 PRIOR APPLICATION NUMBER: GB 9726398.2
 PRIOR FILING DATE: 1997-12-12
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 5
 LENGTH: 598
 TYPE: PRN
 ORGANISM: Neisseria meningitidis
 US-09-377-155-5

	Query Match	Score	DB	Length
Best Local Similarity	95.1%	2235.5	3	598
Matches	442	Pred. No. 1.2e+172		
	Conservative	3	Mismatches 13	Indels 1
QY	4	TDLTSVGEKTSFSFANGKMYNITSPTKLNPAKETAAGNCDPTVLNIGSTLTPTLNT	63	
	140	TDLTSVETEKTSFGNGKMYNITSPTKLNPAKETAGNGDPTVLNIGSTLTPTLNT	199	
Db				
QY	64	GATTNVTINDVNTDDEKKRAASVKDVLNAGWNIKGKPGCTASDNDVRYTYDFEFLSD	123	
Db	200	GATTNVTINDVNTDDEKKRAASVKDVLNAGWNIKGKPGCTASDNDVRYTYDFEFLSD	259	

Db 560 GYAIGYSSISDTCNNVIKGTASGNSRGHFGTSASVGYOM 598

Search completed: October 6, 2003, 09:35:56
Job time : 13.3281 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:31:05 ; Search time 23.0934 Seconds
(Without alignments)
3158.312 Million cell updates/sec

Title: US-09-771-382-35
Perfect score: 2350
Sequence: 1 NNETDLTSVGTETKSFSGANG.....TASGNSRGHGASASVGYOW 461

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PC7_NEW_PUB.pep:*
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9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2350	100.0	461	US-09-771-382-35	Sequence 35, App1
2	2350	100.0	512	US-09-771-382-23	Sequence 23, App1
3	2333	99.3	591	US-09-797-862-11	Sequence 11, App1
4	2333	99.3	591	US-09-797-862-21	Sequence 21, App1
5	2333	99.3	591	US-09-771-382-1	Sequence 1, App1
6	2333	99.3	591	US-09-771-382-5	Sequence 5, App1
7	2329	99.1	592	US-09-797-862-2	Sequence 2, App1
8	2328	99.1	540	US-09-771-382-33	Sequence 33, App1
9	2260.5	96.2	594	US-09-797-862-9	Sequence 9, App1
10	2260.5	96.2	594	US-09-771-382-4	Sequence 4, App1
11	2257.5	96.1	599	US-09-797-862-15	Sequence 15, App1
12	2257.5	96.1	599	US-09-771-382-6	Sequence 6, App1
13	2248.5	95.7	594	US-09-797-862-7	Sequence 7, App1
14	2248.5	95.7	594	US-09-771-382-9	Sequence 9, App1
15	2235.5	95.1	598	US-09-797-862-5	Sequence 5, App1

16	2235.5	95.1	598	10	US-09-797-862-13	Sequence 13, App1
17	2235.5	95.1	598	10	US-09-771-382-7	Sequence 7, App1
18	2235.5	95.1	598	10	US-09-771-382-8	Sequence 8, App1
19	2213.5	94.2	462	10	US-09-771-382-36	Sequence 36, App1
20	2213.5	94.2	513	10	US-09-771-382-24	Sequence 24, App1
21	2207.5	93.9	541	10	US-09-771-382-34	Sequence 34, App1
22	2207.5	93.9	592	10	US-09-797-862-17	Sequence 17, App1
23	2207.5	93.9	592	10	US-09-771-382-2	Sequence 2, App1
24	2148.5	91.4	502	10	US-09-771-382-27	Sequence 27, App1
25	2089.5	88.9	592	10	US-09-771-382-10	Sequence 10, App1
26	2069.5	88.1	589	10	US-09-797-862-19	Sequence 19, App1
27	2069.5	88.1	589	10	US-09-771-382-3	Sequence 3, App1
28	1946.5	82.8	604	10	US-09-771-382-11	Sequence 11, App1
29	1941	82.6	433	10	US-09-771-382-26	Sequence 26, App1
30	1941	82.6	433	10	US-09-771-382-38	Sequence 38, App1
31	1822	77.5	407	10	US-09-771-382-25	Sequence 25, App1
32	1808	76.9	356	10	US-09-771-382-37	Sequence 37, App1
33	901.5	38.4	2353	10	US-09-797-862-33	Sequence 33, App1
34	874	37.2	1098	10	US-09-797-862-32	Sequence 32, App1
35	864.5	36.8	201	10	US-09-771-382-39	Sequence 39, App1
36	358	15.2	2122	10	US-09-813-214A-9	Sequence 9, App1
37	356	15.1	1833	12	US-10-175-275-4	Sequence 4, App1
38	356	15.1	1833	12	US-10-175-282-4	Sequence 4, App1
39	356	15.1	1992	12	US-10-175-275-3	Sequence 3, App1
40	356	15.1	1992	12	US-10-175-282-3	Sequence 3, App1
41	350.5	14.9	1778	12	US-10-238-075-749	Sequence 749, App
42	298	12.7	2039	15	US-10-192-584-7	Sequence 7, App1
43	262.5	11.2	2042	15	US-10-192-584-6	Sequence 6, App1
44	217.5	9.3	1180	12	US-10-193-764-61	Sequence 61, App1
45	217.5	9.3	1188	12	US-10-193-764-59	Sequence 59, App1

ALIGNMENTS

RESULT 1									
US-09-771-382-35									
: Sequence 35, Application US/09771382									
: Patent No. US20020160016A1									
: GENERAL INFORMATION:									
: APPLICANT: Peak, Ian									
: TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN									
: FILE REFERENCE: 8795-2401									
: CURRENT APPLICATION NUMBER: US/09/771,382									
: PRIOR FILING DATE: 2001-01-25									
: PRIOR APPLICATION NUMBER: US 60/177,917									
: NUMBER OF SEQ ID NOS: 52									
: SOFTWARE: PatentIn version 3.0									
: SEQ ID NO 35									
: LENGTH: 461									
: TYPE: PRT									
: ORGANISM: Neisseria meningitidis									
US-09-771-382-35									
Query Match									
Best Local Similarity 100.0%; Score 2350; DB 10; Length 461;									
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	NNETDLTSVGTETKSFSGANGKNVITSDTGLNFAKKTAGTNGDTVHLNIGSTLDTL	60						
Db	1	NNETDLTSVGTETKSFSGANGKNVITSDTGLNFAKKTAGTNGDTVHLNIGSTLDTL	60						
Qy	61	LNTGATNTVNDVNTDDEKRRASVKKVLAAGNKKVKGTTASDVNDVRYRYDVEFL	120						
Db	61	LNTGATNTVNDVNTDDEKRRASVKKVLAAGNKKVKGTTASDVNDVRYRYDVEFL	120						
Qy	121	SADPKTTTVNESDKNKKTEVKTGATSVYKKEGDLVNGKKGSGSSDDEEGLYTA	180						
Db	121	SADPKTTTVNESDKNKKTEVKTGATSVYKKEGDLVNGKKGSGSSDDEEGLYTA	180						
Qy	181	KEVIDAVNKGWRKKTTTANGOTGOADKFETVTSGTNVTASGKGTATVSKDDOGNTV	240						

Db 181 KEVIDAVNKAGRMKTTTANGOTGADKEETVSGTNVTFASGKGTATVSKDDGNTIV 240
OY 241 MYDVNVGDLANVNOLONSGWNLSKAVAGSSGKVISGNVSPSKGMDDEVNINAGNIEI 300
Db 241 MYDVNVGDLANVNOLONSGWNLSKAVAGSSGKVISGNVSPSKGMDDEVNINAGNIEI 300
OY 301 TRNGKNIDIATSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKDKNKPVRIITNVAPEKE 360
Db 301 TRNGKNIDIATSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKDKNKPVRIITNVAPEKE 360
OY 361 GGVTVNAOLKGYAONLNRRIDVNDGNARAGIAOAIATAGLVQAYILPGKSMAIIGGCTYRG 420
Db 361 GGVTVNAOLKGYAONLNRRIDVNDGNARAGIAOAIATAGLVQAYILPGKSMAIIGGCTYRG 420
OY 421 EAGYVAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYOW 461
Db 421 EAGYVAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYOW 461

RESULT 2
US-09-771-382-23
; Sequence 23, Application US/09771382
; Patent No. US20020160016A1
; GENERAL INFORMATION:
; APPLICANT: Peak, Ian
; APPLICANT: Jennings, Michael
; TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
; FILE REFERENCE: 8795-24U1
; CURRENT APPLICATION NUMBER: US/09/771,382
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/177,917
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 512
; TYPE: PRF
; ORGANISM: Neisseria meningitidis
US-09-771-382-23

Query Match 100.0%; Score 2350; DB 10; Length 512;
Best Local Similarity 100.0%; Pred. No. 4.2e-175;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NNETDLTSVTEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVHLNGISTLTDTL 60
Db 52 NNETDLTSVTEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVHLNGISTLTDTL 111
OY 61 LNTGATTNTVNDVTDDEKKRAASVYKVDVLAAGMNIKGVPGTASDNDVDFVRTYDVEFL 120
Db 112 LNTGATTNTVNDVTDDEKKRAASVYKVDVLAAGMNIKGVPGTASDNDVDFVRTYDVEFL 171
OY 121 SADTFTTYNVSKNGKTEVKIGAKTSVIEKDGKLVTKDGKNGSSTDEGGLVTA 180
Db 172 SADTFTTYNVSKNGKTEVKIGAKTSVIEKDGKLVTKDGKNGSSTDEGGLVTA 231
OY 181 KEVIDAVNKAGRMKTTTANGOTGADKEETVSGTNVTFASGKGTATVSKDDGNTIV 240
Db 232 KEVIDAVNKAGRMKTTTANGOTGADKEETVSGTNVTFASGKGTATVSKDDGNTIV 291
OY 241 MYDVNVGDLANVNOLONSGWNLSKAVAGSSGKVISGNVSPSKGMDDEVNINAGNIEI 300
Db 292 MYDVNVGDLANVNOLONSGWNLSKAVAGSSGKVISGNVSPSKGMDDEVNINAGNIEI 351
OY 301 TRNGKNIDIATSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKDKNKPVRIITNVAPEKE 360
Db 352 TRNGKNIDIATSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKDKNKPVRIITNVAPEKE 411
OY 361 GGVTVNAOLKGYAONLNRRIDVNDGNARAGIAOAIATAGLVQAYILPGKSMAIIGGCTYRG 420
Db 412 GGVTVNAOLKGYAONLNRRIDVNDGNARAGIAOAIATAGLVQAYILPGKSMAIIGGCTYRG 471

OY 421 EAGYVAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYOW 461
Db 472 EAGYVAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYOW 512

RESULT 3
US-09-797-862-11
; Sequence 11, Application US/09797862
; Patent No. US20020102276A1
; GENERAL INFORMATION:
; APPLICANT: PEAK, IAN RICHARD ANSELM
; APPLICANT: MOXON, E. RICHARD
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0134
; CURRENT APPLICATION NUMBER: US/09/797,862
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRF
; ORGANISM: Neisseria meningitidis
US-09-797-862-11

Query Match 99.3%; Score 2333; DB 10; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.1e-173;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 TDLSVTEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVHLNGISTLTDTL 63
Db 134 TDLSVTEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVHLNGISTLTDTL 193
OY 64 GATTNTVNDVTDDEKKRAASVYKVDVLAAGMNIKGVPGTASDNDVDFVRTYDVEFLSAD 123
Db 194 GATTNTVNDVTDDEKKRAASVYKVDVLAAGMNIKGVPGTASDNDVDFVRTYDVEFLSAD 253
OY 124 TKTFTTYNVSKNGKTEVKIGAKTSVIEKDGKLVTKDGKNGSSTDEGGLVTAKEY 183
Db 254 TKTFTTYNVSKNGKTEVKIGAKTSVIEKDGKLVTKDGKNGSSTDEGGLVTAKEY 313
OY 184 IDAVNKAGRMKTTTANGOTGADKEETVSGTNVTFASGKGTATVSKDDGNTIVMD 243
Db 314 IDAVNKAGRMKTTTANGOTGADKEETVSGTNVTFASGKGTATVSKDDGNTIVMD 373
OY 244 VNVGDLANVNOLONSGWNLSKAVAGSSGKVISGNVSPSKGMDDEVNINAGNIEITRN 303
Db 374 VNVGDLANVNOLONSGWNLSKAVAGSSGKVISGNVSPSKGMDDEVNINAGNIEITRN 433
OY 304 GKNIDIATSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKDKNKPVRIITNVAPEKEGV 363
Db 434 GKNIDIATSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKDKNKPVRIITNVAPEKEGV 493
OY 364 TNAVQOLKGYAONLNRRIDVNDGNARAGIAOAIATAGLVQAYILPGKSMAIIGGCTYRG 423
Db 494 TNAVQOLKGYAONLNRRIDVNDGNARAGIAOAIATAGLVQAYILPGKSMAIIGGCTYRG 553
OY 424 VAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYOW 461
Db 554 VAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYOW 591

RESULT 4
US-09-797-862-21
; Sequence 21, Application US/09797862
; Patent No. US20020102276A1
; GENERAL INFORMATION:
; APPLICANT: PEAK, IAN RICHARD ANSELM
; APPLICANT: JENNINGS, MICHAEL PAUL

APPLICANT: MOXON, E. RICHARD
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0134
CURRENT APPLICATION NUMBER: US/09/797,862
CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: PCT/A098/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 591
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-797-862-21

Query Match 99.3%; Score 2333; DB 10; Length 591;
Best Local Similarity 100.0%; Pred. No. 1,1e-173;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDLTSGTEKLSFSGANGKNVITSDTKGLNFAKTAGTNGDTYVHLNGISLTLDTLNT 63
DB 134 TDLTSGTEKLSFSGANGKNVITSDTKGLNFAKTAGTNGDTYVHLNGISLTLDTLNT 193
QY 64 GATTNVNDVNTDEDEKRAASVSKDVLNAGNNIKGVKGTASDVDFVRYTDVEFLSAD 123
DB 194 GATTNVNDVNTDEDEKRAASVSKDVLNAGNNIKGVKGTASDVDFVRYTDVEFLSAD 253
QY 124 TKTITTVVESKDNCKTEVKIGAKTSYIKERDGLVTKDGKGENGSTDEGEGLVTAKEV 183
DB 254 TKTITTVVESKDNCKTEVKIGAKTSYIKERDGLVTKDGKGENGSTDEGEGLVTAKEV 313
QY 184 IDAVNKGWRKMTTANGQTQADKFEFTVTSCTVTFASGKTATVSKDQGNITWYD 243
DB 314 IDAVNKGWRKMTTANGQTQADKFEFTVTSCTVTFASGKTATVSKDQGNITWYD 373
QY 244 VNVGDALNVNOLQNSGNLDSKAVAGSSGKVISGNVSPSKGKMDFTVINAGNIEITRN 303
DB 374 VNVGDALNVNOLQNSGNLDSKAVAGSSGKVISGNVSPSKGKMDFTVINAGNIEITRN 433
QY 304 GKNDIATSMTPPOFSSVSLGAGADAPTLVSDGDLANVSKKDNKPVRTTNVAPGVKEGDV 363
DB 434 GKNDIATSMTPPOFSSVSLGAGADAPTLVSDGDLANVSKKDNKPVRTTNVAPGVKEGDV 493
QY 364 TTNVAQLKGVAQNLRNDNDGNARAGIAQAIATAGLVQAVLPKSMMAIGGTYRGEAG 423
DB 494 TTNVAQLKGVAQNLRNDNDGNARAGIAQAIATAGLVQAVLPKSMMAIGGTYRGEAG 553
QY 424 YALGYSSISDGNMIIGKTASGNSRGHFGASASVGYOM 461
DB 554 YALGYSSISDGNMIIGKTASGNSRGHFGASASVGYOM 591

RESULT 5
US-09-771-382-1
Sequence 1, Application US/09771382
Patent No. US20020160016A1

GENERAL INFORMATION:

APPLICANT: Jennings, Michael
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-2401
CURRENT APPLICATION NUMBER: US/09/771,382
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 591
TYPE: PRT
ORGANISM: Neisseria meningitidis

US-09-771-382-1

Query Match 99.3%; Score 2333; DB 10; Length 591;
Best Local Similarity 100.0%; Pred. No. 1,1e-173;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDLTSGTEKLSFSGANGKNVITSDTKGLNFAKTAGTNGDTYVHLNGISLTLDTLNT 63
DB 134 TDLTSGTEKLSFSGANGKNVITSDTKGLNFAKTAGTNGDTYVHLNGISLTLDTLNT 193
QY 64 GATTNVNDVNTDEDEKRAASVSKDVLNAGNNIKGVKGTASDVDFVRYTDVEFLSAD 123
DB 194 GATTNVNDVNTDEDEKRAASVSKDVLNAGNNIKGVKGTASDVDFVRYTDVEFLSAD 253
QY 124 TKTITTVVESKDNCKTEVKIGAKTSYIKERDGLVTKDGKGENGSTDEGEGLVTAKEV 183
DB 254 TKTITTVVESKDNCKTEVKIGAKTSYIKERDGLVTKDGKGENGSTDEGEGLVTAKEV 313
QY 184 IDAVNKGWRKMTTANGQTQADKFEFTVTSCTVTFASGKTATVSKDQGNITWYD 243
DB 314 IDAVNKGWRKMTTANGQTQADKFEFTVTSCTVTFASGKTATVSKDQGNITWYD 373
QY 244 VNVGDALNVNOLQNSGNLDSKAVAGSSGKVISGNVSPSKGKMDFTVINAGNIEITRN 303
DB 374 VNVGDALNVNOLQNSGNLDSKAVAGSSGKVISGNVSPSKGKMDFTVINAGNIEITRN 433
QY 304 GKNDIATSMTPPOFSSVSLGAGADAPTLVSDGDLANVSKKDNKPVRTTNVAPGVKEGDV 363
DB 434 GKNDIATSMTPPOFSSVSLGAGADAPTLVSDGDLANVSKKDNKPVRTTNVAPGVKEGDV 493
QY 364 TTNVAQLKGVAQNLRNDNDGNARAGIAQAIATAGLVQAVLPKSMMAIGGTYRGEAG 423
DB 494 TTNVAQLKGVAQNLRNDNDGNARAGIAQAIATAGLVQAVLPKSMMAIGGTYRGEAG 553
QY 424 YALGYSSISDGNMIIGKTASGNSRGHFGASASVGYOM 461
DB 554 YALGYSSISDGNMIIGKTASGNSRGHFGASASVGYOM 591

RESULT 6
US-09-771-382-5

Sequence 5, Application US/09771382
Patent No. US20020160016A1

GENERAL INFORMATION:

APPLICANT: Jennings, Michael
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-2401
CURRENT APPLICATION NUMBER: US/09/771,382
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 591
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-771-382-5

Query Match 99.3%; Score 2333; DB 10; Length 591;
Best Local Similarity 100.0%; Pred. No. 1,1e-173;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDLTSGTEKLSFSGANGKNVITSDTKGLNFAKTAGTNGDTYVHLNGISLTLDTLNT 63
DB 134 TDLTSGTEKLSFSGANGKNVITSDTKGLNFAKTAGTNGDTYVHLNGISLTLDTLNT 193
QY 64 GATTNVNDVNTDEDEKRAASVSKDVLNAGNNIKGVKGTASDVDFVRYTDVEFLSAD 123
DB 194 GATTNVNDVNTDEDEKRAASVSKDVLNAGNNIKGVKGTASDVDFVRYTDVEFLSAD 253
QY 124 TKTITTVVESKDNCKTEVKIGAKTSYIKERDGLVTKDGKGENGSTDEGEGLVTAKEV 183

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Db 254 TKTITVNESKDNKGKTEKIKGAKTSVLIKEDGKLVTKDGENSSSTDEGGLVTAKEV 313
OY 184 IDAVKAGRMKTTTANGOTGADKFEFVTSCTNTVTFASGKGTATVSKDDGNTTVMYD 243
Db 314 IDAVKAGRMKTTTANGOTGADKFEFVTSCTNTVTFASGKGTATVSKDDGNTTVMYD 373
OY 244 VNVGDALVNNQLONSGWNLDKSAVAGSSGKTVISGNVSPSKGMDETVNNAGNNIEITRN 303
Db 374 VNVGDALVNNQLONSGWNLDKSAVAGSSGKTVISGNVSPSKGMDETVNNAGNNIEITRN 433
OY 304 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDVDALNVGSKKDNKPKVRITNVAPEGKEGV 363
Db 434 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDVDALNVGSKKDNKPKVRITNVAPEGKEGV 493
OY 364 TNVAOLKGYAQNLRNIDVNDGNARAGIAQAATATAGLVOAYLPKSMMAIGGTYRGEAG 423
Db 494 TNVAOLKGYAQNLRNIDVNDGNARAGIAQAATATAGLVOAYLPKSMMAIGGTYRGEAG 553
OY 424 VAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 461
Db 554 VAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 591
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RESULT 7
US-09-797-862-2
; Sequence 2, Application US/09797862
; Patent No. US20020102276A1
; GENERAL INFORMATION:
; APPLICANT: PEAK, IAN RICHARD ANSELM
; APPLICANT: JENNINGS, MICHAEL PAUL
; APPLICANT: MOXON, E. RICHARD
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0134
; CURRENT APPLICATION NUMBER: US-09/797, 862
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-797-862-2
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Query Match 99.1%; Score 2329; DB 10; Length 592;

Best Local Similarity 99.8%; Pred. No. 2.2e-173;

Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 4 TDLTSVGTETKLSFSANGKNKVNITSDTKGLNFAKETAGTNGDTVHLNGIGSTLTDTLLNT 63
Db 135 TDLTSVGTETKLSFSANGKNKVNITSDTKGLNFAKETAGTNGDTVHLNGIGSTLTDTLLNT 194
OY 64 GATTNVTNDVNTDDEKRRASVYKDVNLNAGWNIKGVKPGTTASDNDVFPRTYDTEFLSND 123
Db 195 GATTNVTNDVNTDDEKRRASVYKDVNLNAGWNIKGVKPGTTASDNDVFPRTYDTEFLSND 254
OY 124 TKTITVNESKDNKGKTEKIKGAKTSVLIKEDGKLVTKDGENSSSTDEGGLVTAKEV 183
Db 255 TKTITVNESKDNKGKTEKIKGAKTSVLIKEDGKLVTKDGENSSSTDEGGLVTAKEV 314
OY 184 IDAVKAGRMKTTTANGOTGADKFEFVTSCTNTVTFASGKGTATVSKDDGNTTVMYD 243
Db 315 IDAVKAGRMKTTTANGOTGADKFEFVTSCTNTVTFASGKGTATVSKDDGNTTVMYD 374
OY 244 VNVGDALVNNQLONSGWNLDKSAVAGSSGKTVISGNVSPSKGMDETVNNAGNNIEITRN 303
Db 375 VNVGDALVNNQLONSGWNLDKSAVAGSSGKTVISGNVSPSKGMDETVNNAGNNIEITRN 434
OY 304 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDVDALNVGSKKDNKPKVRITNVAPEGKEGV 363
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Db 435 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDVDALNVGSKKDNKPKVRITNVAPEGKEGV 494
OY 364 TNVAOLKGYAQNLRNIDVNDGNARAGIAQAATATAGLVOAYLPKSMMAIGGTYRGEAG 423
Db 495 TNVAOLKGYAQNLRNIDVNDGNARAGIAQAATATAGLVOAYLPKSMMAIGGTYRGEAG 554
OY 424 VAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 461
Db 555 VAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 592
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RESULT 8
US-09-771-382-33
; Sequence 33, Application US/09771382
; Patent No. US20020160016A1
; GENERAL INFORMATION:
; APPLICANT: Peak, Ian
; APPLICANT: Jennings, Michael
; TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
; FILE REFERENCE: 8795-24U1
; CURRENT APPLICATION NUMBER: US/09/771, 382
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/177, 917
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 33
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-771-382-33
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Query Match 99.1%; Score 2328; DB 10; Length 540;

Best Local Similarity 99.8%; Pred. No. 2.4e-173;

Matches 457; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 4 TDLTSVGTETKLSFSANGKNKVNITSDTKGLNFAKETAGTNGDTVHLNGIGSTLTDTLLNT 63
Db 83 TDLTSVGTETKLSFSANGKNKVNITSDTKGLNFAKETAGTNGDTVHLNGIGSTLTDTLLNT 142
OY 64 GATTNVTNDVNTDDEKRRASVYKDVNLNAGWNIKGVKPGTTASDNDVFPRTYDTEFLSND 123
Db 143 GATTNVTNDVNTDDEKRRASVYKDVNLNAGWNIKGVKPGTTASDNDVFPRTYDTEFLSND 202
OY 124 TKTITVNESKDNKGKTEKIKGAKTSVLIKEDGKLVTKDGENSSSTDEGGLVTAKEV 183
Db 203 TKTITVNESKDNKGKTEKIKGAKTSVLIKEDGKLVTKDGENSSSTDEGGLVTAKEV 262
OY 184 IDAVKAGRMKTTTANGOTGADKFEFVTSCTNTVTFASGKGTATVSKDDGNTTVMYD 243
Db 263 IDAVKAGRMKTTTANGOTGADKFEFVTSCTNTVTFASGKGTATVSKDDGNTTVMYD 322
OY 244 VNVGDALVNNQLONSGWNLDKSAVAGSSGKTVISGNVSPSKGMDETVNNAGNNIEITRN 303
Db 323 VNVGDALVNNQLONSGWNLDKSAVAGSSGKTVISGNVSPSKGMDETVNNAGNNIEITRN 382
OY 304 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDVDALNVGSKKDNKPKVRITNVAPEGKEGV 363
Db 383 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDVDALNVGSKKDNKPKVRITNVAPEGKEGV 442
OY 364 TNVAOLKGYAQNLRNIDVNDGNARAGIAQAATATAGLVOAYLPKSMMAIGGTYRGEAG 423
Db 443 TNVAOLKGYAQNLRNIDVNDGNARAGIAQAATATAGLVOAYLPKSMMAIGGTYRGEAG 502
OY 424 VAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 461
Db 503 VAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 540
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RESULT 9
US-09-797-862-9
; Sequence 9, Application US/09797862

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; Patent No. US20020102276A1
; GENERAL INFORMATION:
; APPLICANT: PEAK, IAN RICHARD ANSELM
; APPLICANT: JENNINGS, MICHAEL PAUL
; APPLICANT: MOXON, E. RICHARD
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0134
; CURRENT APPLICATION NUMBER: US/09/797,862
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-797-862-9

Query Match          96.2%; Score 2260.5; DB 10; Length 594;
Best Local Similarity 97.4%; Pred. No. 5e-168;
Matches 447; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 4 TDLTSVTEKLSFSGANGKVNITSDTKGLNPAKFTAGTNGDTVYHLNGISGTLTDTLLNT 63
DB TDLTSVTEKLSFSGANGKVNITSDTKGLNPAKFTAGTNGDTVYHLNGISGTLTDTLLNT 195
QY 64 GATTNVTNDVNTDDEKRRASVYKVDVLNAGNMIKVKRGTTASDNDVDFVRYDVEFLSAD 123
DB GATTNVTNDVNTDDEKRRASVYKVDVLNAGNMIKVKRGTTASDNDVDFVRYDVEFLSAD 255
QY 124 TKTTTVAVESKDNKREVEKIGAKTSYIKEDGKLVTKGDKGSGSTDEGEGLVTAKEV 183
DB TKTTTVAVESKDNKREVEKIGAKTSYIKEDGKLVTKGDKGSGSTDEGEGLVTAKEV 315
QY 184 IDAVNKAQWRRKTTTANGQGTQADKFEFVTSGTNVTFAASGKTATVSKDDQGNITWYD 243
DB IDAVNKAQWRRKTTTANGQGTQADKFEFVTSGTNVTFAASGKTATVSKDDQGNITWYD 375
QY 316 IDAVNKAQWRRKTTTANGQGTQADKFEFVTSGTNVTFAASGKTATVSKDDQGNITWYD 375
DB VNVGDALNVNOLONGSGNLDKSKAVAGSSGKVISGNSVPSKGMDETVINAGNIEITRN 303
QY 244 VNVGDALNVNOLONGSGNLDKSKAVAGSSGKVISGNSVPSKGMDETVINAGNIEITRN 303
DB VNVGDALNVNOLONGSGNLDKSKAVAGSSGKVISGNSVPSKGMDETVINAGNIEITRN 435
QY 376 VNVGDALNVNOLONGSGNLDKSKAVAGSSGKVISGNSVPSKGMDETVINAGNIEITRN 435
DB GKNDITSMTPQFSSVSLGAGADAPFLSYDGD-ALNVGSKDNKPVRTNVAQVKEGD 362
QY 304 GKNDITSMTPQFSSVSLGAGADAPFLSYDGD-ALNVGSKDNKPVRTNVAQVKEGD 362
DB GKNDITSMTPQFSSVSLGAGADAPFLSYDDEGALNVGSKDNKPVRTNVAQVKEGD 495
QY 436 GKNDITSMTPQFSSVSLGAGADAPFLSYDDEGALNVGSKDNKPVRTNVAQVKEGD 495
DB VTNVAOLKGYAQNINNHIDVNDGNARAGIAQAIATAGIYQAYLPGKSMMAIGGCTYGEA 422
QY 363 VTNVAOLKGYAQNINNHIDVNDGNARAGIAQAIATAGIYQAYLPGKSMMAIGGCTYGEA 422
DB VTNVAOLKGYAQNINNHIDVNDGNARAGIAQAIATAGIYQAYLPGKSMMAIGGCTYGEA 555
QY 423 GYALGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 461
DB 556 GYALGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 594

RESULT 10
US-09-771-382-4
; Sequence 4, Application US/09771382
; Patent No. US20020160016A1
; GENERAL INFORMATION:
; APPLICANT: Peak, Ian
; APPLICANT: Jennings, Michael
; TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
; FILE REFERENCE: 8795-2401
; CURRENT APPLICATION NUMBER: US/09/771,382
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/177,917
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentln version 3.0
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; SEQ ID NO 4
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-771-382-4

Query Match          96.2%; Score 2260.5; DB 10; Length 594;
Best Local Similarity 97.4%; Pred. No. 5e-168;
Matches 447; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 4 TDLTSVTEKLSFSGANGKVNITSDTKGLNPAKFTAGTNGDTVYHLNGISGTLTDTLLNT 63
DB TDLTSVTEKLSFSGANGKVNITSDTKGLNPAKFTAGTNGDTVYHLNGISGTLTDTLLNT 195
QY 64 GATTNVTNDVNTDDEKRRASVYKVDVLNAGNMIKVKRGTTASDNDVDFVRYDVEFLSAD 123
DB GATTNVTNDVNTDDEKRRASVYKVDVLNAGNMIKVKRGTTASDNDVDFVRYDVEFLSAD 255
QY 124 TKTTTVAVESKDNKREVEKIGAKTSYIKEDGKLVTKGDKGSGSTDEGEGLVTAKEV 183
DB TKTTTVAVESKDNKREVEKIGAKTSYIKEDGKLVTKGDKGSGSTDEGEGLVTAKEV 315
QY 184 IDAVNKAQWRRKTTTANGQGTQADKFEFVTSGTNVTFAASGKTATVSKDDQGNITWYD 243
DB IDAVNKAQWRRKTTTANGQGTQADKFEFVTSGTNVTFAASGKTATVSKDDQGNITWYD 375
QY 316 IDAVNKAQWRRKTTTANGQGTQADKFEFVTSGTNVTFAASGKTATVSKDDQGNITWYD 375
DB VNVGDALNVNOLONGSGNLDKSKAVAGSSGKVISGNSVPSKGMDETVINAGNIEITRN 303
QY 244 VNVGDALNVNOLONGSGNLDKSKAVAGSSGKVISGNSVPSKGMDETVINAGNIEITRN 303
DB VNVGDALNVNOLONGSGNLDKSKAVAGSSGKVISGNSVPSKGMDETVINAGNIEITRN 435
QY 376 VNVGDALNVNOLONGSGNLDKSKAVAGSSGKVISGNSVPSKGMDETVINAGNIEITRN 435
DB GKNDITSMTPQFSSVSLGAGADAPFLSYDGD-ALNVGSKDNKPVRTNVAQVKEGD 362
QY 304 GKNDITSMTPQFSSVSLGAGADAPFLSYDGD-ALNVGSKDNKPVRTNVAQVKEGD 362
DB GKNDITSMTPQFSSVSLGAGADAPFLSYDDEGALNVGSKDNKPVRTNVAQVKEGD 495
QY 436 GKNDITSMTPQFSSVSLGAGADAPFLSYDDEGALNVGSKDNKPVRTNVAQVKEGD 495
DB VTNVAOLKGYAQNINNHIDVNDGNARAGIAQAIATAGIYQAYLPGKSMMAIGGCTYGEA 422
QY 363 VTNVAOLKGYAQNINNHIDVNDGNARAGIAQAIATAGIYQAYLPGKSMMAIGGCTYGEA 422
DB VTNVAOLKGYAQNINNHIDVNDGNARAGIAQAIATAGIYQAYLPGKSMMAIGGCTYGEA 555
QY 423 GYALGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 461
DB 556 GYALGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 594

RESULT 11
US-09-797-862-15
; Sequence 15, Application US/09797862
; Patent No. US20020102276A1
; GENERAL INFORMATION:
; APPLICANT: PEAK, IAN RICHARD ANSELM
; APPLICANT: JENNINGS, MICHAEL PAUL
; APPLICANT: MOXON, E. RICHARD
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0134
; CURRENT APPLICATION NUMBER: US/09/797,862
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-797-862-15

Query Match          96.1%; Score 2257.5; DB 10; Length 599;
Best Local Similarity 97.4%; Pred. No. 8.6e-168;
Matches 447; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 4 TDLTSVTEKLSFSGANGKVNITSDTKGLNPAKFTAGTNGDTVYHLNGISGTLTDTLLNT 63
DB TDLTSVTEKLSFSGANGKVNITSDTKGLNPAKFTAGTNGDTVYHLNGISGTLTDTLLNT 195
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Db 141 TDLTSETEKLSFGANGKVNITSDTKGNFAKETAGTNGDTTVHLNGISTLTDTLNT 200
Qy 64 GATTNVTNDNTDDEKKRAASVKDVLNAGMNKGVKPGTTASDNVDFVRYTDFVEFLSAD 123
Db 201 GATTNVTNDNTDDEKKRAASVKDVLNAGMNKGVKPGTTASDNVDFVRYTDFVEFLSAD 260
Qy 124 TTTTIVNVESSKNGKRTVEKIGAKTSVYKEKDGKLVTKGDKENGSSSTDEGGLVYAKEV 183
Db 261 TTTTIVNVESSKNGKRTVEKIGAKTSVYKEKDGKLVTKGDKENGSSSTDEGGLVYAKEV 320
Qy 184 IDAVKAGRMKMTTANAGOTGOADKFEYVTSCTNTVTFASGKGTATVSKDDGNTVYMD 243
Db 321 IDAVKAGRMKMTTANAGOTGOADKFEYVTSCTNTVTFASGKGTATVSKDDGNTVYMD 380
Qy 244 VNVGALNVNOLONGSMNIDSKRAVAGSSGKVISGNVSPSKGMDTVNINAGNIEITRN 303
Db 381 VNVGALNVNOLONGSMNIDSKRAVAGSSGKVISGNVSPSKGMDTVNINAGNIEITRN 440
Qy 304 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDVG-DALNVSKKDNKPVRTTNAPGVKEGD 362
Db 441 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDVG-DALNVSKKDNKPVRTTNAPGVKEGD 500
Qy 363 VTNVAOLKGVNOLNLRIDNVGNARAGIAQAIATAGLVQAVLPKSMMAIGGTYRGHA 422
Db 501 VTNVAOLKGVNOLNLRIDNVGNARAGIAQAIATAGLVQAVLPKSMMAIGGTYRGHA 560
Qy 423 GYAIGYSSISDGGNMIIKGTASGNSRGHFGASASVGYOW 461
Db 561 GYAIGYSSISDGGNMIIKGTASGNSRGHFGASASVGYOW 599
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RESULT 12
US-09-771-382-6
; Sequence 6, Application US/09771382
; Patent No. US20020160016A1
; GENERAL INFORMATION:
; APPLICANT: Peak, Ian
; TITLE OF INVENTION: Jemmings, Michael
; FILE REFERENCE: 8795-2401
; CURRENT APPLICATION NUMBER: US/09/771,382
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/177,917
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 599
; TYPE: PRF
; ORGANISM: Neisseria meningitidis
US-09-771-382-6
```

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Query Match 96.1%; Score 2257.5; DB 10; Length 599;
Best Local Similarity 97.4%; Pred. No. 8.6e-168;
Matches 447; Conservative 2; Mismatches 9; Indels 1; Gaps 1;
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Qy 4 TDLTSETEKLSFGANGKVNITSDTKGNFAKETAGTNGDTTVHLNGISTLTDTLNT 63
Db 141 TDLTSETEKLSFGANGKVNITSDTKGNFAKETAGTNGDTTVHLNGISTLTDTLNT 200
Qy 64 GATTNVTNDNTDDEKKRAASVKDVLNAGMNKGVKPGTTASDNVDFVRYTDFVEFLSAD 123
Db 201 GATTNVTNDNTDDEKKRAASVKDVLNAGMNKGVKPGTTASDNVDFVRYTDFVEFLSAD 260
Qy 124 TTTTIVNVESSKNGKRTVEKIGAKTSVYKEKDGKLVTKGDKENGSSSTDEGGLVYAKEV 183
Db 261 TTTTIVNVESSKNGKRTVEKIGAKTSVYKEKDGKLVTKGDKENGSSSTDEGGLVYAKEV 320
Qy 184 IDAVKAGRMKMTTANAGOTGOADKFEYVTSCTNTVTFASGKGTATVSKDDGNTVYMD 243
Db 321 IDAVKAGRMKMTTANAGOTGOADKFEYVTSCTNTVTFASGKGTATVSKDDGNTVYMD 380
Qy 244 VNVGALNVNOLONGSMNIDSKRAVAGSSGKVISGNVSPSKGMDTVNINAGNIEITRN 303
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Db 381 VNVGALNVNOLONGSMNIDSKRAVAGSSGKVISGNVSPSKGMDTVNINAGNIEITRN 440
Qy 304 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDVG-DALNVSKKDNKPVRTTNAPGVKEGD 362
Db 441 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDVG-DALNVSKKDNKPVRTTNAPGVKEGD 500
Qy 363 VTNVAOLKGVNOLNLRIDNVGNARAGIAQAIATAGLVQAVLPKSMMAIGGTYRGHA 422
Db 501 VTNVAOLKGVNOLNLRIDNVGNARAGIAQAIATAGLVQAVLPKSMMAIGGTYRGHA 560
Qy 423 GYAIGYSSISDGGNMIIKGTASGNSRGHFGASASVGYOW 461
Db 561 GYAIGYSSISDGGNMIIKGTASGNSRGHFGASASVGYOW 599
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RESULT 13
US-09-797-862-7
; Sequence 7, Application US/09797862
; Patent No. US20020102276A1
; GENERAL INFORMATION:
; APPLICANT: PEAK, IAN RICHARD ANSELM
; APPLICANT: MOXON, E. RICHARD
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0134
; CURRENT APPLICATION NUMBER: US/09/797,862
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRF
; ORGANISM: Neisseria meningitidis
US-09-797-862-7
```

```
Query Match 95.7%; Score 2248.5; DB 10; Length 594;
Best Local Similarity 97.2%; Pred. No. 4.3e-167;
Matches 446; Conservative 1; Mismatches 11; Indels 1; Gaps 1;
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Qy 4 TDLTSETEKLSFGANGKVNITSDTKGNFAKETAGTNGDTTVHLNGISTLTDTLNT 63
Db 136 TDLTSETEKLSFGANGKVNITSDTKGNFAKETAGTNGDTTVHLNGISTLTDTLNT 195
Qy 64 GATTNVTNDNTDDEKKRAASVKDVLNAGMNKGVKPGTTASDNVDFVRYTDFVEFLSAD 123
Db 196 GATTNVTNDNTDDEKKRAASVKDVLNAGMNKGVKPGTTASDNVDFVRYTDFVEFLSAD 255
Qy 124 TTTTIVNVESSKNGKRTVEKIGAKTSVYKEKDGKLVTKGDKENGSSSTDEGGLVYAKEV 183
Db 256 TTTTIVNVESSKNGKRTVEKIGAKTSVYKEKDGKLVTKGDKENGSSSTDEGGLVYAKEV 315
Qy 184 IDAVKAGRMKMTTANAGOTGOADKFEYVTSCTNTVTFASGKGTATVSKDDGNTVYMD 243
Db 316 IDAVKAGRMKMTTANAGOTGOADKFEYVTSCTNTVTFASGKGTATVSKDDGNTVYMD 375
Qy 244 VNVGALNVNOLONGSMNIDSKRAVAGSSGKVISGNVSPSKGMDTVNINAGNIEITRN 303
Db 376 VNVGALNVNOLONGSMNIDSKRAVAGSSGKVISGNVSPSKGMDTVNINAGNIEITRN 435
Qy 304 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDVG-DALNVSKKDNKPVRTTNAPGVKEGD 362
Db 436 GKNIDIATSMTPQFSSSVSLGAGADAPTLSDVG-DALNVSKKDNKPVRTTNAPGVKEGD 495
Qy 363 VTNVAOLKGVNOLNLRIDNVGNARAGIAQAIATAGLVQAVLPKSMMAIGGTYRGHA 422
Db 496 VTNVAOLKGVNOLNLRIDNVGNARAGIAQAIATAGLVQAVLPKSMMAIGGTYRGHA 555
Qy 423 GYAIGYSSISDGGNMIIKGTASGNSRGHFGASASVGYOW 461
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Db 556 GYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 594

RESULT 14

US-09-771-382-9
; Sequence 9, Application US/09771382
; Patent No. US20020160016A1
; GENERAL INFORMATION:
; APPLICANT: Peak, Ian
; APPLICANT: Jennings, Michael
; TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
; FILE REFERENCE: 8795-2401
; CURRENT APPLICATION NUMBER: US/09/771,382
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/177,917
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRP
; ORGANISM: Neisseria meningitidis
US-09-771-382-9

Query Match 95.7%; Score 2248.5; DB 10; Length 594;

Best Local Similarity 97.2%; Pred. No. 4.3e-167;
Matches 446; Conservative 1; Mismatches 11; Indels 1; Gaps 1;

QY 4 TDLTSVTEKLSFSANGKRVNITSPTKGLNFAKETAGTNGDPTVHLNGIGSTLTDPLNT 63
Db TDLTSVTEKLSFSANGKRVNITSPTKGLNFAKETAGTNGDPTVHLNGIGSTLTDPLNT 195
QY 64 GATTNTNDNVTDDEKRRASVYKDVNLACGNIKGVKPGTTASDNDVFPRTYDVEFLSAD 123
Db GATTNTNDNVTDDEKRRASVYKDVNLACGNIKGVKPGTTASDNDVFPRTYDVEFLSAD 255
QY 124 TTTTNNVSKDNGKTEVKIGAKTSVIEKDGKLVTKGDKGENSGSTDEGEGLVTAKEY 183
Db TTTTNNVSKDNGKTEVKIGAKTSVIEKDGKLVTKGDKGENSGSTDEGEGLVTAKEY 315
QY 184 IDAVNAGWRMKTATTANGOTGQADKFEYVTSCTNVTFAAGKGTATVSKDDGNTVMYD 243
Db IDAVNAGWRMKTATTANGOTGQADKFEYVTSCTNVTFAAGKGTATVSKDDGNTVMYD 375
QY 244 VNVGDLANNOLONGSMNLDKRAVAGSSGKVISGNVSPSKGKDETVNINAGNNIETRN 303
Db VNVGDLANNOLONGSMNLDKRAVAGSSGKVISGNVSPSKGKDETVNINAGNNIETRN 435
QY 304 GKNIDATSMTPQFSSVSLGAGADAPTLVSVDG-ALNVGSKDKNKPVRITNVA PGYKEG 362
Db GKNIDATSMTPQFSSVSLGAGADAPTLVSVDGALNVGSKDKNKPVRITNVA PGYKEG 495
QY 363 VTNVAQLKGVQNLNRRIDNVGNARAGIAQAATATAGLVQAYLPGKSMAIGGTYRGEA 422
Db VTNVAQLKGVQNLNRRIDNVGNARAGIAQAATATAGLVQAYLPGKSMAIGGTYRGEA 555
QY 423 GYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 461
Db GYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 594

RESULT 15

US-09-797-862-5
; Sequence 5, Application US/09797862
; Patent No. US20020102276A1
; GENERAL INFORMATION:
; APPLICANT: PEAK, IAN RICHARD ANSELM
; APPLICANT: JENNINGS, MICHAEL PAUL
; APPLICANT: MOXON, E. RICHARD
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0134
; CURRENT APPLICATION NUMBER: US/09/797,862

; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-17
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRP
; ORGANISM: Neisseria meningitidis
US-09-797-862-5

Query Match 95.1%; Score 2235.5; DB 10; Length 598;

Best Local Similarity 96.3%; Pred. No. 4.5e-166;
Matches 442; Conservative 3; Mismatches 13; Indels 1; Gaps 1;

QY 4 TDLTSVTEKLSFSANGKRVNITSPTKGLNFAKETAGTNGDPTVHLNGIGSTLTDPLNT 63
Db TDLTSVTEKLSFSANGKRVNITSPTKGLNFAKETAGTNGDPTVHLNGIGSTLTDPLNT 199
QY 64 GATTNTNDNVTDDEKRRASVYKDVNLACGNIKGVKPGTTASDNDVFPRTYDVEFLSAD 123
Db GATTNTNDNVTDDEKRRASVYKDVNLACGNIKGVKPGTTASDNDVFPRTYDVEFLSAD 259
QY 124 TTTTNNVSKDNGKTEVKIGAKTSVIEKDGKLVTKGDKGENSGSTDEGEGLVTAKEY 183
Db TTTTNNVSKDNGKTEVKIGAKTSVIEKDGKLVTKGDKGENSGSTDEGEGLVTAKEY 319
QY 184 IDAVNAGWRMKTATTANGOTGQADKFEYVTSCTNVTFAAGKGTATVSKDDGNTVMYD 243
Db IDAVNAGWRMKTATTANGOTGQADKFEYVTSCTNVTFAAGKGTATVSKDDGNTVMYD 379
QY 244 VNVGDLANNOLONGSMNLDKRAVAGSSGKVISGNVSPSKGKDETVNINAGNNIETRN 303
Db VNVGDLANNOLONGSMNLDKRAVAGSSGKVISGNVSPSKGKDETVNINAGNNIETRN 439
QY 304 GKNIDATSMTPQFSSVSLGAGADAPTLVSVDG-ALNVGSKDKNKPVRITNVA PGYKEG 362
Db GKNIDATSMTPQFSSVSLGAGADAPTLVSVDGALNVGSKDKNKPVRITNVA PGYKEG 499
QY 363 VTNVAQLKGVQNLNRRIDNVGNARAGIAQAATATAGLVQAYLPGKSMAIGGTYRGEA 422
Db VTNVAQLKGVQNLNRRIDNVGNARAGIAQAATATAGLVQAYLPGKSMAIGGTYRGEA 559
QY 423 GYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 461
Db GYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 598

Search completed: October 6, 2003, 10:19:47
Job time: 24.0934 secs

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:10 : Search time 33.8588 Seconds
(without alignments)
3513.485 Million cell updates/sec

Title: US-09-771-382-35
Perfect score: 2350
Sequence: 1 NNEDLTSGTEKLSFSANG.....TASGNSRGHFGASASGYQW 461

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2333	99.3	591	2 0930Y3	093qy3 neisseria m
2	2333	99.3	591	2 09JPS7	09jps7 neisseria m
3	2333	99.3	591	16 09JRI8	09jri8 neisseria m
4	2329	99.1	592	2 09AOF0	09aof0 neisseria m
5	2296	97.7	526	2 09JPS4	09jps4 neisseria m
6	2296	97.7	530	2 09JPS1	09jps1 neisseria m
7	2291	97.5	600	2 09JPS6	09jps6 neisseria m
8	2281.5	97.1	590	2 09JPS3	09jps3 neisseria m
9	2260.5	96.2	594	2 0930Y4	093qy4 neisseria m
10	2257.5	96.1	594	2 09JPI3	09jpi3 neisseria m
11	2257.5	96.1	594	2 09JPS2	09jps2 neisseria m
12	2248.5	95.7	594	2 09JPH8	09jph8 neisseria m
13	2248.5	95.7	594	2 09JPH7	09jph7 neisseria m
14	2241.5	95.4	592	2 09JPS9	09jps9 neisseria m
15	2241.5	95.4	592	2 09JPS0	09jps0 neisseria m
16	2235.5	95.1	598	2 09JPS0	09jps0 neisseria m

17	2235.5	95.1	598	2 0930Y5	093qy5 neisseria m
18	2235.5	95.1	598	2 09JPT0	09jpt0 neisseria m
19	2207.5	93.9	592	2 0930Y2	093qy2 neisseria m
20	2123.5	90.4	599	2 09JPS8	09jps8 neisseria m
21	2117.5	90.1	598	2 09JPR7	09jpr7 neisseria m
22	2115.5	90.0	595	2 09JPH0	09jph0 neisseria m
23	2089.5	88.9	592	16 09JOW4	09jow4 neisseria m
24	2081.5	88.6	589	2 09JPI0	09jpi0 neisseria m
25	2075.5	88.3	600	2 09JPS5	09jps5 neisseria m
26	2069.5	88.1	589	2 0930Y1	093qy1 neisseria m
27	901.5	38.4	2353	2 P71401	P71401 haemophilus
28	874	37.2	1098	2 048152	048152 haemophilus
29	868.5	37.0	1096	2 08GM79	08gm79 haemophilus
30	844.5	35.9	1210	2 08GM74	08gm74 haemophilus
31	836.5	35.6	1210	2 08GM75	08gm75 haemophilus
32	835.5	35.6	1204	2 08GM76	08gm76 haemophilus
33	563	24.0	1002	2 08GM78	08gm78 haemophilus
34	561	23.9	1004	2 08GM77	08gm77 haemophilus
35	405	17.2	1299	16 09FX36	09fx36 pasteurella
36	381.5	16.2	2314	2 08KQW8	08kqw8 moraxella c
37	375.5	16.0	2059	16 09PD50	09pd50 xylella fas
38	365	15.5	1588	16 08XDG4	08xdg4 escherichia
39	360.5	15.3	1190	16 09PC04	09pc04 xylella fas
40	359	15.3	1461	16 08ZL64	08zl64 salmoneilla
41	357	15.2	1107	16 09FZD8	09fzd8 salmoneilla
42	350.5	14.9	1778	16 08RCB2	08rcb2 escherichia
43	346.5	14.7	1964	2 08KQW9	08kqw9 moraxella c
44	341	14.5	2712	16 09FX35	09fx35 pasteurella
45	334.5	14.2	688	2 08RQ60	08rq60 actinobacil

ALIGNMENTS

RESULT 1	ID	0930Y3	PRELIMINARY;	PRT;	591 AA.
AC	0930Y3:				
DT	01-DEC-2001 (TREMUREL. 19, Created)				
DT	01-DEC-2001 (TREMUREL. 19, Last sequence update)				
DT	01-OCT-2002 (TREMUREL. 22, Last annotation update)				
DE	Nha outer membrane protein.				
GN	NHA.				
OS	Neisseria meningitidis.				
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;				
OC	Neisseriaceae; Neisseria.				
OX	NCBI_TaxID=487;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SRRAIN-EG329;				
RA	Peak I.R., Srihanta Y., Dieckelman M., Moxon R., Jennings M.P.;				
RT	"Identification and characterization of a gene encoding a novel outer				
RT	membrane protein of Neisseria meningitidis."				
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: AF157606; AAK68867.1; -				
DR	InterPro: IPR005594; Yada.				
DR	Pfam: PF03895; Yada; 1.				
SQ	SEQUENCE 591 AA; 62048 MW; C0DC600798859C65 CRC64;				
Query Match	99.3%; Score 2333; DB 2; Length 591;				
Best Local Similarity	100.0%; Pred. No. 7.2e-94;				
Matches	458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
OY	4 TDLTSGTEKLSFANGKVNITSPTKGLNFAKETAGTNGDTTVHLNGISLTLDTLANT 63				
DB	134 TDLTSGTEKLSFANGKVNITSPTKGLNFAKETAGTNGDTTVHLNGISLTLDTLANT 193				
OY	64 GATTNTNNDVDEKRAASVDVNLAGNINIGVAPGTASNDVDFRVDFEFLSAD 123				
DB	194 GATTNTNNDVDEKRAASVDVNLAGNINIGVAPGTASNDVDFRVDFEFLSAD 253				
OY	124 TKTTVNVESKDKGKTEVKIGAKTSVIREKDKLVTGKDGKNGSSTDEGELVLAKEV 183				

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Db 254 TKTITVNESKDNCKTEVKIGAKTSYKEKDGKLVTKDKGENSSSTDEGEGLTAYKEV 313
OY 184 IDAVKAKGMRKTTTANGOTGQADKEFTVTSCTNTVTFASGKTTATVSKDQGNITVMD 243
Db 314 IDAVKAKGMRKTTTANGOTGQADKEFTVTSCTNTVTFASGKTTATVSKDQGNITVMD 373
OY 244 VNVGDALVNVQNSGNWLDKSAVAGSSGKYISGVNPSFKGMDFTVINMGNNIETRN 303
Db 374 VNVGDALVNVQNSGNWLDKSAVAGSSGKYISGVNPSFKGMDFTVINMGNNIETRN 433
OY 304 GKNIDIATSMTPQESSVSLGAGADAPTLSDGDALNVGSKDNKRPVRTTNVAPGVKEGDV 363
Db 434 GKNIDIATSMTPQESSVSLGAGADAPTLSDGDALNVGSKDNKRPVRTTNVAPGVKEGDV 493
OY 364 TNVAOLKGVQAOQLNRINDVGNARAGIAQAIATAGLVQAVLPKGSMAIGGGTYRGAAG 423
Db 494 TNVAOLKGVQAOQLNRINDVGNARAGIAQAIATAGLVQAVLPKGSMAIGGGTYRGAAG 553
OY 424 YAIGYSSISDGNWITIKGTASGNSRGHFGASASVGYQW 461
Db 554 YAIGYSSISDGNWITIKGTASGNSRGHFGASASVGYQW 591

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RESULT 2

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ID 09JPS7 PRELIMINARY: PRT: 591 AA.
AC 09JPS7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GMA992.
GN GMA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B2147;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scarlato V., Masiagnani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Barcolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.
RL Science 287:1816-1820(2000).
DR EMBL; AF226366; AAF42515.1; -
DR InterPro; IPR005594; YADA.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 591 AA: 62113 MW: 533453CAE5A91EIF CRC64;

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Query Match 99.3%; Score 2333; DB 2; Length 591;
 Best Local Similarity 100.0%; Pred. No. 7.2e-94;
 Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 4 TDLNSVGTSEKLSFSANGKVKVNTSPTKGLNFAKKTAGTNGDTVYHLNIGSTLTPTLNT 63
Db 134 TDLNSVGTSEKLSFSANGKVKVNTSPTKGLNFAKKTAGTNGDTVYHLNIGSTLTPTLNT 193
OY 64 GATTNVTNDVYDDEKRRASVQVLYNAGWNIKGVPPTTASDNDVFRYDTPVEFLSD 123
Db 194 GATTNVTNDVYDDEKRRASVQVLYNAGWNIKGVPPTTASDNDVFRYDTPVEFLSD 253
OY 124 TKTITVNESKDNCKTEVKIGAKTSYKEKDGKLVTKDKGENSSSTDEGEGLTAYKEV 183
Db 254 TKTITVNESKDNCKTEVKIGAKTSYKEKDGKLVTKDKGENSSSTDEGEGLTAYKEV 313
OY 184 IDAVKAKGMRKTTTANGOTGQADKEFTVTSCTNTVTFASGKTTATVSKDQGNITVMD 243

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Db 314 IDAVKAKGMRKTTTANGOTGQADKEFTVTSCTNTVTFASGKTTATVSKDQGNITVMD 373
OY 244 VNVGDALVNVQNSGNWLDKSAVAGSSGKYISGVNPSFKGMDFTVINMGNNIETRN 303
Db 374 VNVGDALVNVQNSGNWLDKSAVAGSSGKYISGVNPSFKGMDFTVINMGNNIETRN 433
OY 304 GKNIDIATSMTPQESSVSLGAGADAPTLSDGDALNVGSKDNKRPVRTTNVAPGVKEGDV 363
Db 434 GKNIDIATSMTPQESSVSLGAGADAPTLSDGDALNVGSKDNKRPVRTTNVAPGVKEGDV 493
OY 364 TNVAOLKGVQAOQLNRINDVGNARAGIAQAIATAGLVQAVLPKGSMAIGGGTYRGAAG 423
Db 494 TNVAOLKGVQAOQLNRINDVGNARAGIAQAIATAGLVQAVLPKGSMAIGGGTYRGAAG 553
OY 424 YAIGYSSISDGNWITIKGTASGNSRGHFGASASVGYQW 461
Db 554 YAIGYSSISDGNWITIKGTASGNSRGHFGASASVGYQW 591

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RESULT 3

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ID 09JRI8 PRELIMINARY: PRT: 591 AA.
AC 09JRI8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GMA992 (Adhesin) (Nhba outer membrane
protein).
GN GMA992 OR NMB0992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487, 491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MC58 / Serogroup B, B2169, B283, and H44/76;
RX MEDLINE=20175755; PubMed=10710307;
RA Piza M., Scarlato V., Masiagnani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Barcolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwin M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Yamathevan J.,
RA Gill J., Scarlato V., Masiagnani V., Piza M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58.
RL Science 287:1809-1815(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=N.meningitidis; STRAIN=PMC21;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT Identification and characterization of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF226375; AAF42524.1; -
DR EMBL; AE002450; AAF41395.1; -
DR EMBL; AF226367; AAF42516.1; -

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Db 69 TDLTSVEFEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDTVYHLNIGSTLDDTLTNT 128
Qy 64 GATTNVTNDNTDDEKKRAASVKDVLNAGWNIGVYKPGCTASDNDVFEVRYTDVEEFLSAD 123
Db 129 GATTNVTNDNTDDEKKRAASVKDVLNAGWNIGVYKPGCTASDNDVFEVRYTDVEEFLSAD 188
Qy 124 TKTITVNVESKDNKGRTEVKIGAKTSVKEKDGKLVTKGKXGKENGSSSTDEBEGGLTAYKEV 183
Db 189 TKTITVNVESKDNKGRTEVKIGAKTSVKEKDGKLVTKGKXGKENGSSSTDEBEGGLTAYKEV 248
Qy 184 IDAVKAKGRMKRTTTANGOTGADKFEVTSCTNVTFAFGKGTATVASKDOGNITVAYD 243
Db 249 IDAVKAKGRMKRTTTANGOTGADKFEVTSCTNVTFAFGKGTATVASKDOGNITVAYD 308
Qy 244 VNVGDALVNVOLQNSGMWLDKRAVAGSSGKVIISGVNPSKGMDETVINAGNNIEITRN 303
Db 309 VNVGDALVNVOLQNSGMWLDKRAVAGSSGKVIISGVNPSKGMDETVINAGNNIEITRN 368
Qy 304 GKNDIATSMTPQSSSVSLGAGADAPLTVSDGDALNVGSKDKNRPVRTITNAPGVKEGDV 363
Db 369 GKNDIATSMTPQSSSVSLGAGADAPLTVSDGDALNVGSKDKNRPVRTITNAPGVKEGDV 428
Qy 364 TNVAOLKGVAAONLNRRIDNVGDNARAGIAQAIAATGAVQAVLPKSKMAIGGGTYRGEGAG 423
Db 429 TNVAOLKGVAAONLNRRIDNVGDNARAGIAQAIAATGAVQAVLPKSKMAIGGGTYRGEGAG 488
Qy 424 YAIGYSSISDGNWIIKGTASGNSRGRHGASASVGYOW 461
Db 489 YAIGYSSISDGNWIIKGTASGNSRGRHGASASVGYOW 526
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RESULT 6

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QJPS1 PRELIMINARY: PRT; 530 AA.
AC 09JPS1: 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE26;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226371; AAF42520.1; -.
DR InterPro: IPR005594; YADA.
DR Pfam: PF03895; Yada.1.
SQ SEQUENCE 530 AA; 55190 MW; 1F836CA57598515B CRC64;
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Query Match 97.7%; Score 2296; DB 2; Length 530;
Best Local Similarity 98.5%; Pred. No. 2.6e-92;
Matches 451; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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Qy 4 TDLTSVTEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDTVYHLNIGSTLDDTLTNT 63
Db 73 TDLTSVTEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDTVYHLNIGSTLDDTLTNT 132
Qy 64 GATTNVTNDNTDDEKKRAASVKDVLNAGWNIGVYKPGCTASDNDVFEVRYTDVEEFLSAD 123
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Db 133 GATTNVTNDNTDDEKKRAASVKDVLNAGWNIGVYKPGCTASDNDVFEVRYTDVEEFLSAD 192
Qy 124 TKTITVNVESKDNKGRTEVKIGAKTSVKEKDGKLVTKGKXGKENGSSSTDEBEGGLTAYKEV 183
Db 193 TKTITVNVESKDNKGRTEVKIGAKTSVKEKDGKLVTKGKXGKENGSSSTDEBEGGLTAYKEV 252
Qy 184 IDAVKAKGRMKRTTTANGOTGADKFEVTSCTNVTFAFGKGTATVASKDOGNITVAYD 243
Db 253 IDAVKAKGRMKRTTTANGOTGADKFEVTSCTNVTFAFGKGTATVASKDOGNITVAYD 312
Qy 244 VNVGDALVNVOLQNSGMWLDKRAVAGSSGKVIISGVNPSKGMDETVINAGNNIEITRN 303
Db 313 VNVGDALVNVOLQNSGMWLDKRAVAGSSGKVIISGVNPSKGMDETVINAGNNIEITRN 372
Qy 304 GKNDIATSMTPQSSSVSLGAGADAPLTVSDGDALNVGSKDKNRPVRTITNAPGVKEGDV 363
Db 373 GKNDIATSMTPQSSSVSLGAGADAPLTVSDGDALNVGSKDKNRPVRTITNAPGVKEGDV 432
Qy 364 TNVAOLKGVAAONLNRRIDNVGDNARAGIAQAIAATGAVQAVLPKSKMAIGGGTYRGEGAG 423
Db 433 TNVAOLKGVAAONLNRRIDNVGDNARAGIAQAIAATGAVQAVLPKSKMAIGGGTYRGEGAG 492
Qy 424 YAIGYSSISDGNWIIKGTASGNSRGRHGASASVGYOW 461
Db 493 YAIGYSSISDGNWIIKGTASGNSRGRHGASASVGYOW 530
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RESULT 7

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QJPS6 PRELIMINARY: PRT; 600 AA.
AC 09JPS6: 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E26;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226371; AAF42520.1; -.
DR InterPro: IPR005594; YADA.
DR Pfam: PF03895; Yada.1.
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;
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Query Match 97.5%; Score 2291; DB 2; Length 600;
Best Local Similarity 98.5%; Pred. No. 4.9e-92;
Matches 451; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy 4 TDLTSVTEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDTVYHLNIGSTLDDTLTNT 63
Db 143 TDLTSVTEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDTVYHLNIGSTLDDTLTNT 202
Qy 64 GATTNVTNDNTDDEKKRAASVKDVLNAGWNIGVYKPGCTASDNDVFEVRYTDVEEFLSAD 123
Db 203 GATTNVTNDNTDDEKKRAASVKDVLNAGWNIGVYKPGCTASDNDVFEVRYTDVEEFLSAD 262
Qy 124 TKTITVNVESKDNKGRTEVKIGAKTSVKEKDGKLVTKGKXGKENGSSSTDEBEGGLTAYKEV 183
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Db 263 TKTITTVNESKDNKCKTEVIGAKTSYIKKEKDKLVTKGKGNGSSSTDEEGELVTAKEV 322
QY 184 IDAVNKGWRRKTTTANGOTGOADKFETVTSCTVNTVFASGKTATATYSKDDOGNITYWYD 243
Db 323 IDAVNKGWRRKTTTANGOGQADKFETVTSCTVNTVFASGKTATATYSKDDOGNITYWYD 382
QY 244 VNVGDALNVNOLQNSGNLDSKAVAGSSGKVIISGNVSPSKGKMDETVINAGNNIETTRN 303
Db 383 VNVGDALNVNOLQNSGNLDSKAVAGSSGKVIISGNVSPSKGKMDETVINAGNNIETTRN 442
QY 304 GKNIDTATSMTPQSSVSLGAGADAPTLSDVDGALNVGSKDKDKPVRITVAVPVGKGDV 363
Db 443 GKNIDTATSMTPQSSVSLGAGADAPTLSDVDGALNVGSKDKDKPVRITVAVPVGKGDV 502
QY 364 TVNAQLKGVANOLNLRIDNVGNARAGIAQAIAITAGLVQAYLPCKSMMAIGGCTYRGEA 423
Db 503 TVNAQLKGVANOLNLRIDNVGNARAGIAQAIAITAGLVQAYLPCKSMMAIGGCTYRGEA 562
QY 424 YAIYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 461
Db 563 YAIYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 600

RESULT 8
Q9JPS3 PRELIMINARY: PRT: 590 AA.
ID 09JPS3 AC 09JPS3
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE28;
RX MEDLINE=20175756; PubMed=10710308;
RA Piazza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanucci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuli S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL EMBL: AF226378; AAF42527.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada.
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 97.1%; Score 2281.5; DB 2; Length 590;
Best Local Similarity 98.3%; Pred. No. 1.2e-91;
Matches 451; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
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Db 312 IDAVNKGWRRKTTTANGOTGOADKFETVTSCTVNTVFASGKTATATYSKDDOGNITYWYD 371
QY 244 VNVGDALNVNOLQNSGNLDSKAVAGSSGKVIISGNVSPSKGKMDETVINAGNNIETTRN 303
Db 372 VNVGDALNVNOLQNSGNLDSKAVAGSSGKVIISGNVSPSKGKMDETVINAGNNIETTRN 431
QY 304 GKNIDTATSMTPQSSVSLGAGADAPTLSDVDGALNVGSKDKDKPVRITVAVPVGKGDV 362
Db 432 GKNIDTATSMTPQSSVSLGAGADAPTLSDVDGALNVGSKDKDKPVRITVAVPVGKGDV 491
QY 363 VTNVAQLKGVANOLNLRIDNVGNARAGIAQAIAITAGLVQAYLPCKSMMAIGGCTYRGEA 422
Db 492 VTNVAQLKGVANOLNLRIDNVGNARAGIAQAIAITAGLVQAYLPCKSMMAIGGCTYRGEA 551
QY 423 GYAIYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 461
Db 552 GYAIYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 590

RESULT 9
Q930Y4 PRELIMINARY: PRT: 594 AA.
ID 0930Y4 AC 0930Y4
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Nha outer membrane protein.
GN NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG327;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF157605; AAK68866.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada.
SQ SEQUENCE 594 AA; 62297 MW; 9DD48B04B3A8EA2 CRC64;

Query Match 96.2%; Score 2260.5; DB 2; Length 594;
Best Local Similarity 97.4%; Pred. No. 1e-90;
Matches 447; Conservative 4; Mismatches 7; Indels 1; Gaps 1;
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Db 496 VTNNVQLGVGNLNNHIDNDGNARAGIAQAIATAGVQVATLPKSMMAIGGTYRGEA 555
QY 423 GYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOM 461
Db 556 GYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOM 594

RESULT 10

Q9JPI3 PRELIMINARY; PRT; 594 AA.
ID 09JPI3
AC 09JPI3: 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, last annotation update)
GN Outer membrane protein GNA92.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88, and B232;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL: AF226376; AAF42525.1; -
DR EMBL: AF226369; AAF42518.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B90D0A4B6 CRC64;

Query Match 96.1%; Score 2257.5; DB 2; Length 594;

Best Local Similarity 97.4%; Pred. No. 1.4e-90;

Matches 447; Conservative 1; Mismatches 10; Indels 1; Gaps 1;

QY 4 TDLTSGTEKLSFSGANGKRVNTTSDTKGLNFAKTAGTNGDTTVHLNGISTLTPTLLNT 63
Db 136 TDLTSGTEKLSFSGANGKRVNTTSDTKGLNFAKTAGTNGDTTVHLNGISTLTPTLLNT 195
QY 64 GATTNVTNDNVTDDKKRAASVYKDVNLNAGWNIKGVKPGTTASDNDVFTYDTVEFLSAD 123
Db 196 GATTNVTNDNVTDDKKRAASVYKDVNLNAGWNIKGVKPGTTASDNDVFTYDTVEFLSAD 255
QY 124 TKTTVNVEKDKNGKTEVKIGAKTSVKEKDKGLVTGDKGENSSSTDEGEGLYTAKEV 183
Db 256 TKTTVNVEKDKNGKTEVKIGAKTSVKEKDKGLVTGDKGENSSSTDEGEGLYTAKEV 315
QY 184 IDAVKAKGRMKTTFANGOTGADKFEVTSCTNTTFASGKTATVSKDDOGNTTMYD 243
Db 316 IDAVKAKGRMKTTFANGOTGADKFEVTSCTNTTFASGKTATVSKDDOGNTTMYD 375
QY 244 VAVGALVNNQLONSGWNLDKSKAVAGSSGKVTSGNVSPSKGMDFTVINAGNNIEITRN 303
Db 376 VAVGALVNNQLONSGWNLDKSKAVAGSSGKVTSGNVSPSKGMDFTVINAGNNIEITRN 435
QY 304 GKNIDIATSMTPQFSSVSLGAGADAPTLSDVGD -ALNVGSKKDNKPVRTTNVAPGVKEGD 362
Db 436 GKNIDIATSMTPQFSSVSLGAGADAPTLSDVGD -ALNVGSKKDNKPVRTTNVAPGVKEGD 495
QY 423 VTNNVQLGVGNLNNHIDNDGNARAGIAQAIATAGVQVATLPKSMMAIGGTYRGEA 422
Db 496 VTNNVQLGVGNLNNHIDNDGNARAGIAQAIATAGVQVATLPKSMMAIGGTYRGEA 555

QY 423 GYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOM 461
Db 556 GYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOM 594

RESULT 11

Q9JPS2 PRELIMINARY; PRT; 594 AA.
ID 09JPS2
AC 09JPS2: 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, last annotation update)
GN Outer membrane protein GNA92.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE31;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL: AF226379; AAF42528.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 96.1%; Score 2257.5; DB 2; Length 594;

Best Local Similarity 97.4%; Pred. No. 1.4e-90;

Matches 447; Conservative 1; Mismatches 10; Indels 1; Gaps 1;

QY 4 TDLTSGTEKLSFSGANGKRVNTTSDTKGLNFAKTAGTNGDTTVHLNGISTLTPTLLNT 63
Db 136 TDLTSGTEKLSFSGANGKRVNTTSDTKGLNFAKTAGTNGDTTVHLNGISTLTPTLLNT 195
QY 64 GATTNVTNDNVTDDKKRAASVYKDVNLNAGWNIKGVKPGTTASDNDVFTYDTVEFLSAD 123
Db 196 GATTNVTNDNVTDDKKRAASVYKDVNLNAGWNIKGVKPGTTASDNDVFTYDTVEFLSAD 255
QY 124 TKTTVNVEKDKNGKTEVKIGAKTSVKEKDKGLVTGDKGENSSSTDEGEGLYTAKEV 183
Db 256 TKTTVNVEKDKNGKTEVKIGAKTSVKEKDKGLVTGDKGENSSSTDEGEGLYTAKEV 315
QY 184 IDAVKAKGRMKTTFANGOTGADKFEVTSCTNTTFASGKTATVSKDDOGNTTMYD 243
Db 316 IDAVKAKGRMKTTFANGOTGADKFEVTSCTNTTFASGKTATVSKDDOGNTTMYD 375
QY 244 VAVGALVNNQLONSGWNLDKSKAVAGSSGKVTSGNVSPSKGMDFTVINAGNNIEITRN 303
Db 376 VAVGALVNNQLONSGWNLDKSKAVAGSSGKVTSGNVSPSKGMDFTVINAGNNIEITRN 435
QY 304 GKNIDIATSMTPQFSSVSLGAGADAPTLSDVGD -ALNVGSKKDNKPVRTTNVAPGVKEGD 362
Db 436 GKNIDIATSMTPQFSSVSLGAGADAPTLSDVGD -ALNVGSKKDNKPVRTTNVAPGVKEGD 495
QY 363 VTNNVQLGVGNLNNHIDNDGNARAGIAQAIATAGVQVATLPKSMMAIGGTYRGEA 422
Db 496 VTNNVQLGVGNLNNHIDNDGNARAGIAQAIATAGVQVATLPKSMMAIGGTYRGEA 555
QY 423 GYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOM 461
Db 556 GYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOM 594

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RESULT 12
Q9JPR8      PRELIMINARY;      PRT;      599 AA.
AC Q9JPR8;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992 (Nhha outer membrane protein).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH38;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scariato V., Masiagnan V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H38;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF226383; AAF42532.1; -.
DR EMBL: AF157608; AAK68869.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 599 AA; 62844 MW; BBA16BFF53C1970C CRC64;

Query Match      96.1%; Score 2257.5; DB 2; Length 599;
Best Local Similarity 97.4%; Pred. NO. 1.4e-90;
Matches 447; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 4 TDLTSGTEKLSFSAANGKYNITSDPKGLNPAKETAGTNDTTHVHLNGISLTLDLLNT 63
DB 141 TDLTSGTEKLSFGANGKNKYNITSDPKGLNPAKETAGTNDTTHVHLNGISLTLDLLNT 200
QY 64 GATTNTVNDVTDDEKRAASVYKDVNLNAGNNIKGVKPGTASDVNDVFRVYDVEFLSAD 123
DB 201 GATTNTVNDVTDDEKRAASVYKDVNLNAGNNIKGVKPGTASDVNDVFRVYDVEFLSAD 260
QY 124 TKTTTVNESKDKNGKTEVYKIGAKTSYIKERDGLVTKDGKENGSTDEEGGLVTAKEV 183
DB 261 TKTTTVNESKDKNGKTEVYKIGAKTSYIKERDGLVTKDGKENGSTDEEGGLVTAKEV 320
QY 184 IDAVNKGWRRMKTATTAGGOTGADKFEFTVSGTNVTFASGKTATVSKDQGNITVYKD 243
DB 321 IDAVNKGWRRMKTATTAGGOTGADKFEFTVSGTNVTFASGKTATVSKDQGNITVYKD 380
QY 244 VNVGDALNVNQLNSGNLNDLSKAVAGSSGKVISGNVSPSKGKDEYNINAGNNIEITRN 303
DB 381 VNVGDALNVNQLNSGNLNDLSKAVAGSSGKVISGNVSPSKGKDEYNINAGNNIEITRN 440
QY 304 GKNIIDATSMTPQFSSVSLGAGADAPTLSDVG--DALNVGSKDKKPKVRIITNVAAGVEGD 362
DB 441 GKNIIDATSMTPQFSSVSLGAGADAPTLSDVGKALNVGSKDKKPKVRIITNVAAGVEGD 500
QY 363 VTNVAOLKGVNOLNNRINDVGNARAGIAQATATAGLVAAYLPKGSMAIIGGTYNGEA 422
DB 501 VTNVAOLKGVNOLNNRINDVGNARAGIAQATATAGLVAAYLPKGSMAIIGGTYNGEA 560
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QY 423 GYALGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 461
DB 561 GYALGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 599

RESULT 13
Q9JPH7      PRELIMINARY;      PRT;      594 AA.
AC Q9JPH7;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992 (Nhha outer membrane protein).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B2198; and 297-0;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scariato V., Masiagnan V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=B2198;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF226368; AAF42517.1; -.
DR EMBL: AF226358; AAF42507.1; -.
DR EMBL: AF157604; AAK68865.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62361 MW; 436BDEDE68263C5C CRC64;

Query Match      95.7%; Score 2248.5; DB 2; Length 594;
Best Local Similarity 97.2%; Pred. NO. 3.4e-90;
Matches 446; Conservative 1; Mismatches 11; Indels 1; Gaps 1;

QY 4 TDLTSGTEKLSFSAANGKYNITSDPKGLNPAKETAGTNDTTHVHLNGISLTLDLLNT 63
DB 136 TDLTSGTEKLSFGANGKNKYNITSDPKGLNPAKETAGTNDTTHVHLNGISLTLDLLNT 195
QY 64 GATTNTVNDVTDDEKRAASVYKDVNLNAGNNIKGVKPGTASDVNDVFRVYDVEFLSAD 123
DB 196 GATTNTVNDVTDDEKRAASVYKDVNLNAGNNIKGVKPGTASDVNDVFRVYDVEFLSAD 255
QY 124 TKTTTVNESKDKNGKTEVYKIGAKTSYIKERDGLVTKDGKENGSTDEEGGLVTAKEV 183
DB 256 TKTTTVNESKDKNGKTEVYKIGAKTSYIKERDGLVTKDGKENGSTDEEGGLVTAKEV 315
QY 184 IDAVNKGWRRMKTATTAGGOTGADKFEFTVSGTNVTFASGKTATVSKDQGNITVYKD 243
DB 316 IDAVNKGWRRMKTATTAGGOTGADKFEFTVSGTNVTFASGKTATVSKDQGNITVYKD 375
QY 244 VNVGDALNVNQLNSGNLNDLSKAVAGSSGKVISGNVSPSKGKDEYNINAGNNIEITRN 303
DB 376 VNVGDALNVNQLNSGNLNDLSKAVAGSSGKVISGNVSPSKGKDEYNINAGNNIEITRN 435
QY 304 GKNIIDATSMTPQFSSVSLGAGADAPTLSDVG--ALNVGSKDKKPKVRIITNVAAGVEGD 362
DB 436 GKNIIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDKKPKVRIITNVAAGVEGD 495
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OY 363 VTNAQLKGVAONLNLRIDNDGNARAGIAAIAATAGLVOAYLPKSKMAAIGCGTYRGEA 422
 DB 496 VTNAQLKGVAONLNLRIDNDGNARAGIAAIAATAGLVOAYLPKSKMAAIGCGTYRGEA 555
 OY 423 GYALGYSSISDGGNNIITGTASGNSRGHFGASASVGYOM 461
 DB 556 GYALGYSSISDGGNNIITGTASGNSRGHFGASASVGYOM 594

RESULT 14

O9JPR9 PRELIMINARY: PRT: 598 AA.
 AC O9JPR9: 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Outer membrane protein GNA992.
 GN GNA992.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NGH36;
 RX MEDLINE=20175756; PubMed=10710308;
 RA Piza M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
 RA Brocker M., Hundi E., Knapp B., Blair E., Mason T., Tettein H.,
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
 RA Moxon E.R., Grandi G., Rappuoli R.;
 RT "Identification of Vaccine Candidates Against Serogroup B
 Meningococcus by Whole-genome Sequencing.";
 RL Science 287:1816-1820(2000).
 DR EMBL: AF226382; AAF42531.1; -.
 DR InterPro: IPR005594; Yada.
 DR Pfam: PF03895; Yada; 1.
 SQ SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;

Query Match 95.7%; Score 2248.5; DB 2: Length 598;
 Best Local Similarity 97.2%; Pred. No. 3.4e-90;
 Matches 446; Conservative 1; Mismatches 11; Indels 1; Gaps 1;

OY 4 TDLTSGTEKLSFSANGKKNVITSDTKGNFAKETAGTNGDTTVLNLGISTLTPTLLNT 63
 DB 140 TDLTSGTEKLSFSANGKKNVITSDTKGNFAKETAGTNGDTTVLNLGISTLTPTLLNT 199
 OY 64 GATTNVTNDVYTDDEKRAASVKDYLNAGWNKGVKPGTTASDNVDFRTYDTVEFLSAD 123
 DB 200 GATTNVTNDVYTDDEKRAASVKDYLNAGWNKGVKPGTTASDNVDFRTYDTVEFLSAD 259
 OY 124 TKTITVNESKDNKKTVEKIGAKTSVIREKDKLVTKGKGENSSSTDEGGLVTAKEV 183
 DB 260 TKTITVNESKDNKKTVEKIGAKTSVIREKDKLVTKGKGENSSSTDEGGLVTAKEV 319
 OY 184 IDAVNKAQWRKKTITTAANGOTGADKFEFVTSCTNTVTFASGKGTATVSKDDOGNTTAYD 243
 DB 320 IDAVNKAQWRKKTITTAANGOTGADKFEFVTSCTNTVTFASGKGTATVSKDDOGNTTAYD 379
 OY 244 VNVGALVNVNOLONGSNWLDKRAVAGSSGKYISGNVSPSKGMDTVINNGNNIEITRN 303
 DB 380 VNVGALVNVNOLONGSNWLDKRAVAGSSGKYISGNVSPSKGMDTVINNGNNIEITRN 439
 OY 304 GKNIDIATSMTPPESSVSLGAGADAPTLSDVDG-ALNVGSKKDNKPVRTITNAPGVKESD 362
 DB 440 GKNIDIATSMTPPESSVSLGAGADAPTLSDVDGALNVGSKKDNKPVRTITNAPGVKESD 499
 OY 363 VTNAQLKGVAONLNLRIDNDGNARAGIAAIAATAGLVOAYLPKSKMAAIGCGTYRGEA 422
 DB 500 VTNAQLKGVAONLNLRIDNDGNARAGIAAIAATAGLVOAYLPKSKMAAIGCGTYRGEA 559

OY 423 GYALGYSSISDGGNNIITGTASGNSRGHFGASASVGYOM 461
 DB 560 GYALGYSSISDGGNNIITGTASGNSRGHFGASASVGYOM 598

RESULT 15

O9JPR9 PRELIMINARY: PRT: 592 AA.
 AC O9JPR9: 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Outer membrane protein GNA992.
 GN GNA992.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-860800;
 RX MEDLINE=20175756; PubMed=10710308;
 RA Piza M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
 RA Brocker M., Hundi E., Knapp B., Blair E., Mason T., Tettein H.,
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
 RA Moxon E.R., Grandi G., Rappuoli R.;
 RT "Identification of Vaccine Candidates Against Serogroup B
 Meningococcus by Whole-genome Sequencing.";
 RL Science 287:1816-1820(2000).
 DR EMBL: AF226382; AAF42510.1; -.
 DR InterPro: IPR005594; Yada.
 DR Pfam: PF03895; Yada; 1.
 SQ SEQUENCE 592 AA; 61917 MW; 4A3471514FDD3C879 CRC64;

Query Match 95.4%; Score 2241.5; DB 2: Length 592;
 Best Local Similarity 96.9%; Pred. No. 6.7e-90;
 Matches 445; Conservative 1; Mismatches 12; Indels 1; Gaps 1;

OY 4 TDLTSGTEKLSFSANGKKNVITSDTKGNFAKETAGTNGDTTVLNLGISTLTPTLLNT 63
 DB 134 TGLINVTETKLSFSGANGKKNVITSDTKGNFAKETAGTNGDTTVLNLGISTLTPTLLNT 193
 OY 64 GATTNVTNDVYTDDEKRAASVKDYLNAGWNKGVKPGTTASDNVDFRTYDTVEFLSAD 123
 DB 194 GATTNVTNDVYTDDEKRAASVKDYLNAGWNKGVKPGTTASDNVDFRTYDTVEFLSAD 253
 OY 124 TKTITVNESKDNKKTVEKIGAKTSVIREKDKLVTKGKGENSSSTDEGGLVTAKEV 183
 DB 254 TKTITVNESKDNKKTVEKIGAKTSVIREKDKLVTKGKGENSSSTDEGGLVTAKEV 313
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 DB 314 IDAVNKAQWRKKTITTAANGOTGADKFEFVTSCTNTVTFASGKGTATVSKDDOGNTTAYD 373
 OY 244 VNVGALVNVNOLONGSNWLDKRAVAGSSGKYISGNVSPSKGMDTVINNGNNIEITRN 303
 DB 374 VNVGALVNVNOLONGSNWLDKRAVAGSSGKYISGNVSPSKGMDTVINNGNNIEITRN 433
 OY 304 GKNIDIATSMTPPESSVSLGAGADAPTLSDVDG-DALNVGSKKDNKPVRTITNAPGVKESD 362
 DB 434 GKNIDIATSMTPPESSVSLGAGADAPTLSDVDGKALNVGSKKDNKPVRTITNAPGVKESD 493
 OY 363 VTNAQLKGVAONLNLRIDNDGNARAGIAAIAATAGLVOAYLPKSKMAAIGCGTYRGEA 422
 DB 494 VTNAQLKGVAONLNLRIDNDGNARAGIAAIAATAGLVOAYLPKSKMAAIGCGTYRGEA 553
 OY 423 GYALGYSSISDGGNNIITGTASGNSRGHFGASASVGYOM 461
 DB 554 GYALGYSSISDGGNNIITGTASGNSRGHFGASASVGYOM 592

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Job time : 35.8588 secs

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:06:20 ; Search time 7.11902 Seconds
(Without alignments)
3045.266 Million cell updates/sec

Title: US-09-771-382-35

Perfect score: 2350

Sequence: 1 NNCTDLSVGTERTKSPFANG.....TASGNSRGHGASVGYQW 461

Scoring table: BLOSUM62

Gapop 10.0 , Capext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	190.5	8.1	2003	YDBA_ECOLI	P3666 escherichia
2	181.5	7.7	1039	AG43_ECOLI	P39160 escherichia
3	179.5	7.6	2249	OMPA_RICRI	P15921 rickettsia
4	174	7.4	1577	HLVA_PROMI	P16466 proteus mir
5	170.5	7.3	1953	BIGA_SALTY	P25927 salmonella
6	170	7.2	933	SLAP_CAMEE	P35837 campylobact
7	168	7.1	1608	HLVA_SERMA	P15320 serratia ma
8	166.5	7.1	1654	OMPB_RICRI	Q33047 r outer mem
9	166	7.1	1567	ICEN_XANCT	P18127 xanthomonas
10	166	7.1	1655	OMPB_RICCN	Q9K843 r outer mem
11	165.5	7.0	1645	OMPB_RICTY	P36989 r outer mem
12	163.5	7.0	1025	SLAP_CANCR	P35828 caulobacter
13	163.5	7.0	1569	YDBA_ECOLI	P52143 escherichia
14	162	6.9	737	ALYS_ENTFA	P37710 enterococu
15	161.5	6.9	917	HXA3_HAEIN	P45355 haemophilus
16	161.5	6.9	1007	Y741_CHLMU	Q9J166 chlamydia m
17	161.5	6.9	1656	OMPB_RICJA	Q06653 r outer mem
18	161	6.9	550	FLIC_SHEFL	O08860 shigella fl
19	159.5	6.8	1300	120K_RICRI	P14914 rickettsia
20	158.5	6.7	1148	ICEN_PSESX	Q30611 pseudomonas
21	158	6.7	2021	OMPA_RICCN	O52677 rickettsia
22	156	6.6	497	FLIC_ECOLI	P09494 escherichia
23	155.5	6.6	928	PM10_CHLPN	O9R655 chlamydia p
24	155.5	6.6	1286	ALDA_ECOLI	O03155 escherichia
25	154.5	6.6	918	YMBJ_CAREL	P34467 caenorhabdi
26	153.5	6.5	2660	YEBJ_ECO57	O8X877 escherichia
27	152.5	6.5	1196	ICEN_PSESX	Q33479 pseudomonas
28	152	6.5	1643	OMPB_RICPR	O53020 r outer mem
29	151	6.4	642	FLIC_CAMEE	O06946 campylobact
30	150.5	6.4	507	FLIC_SALON	O06974 salmonella
31	150.5	6.4	537	TBE6_STRPY	P18481 streptococ
32	150.5	6.4	954	FLXY_CANCR	P15345 caulobacter
33	149	6.3	367	FLC2_PROMI	P42273 proteus mir

34	149	6.3	928	HXA2_HAEIN	P45354 haemophilus
35	149	6.3	948	HP11_DEIRA	P56867 deinococcus
36	148.5	6.3	507	FLIC_SALBE	O06968 salmonella
37	148.5	6.3	1396	VLTE_BPR5	P13390 bacterioph
38	148.5	6.3	2358	1YEBJ_ECOLI	P76347 escherichia
39	148	6.3	1325	YDEK_ECOLI	P32051 escherichia
40	147.5	6.3	1036	HP12_DEIRA	P13126 deinococcus
41	147.5	6.3	1200	ICEN_PSESY	P06620 pseudomonas
42	147	6.3	1005	Y456_CHLTR	O84462 chlamydia t
43	146.5	6.2	1150	APMU_PIG	P12021 sus scrofa
44	146.5	6.2	1153	PVDB_PLAKN	P50493 plasmodium
45	146.5	6.2	1210	ICEN_PSEFL	P09815 pseudomonas

ALIGNMENTS

RESULT 1
YDBA_ECOLI STANDARD; PRT; 2003 AA.
AC P3666: P76087; P76088; P76856; P76857; P76859;
DT 01-FEB-1994 (Rel. 28, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ydba.
GN YDBA OR B1401/B1405.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Kaba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Asai H., Kashimoto K., Kimura S., Kitkawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Sempel G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 464-2003 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92190338; PubMed=1665988;
RA Moszer I., Glasner P., Danchin A.;
RT "Multiple IS insertion sequences near the replication terminus in
Escherichia coli K-12.";
RL Biochimie 73:1361-1374(1991).
CC -!- SIMILARITY: TO S.TYPHIMURUM ORF NEAR CYSG (AC P25928).
CC -!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION. THE GENE CODING FOR
THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT
BETWEEN AMINO ACIDS 839 AND 840.
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CC -----
DR EMBL; AE000237; AAC74483.1; ALT_SEQ.
DR EMBL; AE000237; AAC74487.1; ALT_SEQ.
DR EMBL; D90778; BAA15009.1; ALT_SEQ.
DR EMBL; D90778; BAA18880.1; ALT_SEQ.
DR EMBL; D90779; BAA18881.1; ALT_SEQ.
DR EMBL; X62680; -; NOT_ANNOTATED_CDS.
DR Ecocore; EG11307; ydbA.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 489 I -> V (IN REF. 2).
FT CONFLICT 495 I -> V (IN REF. 2).
SQ SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220DE CRC64;

Query Match      8.1%; Score 190.5; DB 1; Length 2003;
Best Local Similarity 24.0%; Pred. No. 0.016;
Matches 135; Conservative 66; Mismatches 201; Indels 160; Gaps 31;

QY 1 NNETDLTSTGTEKLSAANKVNITSDTKGLNFAKETAGTNGDTVHLNG-----IG 53
DB 276 DNKGTVTVDPSMGSIQIDGKAIYNN-----GESTITNGTGTQINGDATTANNNG 328
QY 54 STLTDLTLTGATTNTYNTDDEKKRAASVYKVDVLMAGNKGKVPKGTASDNVDFVFT 113
DB 329 KTYVDGKSDTGTETINNNKVIOD-----GDLVSGGGHGT-DITGDSATVDNKGTMV 381
QY 114 YDTVEF-LSADRTTNNVESKD-----NGKTEVKIGAKTSVKEKGLVTG 161
DB 382 TDPESIGIQVDGQAVVNNEGESALTNGGTQIINGDDATTANNNGKTV---DGKDSYG 437
QY 162 KD-KGNG-----STDEEGELVTAK-----VIDA-----VN 188
DB 438 TTAGNNGKVIODGDLDVSGGGHGTIDTSDSATVDKGTPTVTPDPESIGIQIDGQAVN 497
QY 189 KAGWRKTTTANGGOTGOADKFEVTSGTNTFASGKGTATVSKD-----CGNTVMYD 243
DB 498 NGG---ESTITNGGT-----TQINGNAT-ANNNGKTYVDGKSDTGTIRKINIGI--- 544
QY 244 VAVGDLNV-----NOLONGMN-LDSK-----AVAGSGKVIISGVNSPSKGMDETVNI 292
DB 545 VILDGSLTGTGAGHVENIGDNGTVNNKGDIVSDIGSLVINGEATVNSGTGVNS- 603
QY 293 NAGNNEITRNKNIDIASM-TPOPS-----SVSLGA-----GADAPILSVVG 335
DB 604 NEATGFSITNGSKVSLAGSMOVDGFTGVDLNGNNSVTLAKDLKVVGOKATGIVNSG 663
QY 336 DALNV---GSKKDNKPKVRIITNYA---PGV-----KEGDYTNVAKLGVAQN-LNNRI 380
DB 664 DANVTITGNVLDKKTADNMAEYFDPDSVGINVYGSNNVTLLDKLTVSDSEVTSRQ 723
QY 381 DNV-DGNARAGIQAATATAGLV-----QAYLPKSMMAIGGTYRGEAGYAI 426
DB 724 SNLFDGSAE-----KTSGLVYIGDNTVNMNGELIGEKNALADGSGVTSILPTGYSY 776
QY 427 -----GYSSISDGGNMIK 441
DB 777 TSVIVVSGSSVYLNLDGTTISG 798

```

RESULT 2

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AG43_ECOLI
ID AG43_ECOLI STANDARD; PRT; 1039 AA.
AC P39180; P75614; P7360; P97241; Q46771;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 43 precursor (AG43) (Fluffing protein).
GN FLU OR B2000.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.

```

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RC STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,
RA Sivasubram S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horiiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-ML 308-225;
RX Henderson I.R., Owen P.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PRELIMINARY SEQUENCE OF 53-78.
RC STRAIN-ML 308-225;
RX MEDLINE=89291704; PubMed=2661530;
RA Calfee P., Owen P.;
RT "Purification and N-terminal sequence of the alpha subunit of antigen
43, a unique protein complex associated with the outer membrane of
Escherichia coli.";
RL J. Bacteriol. 171:3634-3640(1989).
RN [5]
RP SEQUENCE OF 53-63.
RC STRAIN-K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
RN [6]
RP GENE NAME.
RX MEDLINE=97257509; PubMed=9103983;
RA Henderson I.R., Meenan M., Owen P.;
RT "Antigen 43, a phase-variable bipartite outer membrane protein,
determines colony morphology and autoaggregation in Escherichia coli
K-12.";
RL FEMS Microbiol. Lett. 149:115-120(1997).
CC -1- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION. MAY
FUNCTION AS AN ADHESIN.
CC -1- SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA
CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA
CHAIN).
CC -1- SIMILARITY: TO ADHESIN Aidi-I AND TO BORETELLA PERTACTIN.
CC
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CC
CC EMBL; AE000291; AAC75061.1; ALT_INIT.
CC EMBL; D90838; BAA15825.1; ALT_INIT.
CC EMBL; D90839; BAA15832.1; ALT_INIT.
CC EMBL; U24429; AAB47869.1; -
CC HSSP; P07505; ISRD.
CC Ecocore; EG12686; flu.

```

DR InterPro: IPR006315; Autotransporter.
 DR InterPro: IPR005546; Autotransporter.
 DR Pfam: PF03797; Autotransporter; 1.
 DR Pfam: PF03212; Pertactin; 1.
 DR TIGRFAMs: TIGR01414; autotrans_bar1; 1.
 DR Outer membrane: Signal; Complete proteome.

FT SIGNAL 1 52
 FT CHAIN 53 551
 FT VARIANT 552 1039
 FT VARIANT 2 2
 FT VARIANT 41 42
 FT VARIANT 46 46
 FT VARIANT 157 157
 FT VARIANT 188 188
 FT VARIANT 303 303
 FT VARIANT 320 320
 FT VARIANT 372 372
 FT VARIANT 493 493
 FT VARIANT 497 497
 FT VARIANT 585 585
 FT VARIANT 709 709
 FT VARIANT 721 721
 FT VARIANT 751 753
 FT VARIANT 803 803
 FT VARIANT 815 815
 FT VARIANT 824 824
 FT VARIANT 829 835
 FT VARIANT 845 847
 FT VARIANT 855 855
 FT VARIANT 888 888
 FT VARIANT 1025 1025
 FT CONFLICT 61 63
 SQ SEQUENCE 1039 AA: 106841 MW: 51706478CDEB80 CRC64;
 ANTI GEN 43 ALPHA CHAIN.
 ANTIGEN 43 BETA CHAIN.
 K -> N (IN STRAIN ML 308-225).
 SL -> FE (IN STRAIN ML 308-225).
 T -> K (IN STRAIN ML 308-225).
 W -> L (IN STRAIN ML 308-225).
 V -> F (IN STRAIN ML 308-225).
 ATN -> STI (IN STRAIN ML 308-225).
 A -> T (IN STRAIN ML 308-225).
 N -> Q (IN STRAIN ML 308-225).
 E -> V (IN STRAIN ML 308-225).
 S -> N (IN STRAIN ML 308-225).
 H -> Y (IN STRAIN ML 308-225).
 E -> K (IN STRAIN ML 308-225).
 M -> T (IN STRAIN ML 308-225).
 GHL -> SHF (IN STRAIN ML 308-225).
 S -> P (IN STRAIN ML 308-225).
 A -> V (IN STRAIN ML 308-225).
 C -> S (IN STRAIN ML 308-225).
 LNLVHTS -> MNLITNA (IN STRAIN ML 308-225).
 QGT -> LGA (IN STRAIN ML 308-225).
 S -> T (IN STRAIN ML 308-225).
 Q -> L (IN STRAIN ML 308-225).
 S -> I (IN STRAIN ML 308-225).
 ETW -> TTT (IN REF. 5).
 LNTVHTS -> MNLITNA (IN STRAIN ML 308-225).

Query Match 7.7% Score 181.5; DB 1; Length 1039;
 Best Local Similarity 24.7%; Pred. No. 0.022;
 Matches 112; Conservative 63; Mismatches 146; Indels 133; Gaps 30;

QY 37 ETAGNDTTHLNGI-----GSTLDTLNTAGTAVT---TNDNTDDEK---KRAAS 84
 DB 105 QDGTAKNTTYTSGGLRVNPGSGVSDTVASGGOSLOGRAVNTTLNGSGOMNHEGAIA 164
 QY 85 VKDVLN-AGWNKIKVKKGTASDNVDFVRT-----YDVTEPISADKKTETVNES 133
 DB 165 TGTVINDKGMVY--VKEGTAVDTV--VNTGAEGRPAENGDTGFQFRGDAVRTTN--- 217
 QY 134 KDNCKTEVKIG-AKTSVIEKDKLVTKDKGENSGSTDE---GEGLV---TAKVI 184
 DB 218 -KNGRQIVRAEGTANTTVV-----YAGGDQVTHGHALDITTLNGVQYVANGGTASDVT 269
 QY 185 DAVKAKGRM-----KTTTANGQTGQADKEFTVTSQNTVFRASG---KGTATVYSKD 233
 DB 270 --VNSDMQVTKKNGVAGNTTVN--OKGRL--QVDAGTATNTTLKOGGALVYSTAATV-- 323
 QY 234 DQG-NITVMDVYVNDALNVLNQLNSGMNLSKRAVASSSGVSSGIVSSSPSKKMDERYNI 292
 DB 324 --GINRLGAFSVYCKADNV--VLENGG-RLD-----VLTGHATN-----TRV 362
 QY 293 NAGNNIEITRNGKNIDATSMTPOFSSVSLGAGADAPLTVSDGALNVGSKDKRPVRI 352
 DB 363 DDGGTLDV-RNG-----GTATV-----VSMNGG--VLLADSGAAYSGTSDSK----- 403
 QY 353 NVAPGVEGDTYVNAQLKVAQNLNNRIDVNDGNARAGIAQITAGLVQAYLPDKSMA 412
 DB 404 --AFSISGGQADALMLKSGSFTLN-----AGDTATDTT----- 435
 QY 413 IGGGTVEAGVAYGYSISDPGMMITKSTASGN 446
 DB 436 VNGSLFTARGSTLAGTTTLNNGALITLISGKTVNN 469

RESULT 3

OMP A_RICRI STANDARD: PRT: 2249 AA.

AC P15921;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (rOmpA) (rOmp A).
 GN OMPA.
 OS Rickettsia rickettsii.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 CC Bacteriataceae; Rickettsiaceae; Rickettsia.

OX NCBI_TaxID=783;
 RM [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R;
 RX MEDLINE=90354033; PubMed=2117568;
 RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;
 RT "A protective protein antigen of Rickettsia rickettsii has tandemly repeated, near-identical sequences.";
 RL Infect. Immun. 58:2760-2769(1990).
 CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.
 CC -1- PM: GLYCOSYLATED (PROBABLE).
 CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP B FAMILY.

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 CC -----
 CC EMBL: M31227; AAA26380.1; -.
 DR PIR: A41477; A41477.
 DR InterPro: IPR006315; Autotransporter.
 DR InterPro: IPR005546; Autotransporter.
 DR Pfam: PF03797; Autotransporter; 1.
 DR TIGRFAMs: TIGR01414; autotrans_bar1; 3.
 KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.
 FT SIGNAL 1 28
 FT CHAIN 29 2249
 FT DOMAIN 212 1180
 FT REPEAT 212 286
 FT REPEAT 287 358
 FT REPEAT 359 430
 FT REPEAT 431 505
 FT REPEAT 506 577
 FT REPEAT 578 652
 FT REPEAT 653 724
 FT REPEAT 725 799
 FT REPEAT 800 874
 FT REPEAT 875 949
 FT REPEAT 950 1021
 FT REPEAT 1022 1093
 FT REPEAT 1094 1165
 FT REPEAT 1166 1180
 SQ SEQUENCE 2249 AA: 224333 MW: A9D6646C089DF087 CRC64;
 TYPE I (INCOMPLETE).
 TYPE I (INCOMPLETE).

Query Match 7.6% Score 179.5; DB 1; Length 2249;
 Best Local Similarity 24.4%; Pred. No. 0.067;
 Matches 138; Conservative 45; Mismatches 201; Indels 181; Gaps 28;

QY 1 NNETDLISVTEKEKISFSAKKNVITSD---TKGLNFAKETAGTN-----GDTVHLN 50
 DB 776 DNTTGDNVGVNLN-----NGALSOVYTGIDIGNTSLATISVAGTATIGAVYKATTTKLT 831
 QY 51 GIGSTLDTTLN---TGATTNVT--NDNV----- 74
 DB 832 NAASVLTLLTNANAVLTGAVDNTTGGDNVGLNLGALSOVYTGIDIGNTSLATISVAGTA 891

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OY 75 -----TDEKKRAASVKDVLNAGMNIKGVPCPTASDVNDFVRYDVEFLSADRK 125
DB 892 TIGGAVIKATTTKLTGNAASVLTLTNANAVLTGALDNTGDDNVGLNGLALSOVYTGIDIG 951
OY 126 TTTTVNESDNGKKTVEKIGAKTSYKEKDGKLVYCKDKGENSSDDEBGLVTAKEVID 185
DB 952 NT-----NSLAT-ISVAGATATL-----GGAIVIKATTTT 978
OY 186 AVNKGAWRMKTTTANGOTGADKFEVTSCTVNTFASGKTATVATSKDOGNTTVADVN 245
DB 979 KLTDAASAVKFTNPVYVLTGALDNTGANNGI-VTFGNSSTVGNV-----GNTNALTATVN 1032
OY 246 VGDALNVNOLNSGMNLDKAVAGSSGKVISGNSVPSKGMDETVINAG-----NNIEI 300
DB 1033 VGAGL--LQVGGGVVAKNTINLTNDASAVTFNPVYVLTGALDNTGANNGIYVTFGNSSTV 1090
OY 301 TENGKRIIDATSMTPQFSSVSLGAGADAPTLVSDAL--NGSKDN-KPARITVAVG 357
DB 1091 TGNVGN-----TNALATVNVAG--LLOVGGGVVAKNTINLTNDASAVTFN--PV 1137
OY 358 VKEGDTVNAVOLKGVANLNRIIDVGNARA-----GIAQATAT--AGL-VQAVLPGR 408
DB 1138 VVTGALDNTG-----NANNGLVTFGTGNTVGTGIDGNTNALTATVAVGAGITLQA--GG 1187
OY 409 SMAA-----IGGTYRGEAGYAIGY--SSISDGNMIIK-----440
DB 1188 SLAANNIDFGARSTLEFNGPLDGG-----GKAIPYFKGALANGNALLNVTKLTFTAS 1241
OY 441 ----GASGNSRGH--FGASASVG 458
DB 1242 HLTGTVAEINIGAGLFTIDASVG 1266

RESULT 4
HLXA_PROMI STANDARD: PRT: 1577 AA.
AC P16466;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN HPMA.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.
RC STRAIN-ISOLATE 477-12;
RX MEDLINE=90170827; PubMed=2407716;
RA Uphoff T.S., Welch R.A.;
RT "Nucleotide sequencing of the Proteus mirabilis calcium-independent
RT Serratia marcescens hemolysin genes (shla and shlb).";
RL J. Bacteriol. 172:1206-1216(1990).
CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
CC DEFINED.
CC -1- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM
CC ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA
CC REQUIRES HPMB FUNCTION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -1- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA
CC MAY BE RESPONSIBLE FOR PORE FORMATION.
CC -1- SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
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CC -----
CC EMBL: M30186; AA25657.1; -.
CC DR PIR: A35140; A35140.
CC KW Hemolysis; Toxin; Outer membrane; Signal.
CC FT SIGNAL 1 29
CC FT CHAIN 30 1577 HEMOLYSIN.
CC SQ SEQUENCE 1577 AA; 165869 MW; 175975E0C924BD29 CRC64;

Query Match 7.4%; Score 174; DB 1; Length 1577;
Best Local Similarity 21.4%; Pred No. 0.085;
Matches 126; Conservative 79; Mismatches 171; Indels 214; Gaps 32;

OY 7 TSVGTEKLSFSANGKNKNTSDTKGLNFA-----KETAGT-----N 42
DB 710 TSTETFEQANSTISGANVLDQAN-KDVTFFAGSDLKTTAGNASTIGDNVAVSTENKKQTQTN 768
OY 43 GDTTVH-----LNGIS-----TLTDLILNLTGATNTVND-----72
DB 769 TDTTISGFSYTGVDKVGSKADFOYDKQHTQTEVTKRNGSOTEVAGDILLTANKDLHE 828
OY 73 -----NVTDEKKRAASVKDVLNAGMNI-----KGKPG- 101
DB 829 GASHNVEGRKYQESGENIQLHAVNDSKTSKTDLSLVGIDVGNLDYGVTKPKKALIEDGV 888
OY 102 --TTASDNVDF--VETVDVEFLS--ADTKTTTVNE-----SKDNGKTEVKI 144
DB 889 NNTKPGNNITDLRKVTARDAIANLANLNLNLEFPNVGEVGIKGGGSOQSOTDSQAVSTSI 948
OY 145 GAKTSYIKRKDGKLVYCKDKGENSSDDEBGLVTAKEVIDA-VNKGARMKTTTANGOT 203
DB 949 NMGKIDI-DSNNKL--HDQGHYOSTQEGISLTANTHTSEATLDRHQTTFHEHKGGOI 1004
OY 204 GOADKEFEVTSCTNVTFA-SGKQTPA-----TVSKDQDGNITVYDVNVDGALNVOLQ 256
DB 1005 GVSTK-----TGSIDIVALKGEQTTDNALMETKAGSFTNSGDLSINVE-----NAH 1054
OY 257 NSGMNLDKAVAGSSGKVISGNSVPSKGMDETVINAGNIIETTR-----NG 304
DB 1055 YEGAGFDQAQ-----KGR--TV-INAGDILLAQATDTHSESGSNVNG 1093
OY 305 K-NIDIAITSMTPQFSSVSLGAGADAPTL--SYDGDALNVGSKDKKPAVITNAPRVKRG 361
DB 1094 SANLKVGT--TPE--SKDYGGGFNAGTTTHSKKQTTAKVGTITGSGIELNAGNLTLLQ 1149
OY 362 DVTVNAVOLKGVANLNRIID-----NVGDNARAGIAQ-----ATAAGLVQA 403
DB 1150 --THLSSBDIALNATNKYDLOSASSEHTEKGNLNSGVQAGFGKKMTDDASSVNL-----1204
OY 404 YLPKKSMAAIG-----GGTYRGEAGYAIGYSSISDGNMIIKGT 443
DB 1205 ----GSAQFAIGKQDEKSVSREGT-----INNSGNLTGINS 1238

RESULT 5
BICA_SALTY STANDARD: PRT: 1953 AA.
AC B25927; P25928; Q9XCQ3;
DT 01-MAY-1992 (Rel. 22, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative surface-exposed virulence protein biga precursor.
GN BICA OR STM3478.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AFCC 14028;
RA Stojiljkovic I., Valentine P., Hefron F.;
RT Salmonella typhimurium rfs homolog.
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
```


KW Cell wall; S-layer.
 SQ SEQUENCE 933 AA; 96757 MW; F88C729B4B5B1E9 CRC64;
 Query Match 7.2%; Score 170; DB 1; Length 933;
 Best Local Similarity 22.4%; Pred. No. 0.075;
 Matches 126; Conservative 64; Mismatches 217; Indels 156; Gaps 27;

DB 5 DLTSVTEKLSFSANGKNVNTSD-TKGLNFAKETAGT----- 41
 DB 288 DEVENGEYKGVENGLDIVSFATDASKSVN--ETTGTITTAFTAGTGKVDVACKISAL 345
 QY 42 --NGDTYHLNGIGSTLIDTLNLCATNTVINDNTD-----DEKKRA----- 83
 DB 346 TADSTSVNLATNTITLTSANMATSVNLKORQAKDATITTSAMOQKYNRRNRATITTS 405
 QY 84 -----SVKDVNLNAGNNIKGVKPGCTASDNVDFRTDVEFLSADTKRTTAVN--VEKSD 135
 DB 406 ATAVENLTVKATNALNGMDKLATVTLDNAALTAIDI-----KSASTLNLINSSV 458
 QY 136 NG-----KKTEVKGAKTSVIREK-----DGKLVTKDKGNGSSSTD 172
 DB 459 NGPKHLVSKRRYCKFRPAKVKLNTAATDQVTLKANATDNLSEFDSATKTSVTA 518
 QY 173 EGEG---LYTAKEVIDAVNKKGMKTTTAN-----GQTGQADKEFTVTSCTVTTAS 222
 DB 519 SSGSGTFLVKGAEVETLVN-----IDTTFANALOSVSGKTGQGGKF--SVKGTGDDKIE 572
 QY 223 GKGTATVSK--DDOGNITVMVDVNGDALNVNOLONGMNLDSKAVAG---SSGKVTSG 277
 DB 573 FVGTTLTGSIYDAPGNTITAKSKAALTANFTMIKNENVAISDAVATADLSSAFKNS 632
 QY 278 NVSPSKGMDETVNINANNIEITRNGN-----IDATSMTPQSSS 319
 DB 633 VIITTEKADPTTLTINKDQVINFPAADAGSVKLTVKLNVDYATMIVKIVYLDAAAKDN 692
 QY 320 VSLGAGAPPLTSDVG--DALNWS-KDKNKPVRTTNVAPGVKEDVTNV---AQL--- 369
 DB 693 IALGTAADKALVIDTGETIENITISLVKATSPETTANV-NAKLVDVTSIIIDGQITLG 751
 QY 370 -KGVANQNLNIDVNDGNA-RAGI---AQAIATAGLVQAYLPGKSMAIGGCTVGEAGY 424
 DB 752 HAGTAGTGYSKVSMIDALAKGLTFDASAI-TLG-----ANATIKGS----- 794
 QY 425 AIGYSSIS-DGANNIITKGTASGN 446
 DB 795 --GADSTIVKGNIVVDLVAGSD 815

RESULT 7
 HLTA_SERMA STANDARD: PRT; 1608 AA.
 AC P15320;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-NOV-1990 (Rel. 16, Last annotation update)
 DE Hemolysin precursor.
 GN SHLA.
 OS *Serratia marcescens*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Serratia.
 OX NCBI_Taxid=615;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
 RC STRAIN=SN8;
 RX MEDLINE=88257037; PubMed=3290200;
 RA Poole K., Schiebel E., Braun V. ;
 RT "Molecular characterization of the hemolysin determinant of *Serratia marcescens*,"
 RL J. Bacteriol. 170:3177-3188(1988).
 CC -i- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANS AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.
 CC -i- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM

CC ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA
 CC REQUIRES SHLB FUNCTION.
 CC -i- SUBCELLULAR LOCATION: Outer membrane.
 CC -i- SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
 CC -----
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 CC -----
 DR EMBL; M22618; AAA50323.1; -
 DR PIR; A28182; A28182.
 KW Hemolysis; Toxin; Outer membrane; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 1608 HEMOLYSIN.
 SQ SEQUENCE 1608 AA; 165078 MW; D69B476FE7DAD51 CRC64;

Query Match 7.1%; Score 168; DB 1; Length 1608;
 Best Local Similarity 22.3%; Pred. No. 0.18;
 Matches 125; Conservative 73; Mismatches 207; Indels 156; Gaps 27;

QY 1 NNEIDLSVTEKLSFSANGNK-VNIT-SDTKGLNFAKETAGTNGDTVHLNGIGSTLTD 58
 DB 558 SHASELTGSGTLRL-----NGOQGVITTSKARQGVGEVTA-TTGGLRLID-NALETVDK 611
 QY 59 TLLNLTGATNTVNDVNDDEKKRAASVKNVNLNAGNNIGVAPGTTASDNVDFVRYDVE 118
 DB 612 IDARTGFANITSSHKADNSYOSTASEL-----KSDTNLTVSHKADV 657
 QY 119 F-----LSADTKTTTAVN----- 132
 DB 658 IGSQVASGSELVSKEKTGINVKAERQONIDEKLTALTVNGYAKKAGDKOYRAGLRHEH 717
 QY 133 SKDNCKTEVYKIGAKTSVIREKDGKLVTKGRKGENGS--TDEGEGLVTAKEV--IDAVN 188
 DB 718 TRDSEKTRRTENSA--SSLGSGSVYKLAKEKVTESGKLVADKDGASVSGNKFVSLADD 775
 QY 189 KAGWEMKTTTANG--OTGOADKEFTVSGTNVFPASGKTATVSK-----DDOGNIT 239
 DB 776 KTASNTDQTKIGGGYTYTGIDK--LGGYVAGYEENK-TQOOSKAITSGSDVKGNLT 831
 QY 240 VMYDVNVDALNVNQLONGMNLDSKAVAGSSGKVISGNSVPSKGMDETVNINANNIE 299
 DB 832 ----INARDKLQOQAOHSGVGAQENAAVDHLAADPTASTTTTKTDVGVNI----- 880
 QY 300 ITRNGKNIDTASMTPOSSVSLG-----GADAPTLSDGDALNWSK--D 345
 DB 881 ---GANVDYSAVTRPVERAVGAKAKLDATGIVINDIGIGAPNVLGIDGAGGSSSEKRS 936
 QY 346 NKPVRTNVAVGV---KEGV---TNVAOLKGAQNLN-----NRIDVNDNA 387
 DB 937 SSQAVSSVQAGSIDINAKGEYRROGTQYQASKG-AVNLTLADSHRSEALNROBQSDYT 995
 QY 388 RAGIAQAIATAGLVQAYLPGKSMAIG---GTYRGEAGYAIGYSSISDGNW----- 437
 DB 996 R-----GSAG-VVVYTTTGSIDLVDKAGGCGTORSNSASQAVTGSIDAANGINVMK 1047
 QY 438 ---IKGTASGNSRKHFGASA 455
 DB 1048 KDAILYGTALNGRGKTAVNA 1068

RESULT 8
 OMPB_RICRI STANDARD: PRT; 1654 AA.
 AC O53047;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Outer membrane protein B precursor (168 kDa surface-layer protein)

[illegible]

Db 569 NGGTIKLT-STGNNIIVDFDLAIATPDQGVNDASSLTNAQFLTITNGKIGTIGANKTKLGQ 627D
 Qy 269 ---GSSGKYIS-GNV-----SSSKGMDETVAINNGNN 257
 Db 628 FNIGSSYVATNSGNVAINELVIGNDGAVOFAHDYLTITRTNAGQGKILFPNPNVNNGT 687
 Qy 298 IETTRNGKNIDATSMTPQFSSVSLGAGADAPTLTSDGDALNVSCKDKDNKPRIT ---N 353
 Db 688 LAA---GTNIGSATINPLAEINFGSGVNDT-----VNTVEGVNLTATNTTTIDAN 736
 Qy 354 VAAQVKEQEDVTNVAQLKGAQNINRIRIDVDCNARAGIAQAIATAGLQVAILPKSMAAI 413
 Db 737 VGSFEVNAAGTINIVS-GTVGGQGGKMFNTV-----ALENTTYKFL 776
 Qy 414 GGCTYRGEACYAIGYISIDSGGNMILKTGASNSRG 449
 Db 777 GNAIFNGNTTIAAN-STLDIGGNYTADCVASADGTG 811

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RESULT 9
ICEN_XANCT      STANDARD:      PRT: 1567 AA.
ID              ICEN_XANCT
AC              P18127;
DT              01-NOV-1990 (Rel. 16, Created)
DT              01-NOV-1990 (Rel. 16, Last sequence update)
DT              16-OCT-2001 (Rel. 40, Last annotation update)
DE              Ice nucleation protein.
GN              INAX.
OS              Xanthomonas campestris (pv. translucens).
OC              Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC              Xanthomonadaceae; Xanthomonas.
OX              NCBI_TaxID=343;
RN              [1]
RP              SEQUENCE FROM N.A.
RC              STRAIN=X56S;
RX              MEDLINE=91080859; PubMed=2259339;
RA              Zhao J., Orser C.S.;
RT              "Conserved repetition in the ice nucleation gene inax from
RT              Xanthomonas campestris pv. translucens.";
RL              Mol. Gen. Genet. 223:163-166(1990).
CC              -I- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
CC              CRYSTALLIZATION IN SUPERCOOLED WATER.
CC              -I- SUBCELLULAR LOCATION: Outer membrane (by similarity).
CC              -I- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
CC              OCTAPEPTIDE A-G-Y-G-S-T-T; FURTHER ON A 16-RESIDUE AND A
CC              REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
CC              -I- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE
CC              NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
CC              -I- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
CC              FAMILY.
CC              -----
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CC              at the European Bioinformatics Institute. There are no restrictions on its
CC              use by non-profit institutions as long as its content is in no way
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CC              -----
DR              EMBL: X52970; CAA37140.1; -.
DR              HSSP: P06620; IINA.
DR              InterPro: IPR0000258; Ice_nucleatn.
DR              Pfam: PF00818; Ice_nucleation; 81.
DR              PRINTS: PR00327; ICENUCLEATN.
DR              PROSITE: PS00314; ICE_NUCLEATION; 57.
KW              Ice nucleation; Repeat; Outer membrane.
SQ              SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;
Query Match          7.1%; Score 166; DB 1; Length 1567;
Best Local Similarity 20.9%; Pred. No. 0.22;
Matches 100; Conservative 69; Mismatches 222; Indels 88; Gaps 18;

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```
OY 15 SFSANGKNVNTSDTRKGLNFAKE-----TACTNEDTVHLNGISLT--DTLLN 62
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 832 STQTSGLSLAGYSTQTAREGSDVYAGYSTGTAGADSTLLISGYSTQTAGSDSLT 891
OY 63 TGAATNVTNDTDEKRRASVKNVLAAGNVIKGVKGTTSADVDFRTDYEFLLSA 122
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 892 AGYGSTQARAKSD-----VTAGYGSTG---TAGADSTLLAGYSTQTSQS 934
OY 123 DTKTTTVAVESKDNKKTTEVKIGAKTSYIKEDGLVTKDCKGNGSSTDEGEGLVPAKE 182
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 935 DSSLTLAGYSTQTARAKSDMTAGYSTGTAGADSTLLING-----YGSQTSS----- 982
OY 133 VIDAVNKGWRMKTTTANGQGTQADKFEYVSGTAVTRASGKGTATVSKDDQGNITVWY 242
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 983 --DSSLTLAGYSTQTAREGSDVYAGYSTGTAGADSTLLAGYGSTQTAGSD--SSLTAGY 1038
OY 243 DVNVDALNVNQLQNSGNLDSKAVAGSSGVYISGNVSPSKMDEYNINAGNMEITR 302
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1039 -----GSTQTARQGSVYTAGYGSTGTAGADSTLLIAGYSTQTARQSDSSLTLAGYGST-QTAR 1093
OY 303 NGKNIDVATSMTPQPSVSLGAGADAPTLVVDGDLNVGSKKDNKPVRTTNYAPGV--- 358
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1094 QGSDI-----TAGYGSTGT-AGADSSLTLAGYGSTQTAGYD-----SNLTAGYGSTQ 1138
OY 359 ---KGDVYVNAQLKGVAKQNLNRIQNDVGNARAGIQAIAIATA-GLVQAYLPFGKSMATG 414
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1139 TAREDSLTLAGYSTGTAGHDSLLTLAGYSTQTAGYNSLTITGYSTQTAGRESSLTAGY 1198
OY 415 GGTYSGEAGY---AIGYSSISDGG--NMILGTASGNSRGH-----FGASASVGVQ 460
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1199 GST--STAGYDSTLAGYGSTQTAGYKSTLTLAGYNSNSTAGHSSLLAGYGSTQIAGYE 1255

RESULT 10
OMP. R1CCN STANDARD: PRT: 1655 AA.
ID OMP. R1CCN STANDARD: PRT: 1655 AA.
AC Q9KKA3; Q9KKA9; Q9XC45;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scs5) (ompB)
DE (Romp B) [Contains: 120 kDa surface-exposed protein (surface protein
antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptidase].
GN OMPB OR RCI085.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OY NCBI_TaxId=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=2142074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RT Science 293:2093-2098(2001).
RN [2]
RP SEQUENCE OF 33-1649 FROM N.A.
RC STRAIN=Indian tick typhus, and Malish 7;
RX MEDLINE=20393643; PubMed=10939649;
RA Roux V., Raoult D.;
RT "Phylogenetic analysis of members of the genus Rickettsia using the
RT gene coding the outer-membrane protein rompB (ompB).";
RL Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
RN [3]
RP SEQUENCE OF 353-1655 FROM N.A.
RC STRAIN=Malish 7;
RA Stenos J., Walker D.;
RT "The rickettsial outer membrane protein A and B genes of Rickettsia
RT australis, the most divergent rickettsia of the spotted fever group.";
RL Submitted (May-1999) to the EMBL/GenBank/DBD databases.
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CC -I- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
CC SIMILARITY).
CC -I- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
CC (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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CC -----
DR EMBL: AE008659; AAL03623.1; -.
DR EMBL: AF123721; AAF34124.1; -.
DR EMBL: AF123726; AAF34129.1; -.
DR EMBL: AF149110; AAD39533.1; -.
DR PIR: E97835; E97835.
DR InterPro: IPR006315; Autotransport.
DR InterPro: IPR005346; Autotransporter.
DR Pfam: PF03797; Autotransporter.1.
DR TIGRFAMs: TIGR01414; autotrans_bar1.2.
KW Antigen; S-layer; Cell wall; Complete proteome.
FT CHAIN 1..1334 120 kDa SURFACE-EXPOSED PROTEIN.
FT 1335..1655 32 kDa BETA PEPTIDE.
FT 61..61 P -> A (IN STRAIN INDIAN TICK TYPHUS).
FT 75..75 V -> S (IN STRAIN INDIAN TICK TYPHUS).
FT 78..78 K -> N (IN STRAIN INDIAN TICK TYPHUS).
FT 251..251 V -> A (IN STRAIN INDIAN TICK TYPHUS).
FT 413..413 I -> D (IN STRAIN INDIAN TICK TYPHUS).
FT 959..959 I -> V (IN STRAIN INDIAN TICK TYPHUS).
FT 988..988 A -> T (IN STRAIN INDIAN TICK TYPHUS).
FT 1139..1139 R -> L (IN STRAIN INDIAN TICK TYPHUS).
FT 1139..1139 KD -> GH (IN REF. 3).
FT 353..354 E -> S (IN REF. 3).
FT 776..776 F -> D (IN REF. 3).
FT 1159..1159 G -> S (IN REF. 3).
FT 1177..1177 G -> S (IN REF. 3).
FT 1492..1492 H -> R (IN REF. 3).
SQ SEQUENCE 1655 AA; 168342 MW; E49E9377D5FCB37 CRC64;

Query Match 7.1%; Score 166; DB 1; Length 1655;
Best Local Similarity 23.6%; Pred. No. 0.23;
Matches 118; Conservative 57; Mismatches 230; Indels 94; Gaps 23;

OY 19 NGKNVNTSDTRKGLNFAKETAGTNGDTT-----VHLNGISLTLDLTLTGATNTVNDNV 74
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 340 NGKAVTIQGVYAKDMVIOASANAAGOVNFRHIVDVGDTGTAFKTAASVATLQNSNFGT 399
OY 75 TDDEKRRASVND---VINAGNINGVKPGCTASNDVFVRVYD---TYEFLSADTKTTTY 128
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 400 TDFGNLAQIIVPNTMTLNGNTGDASNGNTAG-----VTFEDNGTLTASASADANAV 454
OY 129 VN-----VESKDNQ-----KRTEVIGAKTSYIKEDGLVTKGDKG-----ENG 169
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 455 TNNITAIKASGAGVVOGSTHAELRLGAGSVFELADGTVINGKVNQATLVGALAGT 514
OY 170 STDEGEGLVTAKEVIDAVNKGWRMKTTTANGQGTQADKFEYV-----SGTNVTF 220
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 515 ILLDSATITG---DIGNAG-----AALQGITLTLANDATKTLTGANIIIGANGCTINE 566
OY 221 ASGKTITATVSKDDGDNITVMDV-----NVGALNVNQLQNSGNVINDSKAVAGSSGK 273
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 567 QANGSTIKTFS--TQNNIVVDFDLAIVDQGTGVASSLTNQTLLTNGKIGTVANNKT 624
OY 274 VISGNVSPSKGM-DETVNIN--AGNN--LEIFNKGKIIDATSMTPQ---FSSV--- 320
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 625 LGQFNIGSKTVLSGDVAIVNGLVGNNGAVQFAINTYLTITRTNAAGGKIIFNPVNN 684
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RT      crescentus paracrystalline surface layer protein.";
RL      Can. J. Microbiol. 38:193-202(1992).
RN
RP      [2]
RP      REVISIONS TO 376: 636 AND 842-843.
RA      Awram P.;
RL      Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN
RP      [3]
RP      SEQUENCE FROM N.A.
RA      Bingle W.H., Awram P.A., Nornellint J.F., Smit J.K.;
RT      "The secretion signal of C. crescentus S-layer protein is located in
RT      the C-terminal 82 amino acids of the molecule.";
RN
RP      [4]
RP      Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN
RP      SEQUENCE FROM N.A.
RA      MEDLINE-21173698; PubMed-11295647;
RC      STRAIN-ATCC 19089 / CB15;
RX      MEDLINE-21173698; PubMed-11295647;
RA      Niemman W.C., Feldblum T.V., Land M.T., Paulsen I.T., Nelson K.E.,
RA      Eisen V., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA      Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA      Deboy R.T., Dodson R.J., Durkin A.S., Gilm M.L., Haft D.H.,
RA      Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA      Utterback T., Tran K., Wolf A., Yamachyan J., Ermolaeva M., White O.,
RA      Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT      "Complete genome sequence of Caulobacter crescentus.";
RL      Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
RN
RP      [5]
RP      SEQUENCE OF 1-313 FROM N.A., AND SEQUENCE OF 1-20.
RC      STRAIN-ATCC 19089 / CB15;
RX      MEDLINE-89008089; PubMed-3049545;
RA      Fisher J.A., Smit J.K., Agabian N.;
RT      "Transcriptional analysis of the major surface array gene of
RT      Caulobacter crescentus.";
RL      J. Bacteriol. 170:4706-4713(1988).
RN
RP      [6]
RP      CHARACTERIZATION.
RC      STRAIN-ATCC 19089 / CB15;
RX      MEDLINE-98292737; PubMed-9620954;
RA      Awram P., Smit J.K.;
RT      "The Caulobacter crescentus paracrystalline S-layer protein is
RT      secreted by an ABC transporter (type I) secretion apparatus.";
RL      J. Bacteriol. 180:3062-3069(1998).
RN
RP      -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
RT      OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. PROBABLY ACTS AS A
RT      PHYSICAL BARRIER TO PARASITES AND LYTIC ENZYMES.
RN
RP      -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
RT      LAYER WITH HEXAGONAL SYMMETRY. SECRETED BY AN ABC TRANSPORTER
RT      (TYPE I) SECRETION APPARATUS.
RN
RP      -1- MISCELLANEOUS: THE CALCIUM BINDING OF THIS PROTEIN MAY MEDIATE
RT      SURFACE ATTACHMENT BY IONIC BRIDGING BETWEEN THE S-LAYER AND A
RT      SPECIFIC MEMBRANE-ASSOCIATED OLIGOSACCHARIDE.
RN
RP      -----
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CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-slb.ch/announce/
CC      or send an email to license@isb-slb.ch).
CC
CC      EMBL; AF062345; AAC38665.2; -
CC      EMBL; AF193063; AAF19365.1; -
CC      EMBL; AE005779; AAK22991.1; ALT_INIT.
CC      PIR; A48995; A48995.
CC      HSSP; P22629; ISMC.
CC      TIGR; CC1007; -
CC      InterPro; IPR001343; HemlYsn_Ca_bind.
CC      Pfam; PF00353; hemlYsnCbind; 3.
CC      PRINTS; PR00313; CABNDNGRPF.
CC      Cell wall, S-layer, Calcium-binding; Complete proteome.
CC      INT. MET.
CC      SEQUENCE 1025 AA; 96001 MW; AD7A326E1363DBAC CRC64;

```

Query Match	7.0%;	Score 163.5;	DB 1;	Length 1025;
Best Local Similarity	23.8%;	Pred. No. 0.18;		
Matches	129;	Conservative	63;	Mismatches 199; Indels 153; Gaps 26
QY	8	SVCTEKLSFSAN-----GKNVITSDPTKGLNFAKETAGTNGDTTVHLN	50	
Db	254	TTGTDTLTGTANNNDPTFVAGEVAGATLTIVGDTLSCGACTDVLNWWQAALVTLPTGVTL	313	
QY	51	GI-----GSTLT-----DTLNT---GATTNT---NDNVTDEKKRAASVDV	88	
Db	314	GIEITMNVYSGAAILINTSSGVTGLTALNTNPGAQVYTAGAGONLTTTAAQAN-NVA	372	
QY	89	LNAGMNI-----KGVKPGFTASDNDVFTYDPTVEFLSDFTKTTVNVASKDKKTEVK	144	
Db	373	VDBGANVTVASTGVTSGIT-----TVCANSAAGTIVSVANSSSTTTGAILAV	420	
QY	145	GAKTSV-IKEKDKLV---TGKDKGENSSTDEG-----EGLVTAKEVIDAVNK	189	
Db	421	TGGTAIVTAQVAGANVNTLTQADVTVYVNGSSTTAVTVTQPAANTAGATVAGRVGAVT-	479	
QY	190	AGFMKKTITANGQIGQADKFTVYSG-----TNYTFASGKTITATVSKDDGDN	237	
Db	480	-----ITDSSAASATTAAGIKATVTLGSGAATIDSSALTTVNL-SGCTSLIGIGR---GA	530	
QY	238	ITVWYDVNVGALVNWQNLQNSGMNLSKAAVAGS-----SGKVISGVNVPSPKGMDETV	290	
Db	531	LTATPTAT-LTLVNVNGLTITGALTDSAPAADGFTTININGSTASSTIASLVAADATTL	589	
QY	291	NINAGNNIEITRN-----GKNI-DIATSMTPQFSSVSGAGADAPTLSD	334	
Db	590	NISDARTITISHRAALTGITVNVSGATLGAELATPLV--FTG---GAGADSLILDAT	644	
QY	335	GDALVSGSKDKNKPVRITNVAPG--VKEGDTVNAQLKGVAONLNRIQNDV-----	384	
Db	645	TKAIVMAGAGDPTVYVSSATLGAAGSGVANGDGTDV-----LVA NVGSSFSADPARGFET	699	
QY	385	-----GNRAG-----IAQAITAGLVQ---AYLPCKSMALGGGTTCGEACATGY	428	
Db	700	LRVAGAAAGGSHNANGFTALQLGATAGATFTTNAVNVGLTAAPTGTTVTLANAGT	759	
QY	429	SSI 431		
Db	760	SDV 762		

RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
RA Oshima T., Oyama S., Saito N., Sampel G., Satoh Y., Sivasundaram S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horuchi T.;
RT "Construction of a continuous 874-kb sequence of the *Escherichia coli*
RT K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
CC -1- SUBCELLULAR LOCATION: Outer membrane (Potential).
CC -1- SIMILARITY: STRONG, TO BORDETELLA PERTACTIN.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U36840; AAA79815.1; ALT_SEQ.
DR EMBL: AE000350; AAC75695.1; -.
DR EMBL: D90889; BAA16514.1; ALT_INIT.
DR EMBL: D90890; BAA16518.1; ALT_INIT.
DR PIR: A65044; A65044.
DR Ecogene: EG13213; YPJA.
DR InterPro: IPR006315; Autotransport.
DR InterPro: IPR005546; Autotransporter.
DR InterPro: IPR004899; Pertactin.
DR InterPro: IPR003991; Pertactin_C.
DR Pfam: PF03797; Autotransporter; 1.
DR Pfam: PF03212; Pertactin; 1.
DR PRINTS: PR01484; PERTACTIN.FAMILY.
DR TIGRFAWS: TIGR01414; autotrans_bar1; 2.
DR Hypothetical protein. Outer membrane. Complete proteome.
KM SEQUENCE 1569 AA; 162774 MW; DD006A9A32154596 CRC64;
SQ
Query Match 7.0%; Score 163.5; DB 1; Length 1569;
Best Local Similarity 19.8%; Pred. No. 0.29;
Matches 95; Conservative 86; Mismatches 235; Indels 63; Gaps 17;
QY 1 NNETDLTSVTEKLSANGKNVNTSDPKGLNFAKETAGCTVHLNG----- 51
DB 410 NNTNTINGTONINNYGATGTNINSSTONIK-----SGGADTTIISSSROYEKDG 464
QY 52 --IGSTLT--DTLNTGATNTNDVNTDDEKKRAASKVDLNAQMNK--YKPGT 103
DB 465 TAIQSNTISAGSLIVTGGIAHGVN-----QETGSALVANT-GAETDIEGKLSHFTI 517
QY 104 ASDNDFVETPTVEFLSADFTKTTVNVESKDNKKTEVKGAKTSVIREKDKLTGKD 163
DB 518 TGGEANYVYLENTGE-LTVVAKTSAKNT-TIDTGGKLIYQKEKKTSTFLNNGVLEVD 575
QY 164 KEENSGSDEBEGLV---TAKEVIDAVNKAQ--WPKTTTANGQGTQADKEPTVSGTN 217
DB 576 GGEAKHVEQSGGALASTTSGTLIEGTNSYGPDAFIIRNSPEAKNVYLENAGSLTVYTGSR 635
QY 218 V--TPASGKGTATVSKD-----DQGNITVMDVNVGDLANVQNLQNSMNDLSKRVAS 270
DB 636 AVDTTIINANGKMDVYTGKDVGLNSAGTOTTASATSDAKNTKGGQIYVGLATEMNIES 695
QY 271 SGRVTSIGNVSPSKGKDEVTNINAGNNIEITFRNGKIDIDATSTPQSSVSLGAGADAPT 330
DB 696 GEGQIVDGGST-----EKTHINGNQ-TVQNYGKAIN--TIDVSLQIIMANGTAEESI 745
QY 331 LSYVDGDLNVGSKDKNRPRTNVAPGVKEGDTVNAQLKGYAQNINRINDVNGNARAG 390
DB 746 INGGSGVNVGGLAENSIVLNDGTLIDVREKSGATGIDQSSGALVATPATRTVYTRAG 805
QY 391 IQAATATAGLVQAYLPCKSMALIGGFTVGEAGVAYAGVSSISDGGWII--IGTASGNS 447
DB 806 VAFSTIEGQ-----ANNITLANGCVLTVESDTSDDKTVQVMNGGREIVKATATGTT 857

RESULT 14
ALYS_ENTFEA STANDARD; PRT; 737 AA.
AC P37710;
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Autolysin precursor (EC 3.2.1.1-) (Peptidoglycan hydrolase)
DE (Beta-glycosidase).
GN EF0799.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91358349; PubMed=1679432;
RA Bellevue C., Potvin C., Trudel J., Asselin A., Bellemare G.;
RT "Cloning, sequencing, and expression in *Escherichia coli* of a
RT Streptococcus faecalis autolysin.";
RL J. Bacteriol. 173:5619-5623(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
RA Daugherty S., Deboy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
RA Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
RA Ultebrack T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis.";
RL Science 299:2071-2074(2003).
CC -1- FUNCTION: Hydrolyzes the cell wall of *E. faecalis* and
CC M. lysodeikticus. May play an important role in cell wall growth
CC and cell separation.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- DOMAIN: LYSM REPEATS ARE THOUGHT TO BE INVOLVED IN PEPTIDGLYCAN
CC BINDING.
CC -1- SIMILARITY: BELONGS TO FAMILY 73 OF GLYCOSYL HYDROLASES.
CC -1- SIMILARITY: Contains 6 LysM repeats.
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CC -----
DR EMBL: M58002; AAA67325.1; -.
DR EMBL: AE016949; AAO80613.1; -.
DR PIR: A38109; A38109.
DR TIGR: EF0799;
DR InterPro: IPR002901; Amidase_4.
DR InterPro: IPR002482; LysM.
DR Pfam: PF01832; Amidase_4; 1.
DR Pfam: PF01476; LysM; 5.
DR SMART: SM00257; LysM; 6.
DR SMART: SM00047; Lys2; 1.
DR Hydrolase; Glycosidase; Bacteriolytic enzyme; Cell wall;
KM Cell division; Septation; Repeat; Signal.
FT SIGNAL 53
FT CHAIN 737
FT REPEAT 363
FT REPEAT 405
FT REPEAT 431
FT REPEAT 499
FT REPEAT 567
FT REPEAT 609
FT REPEAT 633
FT REPEAT 695
FT REPEAT 737
FT REPEAT 85
FT CONFLICT 118
A -> V (IN REF. 1).
A -> V (IN REF. 1).

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FT CONFLICT 143 143 A -> T (IN REF. 1).
FT CONFLICT 417 417 S -> N (IN REF. 1).
FT CONFLICT 449 449 S -> T (IN REF. 1).
FT CONFLICT 476 476 A -> T (IN REF. 1).
FT CONFLICT 484 484 N -> S (IN REF. 1).
FT CONFLICT 567 632 MISSING (IN REF. 1).
SQ SEQUENCE 737 AA; 77025 MW; ABB16BD506AC7507 CRC64;

Query Match
Best Local Similarity 6.9%; Score 162; DB 1; Length 737;
Matches 94; Conservative 47; Mismatches 182; Indels 80; Gaps 18;

OY 15 SFSANGKVNITSDTKLNF-----KETAGNGDTYVHLNGISGLTIDTLNTGATNTVT 70
DB 268 SFDONAHVLTSTSFQAGVYYAGAWKSNSTSSYRDATAVLT--GRAYDPSYNAKLNNVIT 325
OY 71 NDVNTDEKKRAASVKDVLNAGWNKIG--VKPGTASNDVDFVRY-----DIVEFLSA 122
DB 326 AVNLTQ-----YDPPSSGGNTGGTVPNPGTGSNNQSGTNTYTVKSGDTLNTAA 376
OY 123 DTKTTTVVESKDNKTEVKIKAKTSYIKKEDKLTVTGKDKGENGSSTDE-GEGLVTAK 181
DB 377 QYGVSVANLRSMNGISGLIFVGGKLYVKKASGN--TG-GSGSGSNNQSGTNTYTV 433
OY 182 EVIDAVNKAQWRMKTATTANGQTGADEFTVTSNTVTF--ASGK--GTTATVSKDDG 236
DB 434 KSGDTLNKIAQYGVSVANLRSMNGISGLIFVGGKLYVKKASGNQSGTNTYTVKSGDTLN 493
OY 237 NITWYDNDVGDALN-----VNOLONSGWNLDKSKANAGSSGYI-----SGNVSPSKG 284
DB 494 GTNTYTIKSGDTLNKIAQYGVSVANLRSMNGISGLIFVGGKLYVKKASGNQSGTNTYTV 552
OY 285 KMDETVINAGNNIEITPENGKINIDJANSMTPQSFSSVLGAGADAPTL-----SYDGDAL-- 338
DB 553 -----NGGSN--NNQSGTNTYTIKSGDTLNKISAQFGVSVANLQAMNNISGLIFA 602
OY 339 -----NVGSKDKPKPVRIITNVAFG-----YKGGDYTN 365
DB 603 GOKIIVKKGANGSGTNTNKP--TNNGGAVTSTYTIKSGDTLN 642

RESULT 15
HXK3_HAEIN STANDARD; PRT; 917 AA.
AC P45355;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Heme/hemopexin-binding protein precursor (Heme:hemopexin utilization
protein A).
GN HXUA.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NH1 N182;
RX MEDLINE=95115556; PubMed=7815944;
RA Cope L.D., Thomas S.E., Latimer J.L., Slaughter C.A.,
RA Mueller-Eberhard U., Hansen E.J.;
RA "The 100 kDa heme:hemopexin-binding protein of Haemophilus
RT influenzae: structure and localization.";
RL Mol. Microbiol. 13:863-873(1994).
CC -1- FUNCTION: BINDS HEME/HEMOPEXIN COMPLEXES.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -----
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CC -----
CC EMBL; U08349; AAA74139.1;
DR Transport; Signal; Repeat.
KM SIGNAL 1 21
FT CHAIN 22 917
FT DOMAIN 24 38
FT REPEAT 24 28
FT REPEAT 29 33
FT REPEAT 34 38
FT DOMAIN 111 668
FT REPEAT 111 116
FT REPEAT 203 208
FT REPEAT 277 282
FT REPEAT 399 404
FT REPEAT 624 629
FT REPEAT 663 668
FT DOMAIN 159 170
FT REPEAT 159 164
FT REPEAT 165 170
SQ SEQUENCE 917 AA; 100148 MW; 7FF39BB8C046539D CRC64;

Query Match
Best Local Similarity 6.9%; Score 161.5; DB 1; Length 917;
Matches 104; Conservative 76; Mismatches 187; Indels 119; Gaps 21;

OY 2 NEPLDTSVTEKLSFSANGKVNITSDTKLNFAKETAGTN-----GDTYVHLNGISGL 56
DB 131 NVAGLLATNTKLEISSESNSTYQTRTKDKDQVYEGVINEGRLKAKDFVLLNG----- 185
OY 57 TDTLNTGATNTVNDVNTDDEKKRAASVKDVLNAGWNKIGVKGFTASDNVDFVRYDT 116
DB 186 -DEVINNG-----NINV--EKNSTINGKLYLSSGYNT-----FTLSDS----- 221
OY 117 VEPISADTKTTVN--VESKDNKTEVKIKAK-----TSVIEKDKG 157
DB 222 --GISVALEDNTVAGIYONEGSIKAGEITLTSKGRKELDSLVMNNGYLETKVSNRNG 279
OY 158 LVTKRKGE--NGSSTDEGEGLVTAKEVIDAVNKAQWRMKTATTANGQTGADEFTVTS 216
DB 280 VVLADNVQLNNEENINGEIVNFGTEVTSNEDK--KLTISKTSKVTSPKIFKGSV 336
OY 217 NVTFASGKGTATYVSKDDGNITVYDVVNGDALNVNOLN--SGMNLDS-----KAVA 268
DB 337 NINGNFGRENGSTHYNEERKTLNTEVINIDVGAENIRIADKDKTETDSFIQTEALSLL 396
OY 269 GSGKV-----ISGNVS-----PSKGMQD--ETVININA--GNNIEITRNGK 305
DB 397 ANNGKVNLRKNDVINSININIDSRGTDLSLKLNTNQGHIINIDHADINSKGRLEFVTSIQN 456
OY 306 NIDATSKMTPQSFSSVLGAGADAPTLSDVDALNVGSKDKPKPVRIIT--NVAPGVKEG 364
DB 457 DVDRKSNITTTDSKININLNGAMGLGRSVNEDDVATPMKRAKSKRKFNV-----DMR 509
OY 365 NVAQLKGYAONLNRRIDNV--DGNARAGIAQAIATAGLVQAYLPKGSMAIGGCTTGE 421
DB 510 NV-----VFNOQVDEVILIAGFEKRYNLDKIVAT-----GOTNFYDGVGSRRN 551
OY 422 AGYAIG 427
DB 552 SRYEYG 557

Search completed: October 6, 2003, 09:24:14
Job time : 9.11902 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:35 ; Search time 13.1962 Seconds
(without alignments)
3359.577 Million cell updates/sec

Title: US-09-771-382-35

Perfect score: 2350

Sequence: 1 NNEFDLTSVGTETKLSFGANG.....TASGNSNGHFGASASVGYQW 461

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_76:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2333	99.3	591	2	G81133
2	2089.5	88.9	592	2	A81888
3	393.5	16.7	298	2	I64138
4	375.5	16.0	2059	2	D82671
5	365	15.5	1588	2	A86036
6	360.5	15.3	1190	2	H91188
7	357	15.2	1107	2	A82615
8	328.5	14.0	658	2	AC0976
9	205	8.7	1536	2	A43855
10	195	8.3	585	2	F90961
11	195	8.3	585	2	F85809
12	194.5	8.3	4919	2	T31105
13	194	8.3	936	2	I40711
14	192.5	8.2	1910	2	AF0394
15	190.5	8.1	1004	2	C82672
16	190.5	8.1	2020	2	C48339
17	185	7.9	365	2	AB3486
18	184	7.8	1477	2	B43855
19	182.5	7.8	1109	2	A56143
20	182.5	7.8	1099	2	S76109
21	181.5	7.7	1091	2	G64964
22	181.5	7.7	364	2	A81019
23	180.5	7.7	584	2	C48658
24	180.5	7.7	3705	2	B98047
25	180	7.6	2249	2	AD0123
26	179.5	7.5	980	2	A41477
27	177	7.5	980	2	H90681
28	177	7.5	980	2	D85532
29	177	7.5	980	2	D85532

30	177	7.5	2232	2	T34434	hypothetical prote
31	176.5	7.5	5188	2	E80547	probable RTX faml
32	176	7.5	1461	2	B95696	hypothetical prote
33	175.5	7.5	1428	2	AC2224	hypothetical prote
34	175.5	7.5	2273	2	T09083	hemagglutinin/hemo
35	175.5	7.5	2468	2	A83412	hypothetical prote
36	175.5	7.5	3013	2	AB0480	probable invasin y
37	174.5	7.4	5291	2	F90696	hypothetical prote
38	174	7.4	1577	2	A35140	hemolysin A precu
39	173.5	7.4	1651	2	JC1340	outer membrane pro
40	173	7.4	1430	2	AF0351	probable autotrans
41	172.5	7.3	4152	2	T31102	filamentous hemag
42	172	7.3	1461	2	A85547	hypothetical prote
43	171.5	7.3	1635	2	A10452	hemolysin (importe
44	170	7.2	893	2	A37284	surface-array prot
45	169	7.2	883	2	AC2444	hypothetical prote

ALIGNMENTS

RESULT 1									
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)									
C:Species: Neisseria meningitidis									
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001									
C:Accession: G81133									
R:Retelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, R.; Hickey, E.R.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. et al.; Olin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000									
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappunli, R. A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: A81000; MUID:2017575; PMID:10710307									
A:Accession: G81133									
A:Status: preliminary									
A:Molecule type: DNA									
A:Residues: 1-591 <TEF>									
A:Cross-references: GB:AE00450; GB:AE002098; NID:g7226229; PIDN:AA41395.1; PID:g722									
A:Experimental source: serogroup B, strain MC58									
C:Genetics:									
A:Gene: NMB0992									
Query Match									
Best Local Similarity 99.3%; Score 2333; DB 2; Length 591;									
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	4	TDLTSVGTETKLSFGANGKVNITSDTKGLNFAKFTAGTNGDPTVHLNGIGSTLTDTLLNT	63						
DB	134	TDLTSVGTETKLSFGANGKVNITSDTKGLNFAKFTAGTNGDPTVHLNGIGSTLTDTLLNT	193						
QY	64	GATTNTVNDVNTDEKKRAASVKDYLANGMNKKVKKDGTASDVNDVFRIVYVEPLSAD	123						
DB	194	GATTNTVNDVNTDEKKRAASVKDYLANGMNKKVKKDGTASDVNDVFRIVYVEPLSAD	253						
QY	124	TKTTTVNESKDNCKTEVKIGAKTSYIKEDGLVYKDGKNGENSSSTDEEGVLYTKEV	183						
DB	254	TKTTTVNESKDNCKTEVKIGAKTSYIKEDGLVYKDGKNGENSSSTDEEGVLYTKEV	313						
QY	184	IDAVNKGWRKTKTTTANGOTQADKFEYVSGTAVTFASGKTATVYSKDQGNITWYD	243						
DB	314	IDAVNKGWRKTKTTTANGOTQADKFEYVSGTAVTFASGKTATVYSKDQGNITWYD	373						
QY	244	VNVGDALNVNOLNSGWNLSKAVAGSSGKVISNVSPSKGMDVYVINAANNIEITRN	303						
DB	374	VNVGDALNVNOLNSGWNLSKAVAGSSGKVISNVSPSKGMDVYVINAANNIEITRN	433						
QY	304	GKNIDVATSPMPPOSSVSLGAGADAPTLVSVDGLNLGSKKDNKPVRTTNVAPGVKGDV	363						
DB	434	GKNIDVATSPMPPOSSVSLGAGADAPTLVSVDGLNLGSKKDNKPVRTTNVAPGVKGDV	493						
QY	364	TNVAQLGVAGQNLNRRIDNVNAGNAGIAQAIATAGVQVATLPKSKMAATGCTTYREAG	423						

QY 336 DALNNGSKDNKPNRTTNAPGVKEGDYTNNAQLKVAQ-----NLNKRDNVD 384
DB 1466 -----RLSNYSAGVNNNDVYNAQLKQSVETKQYTDQRVMEVNDKLSKTE 1511
QY 385 GNAAGACIAQAIATAGVAYVLPKRSMAATGCGTYRGEAGYAGISYSSDGMNITIGTAS 444
DB 1512 SKLSGGIATAMAMTGLPQAYTPGASMASIGGCTYNGESAVALGVSVMSANGRWYKLOOS 1571
QY 445 GNSRGHFGASASVAYQW 461
DB 1572 TNSGGEYSALGAGIQW 1588

RESULT 7
AB2615
surface protein Xf1981 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision: 20-Aug-2000 #text_change: 20-Aug-2000
C:Accession: AB2615
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: AB2515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: AB2615
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1190 <SIN>
A:Cross-references: GB:AE004017; GB:AE003849; NID:g9107083; PIDN:AAF84783.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Brienes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carier, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincanl, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.C.; Kuramae, E.E.; Laigt
chdo, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, R.C.; Palmieri, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tashiro, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:genetics:
A:gene: Xf1981

Query Match 15.3%; Score 360.5; DB 2; Length 1190;
Best Local Similarity 25.3%; Pred. No. 1.2e-11;
Matches 135; Conservative 68; Mismatches 188; Indels 143; Gaps 20;

QY 8 SVGTETKLSFSAN-----GNKVNTSDTKGLNFAKKTAG-----TNGDT 45
DB 720 SGMNMLASGANSNNVAPESVDLKNITDGNIVYSKSSGNDVLFNLSSLLKDKLKVGT 779
QY 46 TVHLNGIGSTLFDLTLCATTTNNDVNTDEKKFAASVKDVLNAG-WNIKGVKGTGA 104
DB 780 VWTTCNV-----TVSGSVTLGSMGLVTTDGPVSYSGL-----NAGSOKITVVAAGTAD 828
QY 105 SD-----NVDFFRYDVEFLSNQTKTTFVVEKDKGKTEVKGAK 147
DB 829 TDAVNLSQLNTAMAGSGAKSVHYSYTD-----GTTGGNNGDAGTGTSTIAVGVTL 882
QY 148 TSVIEKDKGLVTKDKGKENG-SPTDEGGLVTAKEVIDAVNKAAGRMKTTTANGQTGA 206
DB 883 ASA-----EGATAVGSAASAASGKSTAIIGNAVASADGVALGD-GAKDKARAGESTTGK 937
QY 207 DKFEYVTSCTNTFASGKTTATVSKDGCNITVAVDVGALNVNL-----QNSGMNL 262
DB 938 SGLQNTVTVGVSDGASGKETRTVS-----NVADAKEAT--DAVNLRLQDRVAQDANRYV 990
QY 263 DKRAVAGSSGKVIISGVNVSFKGMDETVYINAGNNTETIRNKGKNDIATSMTPQPSVSL 322

DB 991 DNKIESLSCGTF-----VAVNSLN-----SAPF-----I 1016
QY 323 GAGADAPLTSLV-----DGDALNVGSK-----KDNKPV-----RI 351
DB 1017 AAGVATATGATGATASGADSIAMGNKASASADNNAVAGHNVADRANTVSVGSAGEBQV 1076
QY 352 TVNAPGVKGDYTNNAQLKGVANLNKRIDNVGNAR-----AGIAQAITAGVAYLPFG 407
DB 1077 TVNAGTADTDAVNVNSQLNQGLITAKQYTDGVVGLRRPTDGGVAAALITANLPLQAYIPG 1136
QY 408 KSNMAIGGTYRGEAGYAGISYSSDGMNITIGTASNGRHFASASVAYQW 461
DB 1137 RGMTSVGSYIRGQSAIAVGVSVSESGNWKVRFSGSANTRQOVIGAGVGIQW 1190

RESULT 8
AC0976
probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serova
C:Species: Salmonella enterica subsp. enterica serovar typhl
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision: 09-Nov-2001 #text_change: 18-Nov-2002
C:Accession: AC0976
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
S.; Moulder, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AC0976
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1107 <PAR>
A:Cross-references: GB:AL51382; PIDN:CAD03303.1; PID:g16504923; GSPDB:GN00176
C:genetics:
A:gene: sapB

Query Match 15.2%; Score 357; DB 2; Length 1107;
Best Local Similarity 21.8%; Pred. No. 1.6e-11;
Matches 150; Conservative 92; Mismatches 190; Indels 256; Gaps 25;

QY 15 SFSAN--GNKVNTSDTKGLNFAKKTAGTNG-----DTVHLNGIGSTLFDLTLCATTN 68
DB 435 AFSANHGSKTKITTVNAAALSDSTDAVNSQLVETYNQVNTSALND--INT-STTN 491
QY 69 VTNDVNTDEKKRAASVKDVLNAGWNKGVKGTATSDVDPV-----RTYDT----- 116
DB 492 LCTDALSMWDEGAFSASHTGKTITVVAAGELASBSTDALNSQLVETYNMLISQVNE 551
QY 117 -VEFLSADTKTTTVN-----VESKDKGKTEVKGAKTSVIREKDKLVTKDK-- 164
DB 552 SISQLAGDSEFEYITENGTVKRYIRTNNGLEGO-----DAYATGNATAVGYDAVAS 604
QY 165 -----GENGSSTDEG-----EGIV-----TAKVIOAV 187
DB 605 GAGCIALGONSSSIEGSIALGSGSTSNRAITTTGIRETSATSDGVVIGYNTTDELLGL 664
QY 188 NKA-----GWRMKTTFANGQTGQ-----ADKFETVTSCTNTFASGKG 225
DB 665 SLCTGDESTRQITNVADGSEADAVTVROLQNAIGAATVTPPKRYHANSTEEDSLAVGND 724
QY 226 TTA-----TVSKDDGQ-----NITVAVDVNVGALNVN-----QL 255
DB 725 SLAMGAKTIVNADAGIGLINTLVAMDAINGIAISNARANHANSIAMGNSQTTGCAQT 784
QY 256 QNSGMNLDSK-----ANAGSSGKVISGNSVPSKGMDEYVNIAG-----NNIETRRG 304
DB 785 DVTAYNMDPQNSVGEFVSSEDEGQRTITVNAAGSADTDA-----VNVGQLKTVDAQVSRT 841
QY 305 KNI-----DIATSMTPQF-----SSVSLGAGAD 327
DB 842 QSTTNLNTQVSNLDRVNTNIENGIDGIYTTGTSKTKFKTNTDADANAAGADAVAGSGSI 901

[illegible][illegible]

Db	1154	GS-----SAGTG-----	DYFTNVELNATAGNVSIAETK	1183
QY	371	GVAQNINNRIDNVDGN----	ARAGIAQAIATAGLVOAYLPGKSMMAIGGGTYRGAGYAI	426
Db	1184	TALSTSLNAYLSIGGNNSIKAONG-----	WLIKKA-----FWTTOGAGI	1222
QY	427	GY---SSISDGGNWIKTASG	445	
Db	1223	GFRANSSLSVDGNIIKGETEG	1244	

Search completed: October 6, 2003, 09:33:34
Job time : 15.1962 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

```
Run on:      October 6, 2003, 09:05:45 ; Search time 43.9664 Seconds
              (without alignments)
              1848.329 Million cell updates/sec
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Title: US-09-771-382-23

Sequence: 1 MNKIYRIWNSALNAVVS.....TASGNSRGHFGASASVGYQW 512

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database : A_Geneseq_19Jun03: *

- 1: /SIDS1/gcgcdgata/geneeseq/geneesqp-emb1/AA1980.DAT.*
- 2: /SIDS1/gcgcdgata/geneeseq/geneesqp-emb1/AA1981.DAT.*
- 3: /SIDS1/gcgcdgata/geneeseq/geneesqp-emb1/AA1982.DAT.*
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- 5: /SIDS1/gcgcdgata/geneeseq/geneesqp-emb1/AA1984.DAT.*
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- 7: /SIDS1/gcgcdgata/geneeseq/geneesqp-emb1/AA1986.DAT.*
- 8: /SIDS1/gcgcdgata/geneeseq/geneesqp-emb1/AA1987.DAT.*
- 9: /SIDS1/gcgcdgata/geneeseq/geneesqp-emb1/AA1988.DAT.*
- 10: /SIDS1/gcgcdgata/geneeseq/geneesqp-emb1/AA1989.DAT.*
- 11: /SIDS1/gcgcdgata/geneeseq/geneesqp-emb1/AA1990.DAT.*
- 12: /SIDS1/gcgcdgata/geneeseq/geneesqp-emb1/AA1991.DAT.*
- 13: /SIDS1/gcgcdgata/geneeseq/geneesqp-emb1/AA1992.DAT.*
- 14: /SIDS1/gcgcdgata/geneeseq/geneesqp-emb1/AA1993.DAT.*
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- 18: /SIDS1/gcgcdgata/geneeseq/geneesqp-emb1/AA1997.DAT.*
- 19: /SIDS1/gcgcdgata/geneeseq/geneesqp-emb1/AA1998.DAT.*
- 20: /SIDS1/gcgcdgata/geneeseq/geneesqp-emb1/AA2000.DAT.*
- 21: /SIDS1/gcgcdgata/geneeseq/geneesqp-emb1/AA2000.DAT.*
- 22: /SIDS1/gcgcdgata/geneeseq/geneesqp-emb1/AA2001.DAT.*
- 23: /SIDS1/gcgcdgata/geneeseq/geneesqp-emb1/AA2002.DAT.*
- 24: /SIDS1/gcgcdgata/geneeseq/geneesqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2600	100.0	512	22	AAU06182	N_meningitidis P
2	2550.5	98.1	591	20	AAV27202	Amino acid sequen
3	2550.5	98.1	591	20	AAV23746	A surface protein
4	2550.5	98.1	591	22	AAU06171	N_meningitidis p
5	2546	97.9	592	20	AAV23737	A surface protein
6	2543.5	97.8	591	21	AAV57045	BASB029 amino aci
7	2538.5	97.6	591	20	AAV23741	A surface protein
8	2538.5	97.6	591	22	AAU06175	N_meningitidis E
9	2456.5	94.5	513	22	AAU06183	N_meningitidis H

10	2453.5	94.4	599	20	AAV33743	A surface protein
11	2453.5	94.4	599	22	AAU06176	N. meningitidis H3
12	2449	94.2	594	20	AAV33740	A. surface protein
13	2449	94.2	594	21	AAV57044	BAB5029 amino acid
14	2449	94.2	594	22	AAU06174	N. meningitidis EG
15	2442	93.9	594	20	AAV33739	A surface protein
16	2442	93.9	594	22	AAU06179	N. meningitidis BZ
17	2427	93.3	598	20	AAV33742	A surface protein
18	2427	93.3	598	22	AAU06177	N. meningitidis H1
19	2418	93.0	598	20	AAV33738	A surface protein
20	2418	93.0	598	22	AAU06178	N. meningitidis BZ
21	2407	92.6	592	20	AAV33744	A surface protein
22	2407	92.6	592	22	AAU06172	N. meningitidis H4
23	2383	91.7	592	22	AAU06166	N. meningitidis P4
24	2289	88.0	592	22	AAU06180	N. meningitidis P4
25	2260	86.9	592	20	AAV37203	N. meningitidis 2Z
26	2234.5	86.7	589	20	AAV33745	A surface protein
27	2254.5	86.7	589	22	AAU06173	N. meningitidis P2
28	2147.5	82.6	433	22	AAU06185	N. meningitidis PM
29	2098	80.7	604	22	AAU06184	N. meningitidis PM
30	2000.5	76.9	407	22	AAU06184	N. meningitidis PM
31	991	38.1	1094	21	AAAB33858	Haemophilus influenzae
32	991	38.1	1098	17	AAAB33852	Haemophilus adhesion
33	956.5	36.8	2411	21	AAAB33860	Haemophilus influenzae
34	954.5	36.7	2353	17	AAAB33939	Haemophilus adhesion
35	789.5	30.4	679	17	AAAB33934	Haemophilus influenzae
36	789.5	30.4	679	21	AAAB33855	Haemophilus influenzae
37	780.5	30.0	245	20	AAV37201	Amino acid sequence
38	683	26.3	1004	21	AAAB33857	Haemophilus influenzae
39	679	26.1	1002	21	AAAB33854	Haemophilus influenzae
40	600	23.1	116	21	AAAB33782	Nonserial conserved
41	573	22.0	1104	21	AAAB33856	Haemophilus influenzae
42	573	22.0	1104	21	AAAB33855	Haemophilus influenzae
43	536.5	20.6	298	24	AAAB30477	Haemophilus influenzae
44	386.5	14.9	2314	22	AAAB59137	M. catarrhalis sur
45	383	14.7	2139	24	AAAB59126	M. catarrhalis sur

ALIGNMENTS

RESULT 1	
AAU06182	
ID	AAU06182 standard; Protein; 512 AA.
XX	
AC	AAU06182;
XX	
DT	24-OCT-2001 (first entry)
XX	
DE	N. meningitidis PMC21 Nhma deletion mutant #1.
XX	
KW	Surface antigen Nhhb; meningococcal disease; meningitis vaccine
KW	mutant; mutein.
XX	
OS	Neisseria meningitidis strain PMC21.
OS	Synthetic.
XX	
Key	Location/Qualifiers
FF	1..51
FT	/label= Signal_peptide
FT	52..512
FT	/label= Mature_Nhma_deletion_mutant_#1
FT	/note= "Predicted mature protein, specifically
FT	claimed in claim 12"
XX	
PN	WO200155182-A1.
XX	
PD	02-AUG-2001.
XX	
PF	25-JAN-2001; 2001WO-AU00069.
XX	
PR	25-JAN-2000; 2000US-0177917.
XX	

WO200155182-A1

02-AUG-2001

25-JAN-2001; 2001WO-AU00069.

25-JAN-2000; 2000US-0177917.

PA (UYOU) UNITV QUEENSLAND.
XX
XX PI Peak IRA, Jennings MP;
XX
XX DR MPI: 2001-488774/53.
XX N-PSDB; AAS09172.
XX
XX PT New Nhba surface antigen polypeptides and polynucleotides from
XX Neisseria meningitidis, useful in producing vaccines for treating or
XX preventing broad spectrum of Neisseria meningitidis -
PS
PS Claim 12; Fig 5; 91pp: English.
XX
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen Nhba
XX (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are
XX characterised by deletions of non-conserved amino acids, particularly
XX the deletion of variable regions. The deletion mutants are useful in
XX diagnostics, therapeutic and prophylactic vaccines against a broader
XX spectrum of N. meningitidis, and in designing and/or screening of
XX medicaments. The mutant proteins when used as a vaccine can effectively
XX immunise against a broader spectrum of N. meningitidis strains than
XX would be expected from a corresponding wild-type surface antigen.
XX The present sequence represents N. meningitidis strain PMC21 surface
XX antigen Nhba deletion mutant #1.
SQ

Sequence 512 AA:

Query Match 100.0%; Score 2600; DB 22; Length 512;
Best Local Similarity 100.0%; Pred. No. 7.8e-154;
Matches 512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIIWSALNMAVYSELTRNHTKRASATVKTAVLATLLFATVQASANNEDLTSV 60
DB 1 MNKIYRIIWSALNMAVYSELTRNHTKRASATVKTAVLATLLFATVQASANNEDLTSV 60
QY 61 GREKISFSANGKRVNTSDTKGLNFAKETAGTNGDTTVHLNIGSTLPTLTLTGATTV 120
DB 61 GREKISFSANGKRVNTSDTKGLNFAKETAGTNGDTTVHLNIGSTLPTLTLTGATTV 120
QY 121 TNDNVTDEKRRASVADVNLNAGWNIKGVKPGTTASDNDVFRTYDVEFLSADTKTTV 180
DB 121 TNDNVTDEKRRASVADVNLNAGWNIKGVKPGTTASDNDVFRTYDVEFLSADTKTTV 180
QY 181 NVESKDNKRTVEKIGAKTSVKEKDKLVTKDKGENSSSTDEGEGLVTAKEVIDAVNK 240
DB 181 NVESKDNKRTVEKIGAKTSVKEKDKLVTKDKGENSSSTDEGEGLVTAKEVIDAVNK 240
QY 241 AGWRKMTTANQOTGADKFEYVTSNTTFFASGKGTATVSKDDGNTTVMYDVAVGDA 300
DB 241 AGWRKMTTANQOTGADKFEYVTSNTTFFASGKGTATVSKDDGNTTVMYDVAVGDA 300
QY 301 LNVNOLONGSMNLDSRAVAGSSGKVTSGNVSPSKGMDFTVININAGNIEITRNGKNIDI 360
DB 301 LNVNOLONGSMNLDSRAVAGSSGKVTSGNVSPSKGMDFTVININAGNIEITRNGKNIDI 360
QY 361 AFSMTPOFSSSVSLGAGADAPTLISVDGALNVGSKDKNKEPVRTTNVAPGVKEGDTVAOL 420
DB 361 AFSMTPOFSSSVSLGAGADAPTLISVDGALNVGSKDKNKEPVRTTNVAPGVKEGDTVAOL 420
QY 421 KQVAAONLNRRINDNVGNARAGTAQAATATAGLVQAYIPGSSMAIGGGTTRGEGAGYIGS 480
DB 421 KQVAAONLNRRINDNVGNARAGTAQAATATAGLVQAYIPGSSMAIGGGTTRGEGAGYIGS 480
QY 481 SISDGNMTIKGTASGNSRGHFGASASVGYOW 512
DB 481 SISDGNMTIKGTASGNSRGHFGASASVGYOW 512

RESULT 2
AAV27202
ID AAV27202 standard; Protein; 591 AA.
XX

AC AAV27202;
XX
XX 24-SEP-1999 (first entry)
XX
XX Amino acid sequence of N. meningitidis protein ORF40-1.
DE
XX Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;
XX bacterial infection; treatment.
KW
XX Neisseria meningitidis.
OS

PN WO936544-A2.
XX
XX 22-JUL-1999.
PD
XX 14-JAN-1999; 99WO-1B00103.
PF
XX 09-OCT-1998; 98GB-0022143.
PR 14-JAN-1998; 98GB-0000760.
PR 01-SEP-1998; 98GB-0019015.
XX
XX (CHIR-) CHIRON SPA.
PA
XX Grandi G, Masiagnani V, Piazza M, Rappuoli R, Scarlato V;
PI
XX MPI: 1999-444400/37.
DR
XX N-PSDB; AAX99124.
DR

PT New protein and its nucleotide sequence, useful in vaccines or
diagnostic compositions for treating and/or preventing Neisseria
meningitidis infections
PT
XX
XX Claim 1; Page 62; 123pp: English.

PS The invention provides proteins (AAV27201-245) from Neisseria
XX meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)
XX encoding the proteins. Compositions comprising the protein, nucleic acid
XX or antibody specific to the protein are useful as pharmaceuticals, e.g. a
XX vaccine composition or a diagnostic composition. The composition is also
XX useful for treating or preventing an infection due to Neisseria
XX bacteria, especially Neisseria meningitidis.
XX

SQ Sequence 591 AA:

Query Match 98.1%; Score 2550.5; DB 20; Length 591;
Best Local Similarity 86.6%; Pred. No. 1.1e-150;
Matches 512; Conservative 0; Mismatches 0; Indels 79; Gaps 1;

QY 1 MNKIYRIIWSALNMAVYSELTRNHTKRASATVKTAVLATLLFATVQASANNEDLTSV 54
DB 1 MNKIYRIIWSALNMAVYSELTRNHTKRASATVKTAVLATLLFATVQASANNEDLTSV 60
QY 55 -----TDLTSVTEKLELSEFANGKRVNTSDTKGLNFAKETAGTNGDTTVHLN 54
DB 55 -----TDLTSVTEKLELSEFANGKRVNTSDTKGLNFAKETAGTNGDTTVHLN 60
QY 61 YLDPVORTAVLIVNSDKRGTEKEVEENSOMAVYFNEKGVLTAREITLAKGDNLIKIKO 120
DB 61 YLDPVORTAVLIVNSDKRGTEKEVEENSOMAVYFNEKGVLTAREITLAKGDNLIKIKO 120
QY 121 NCTNFYSILKDETDLTLSVTEKLELSEFANGKRVNTSDTKGLNFAKETAGTNGDTTVHLN 180
DB 121 NCTNFYSILKDETDLTLSVTEKLELSEFANGKRVNTSDTKGLNFAKETAGTNGDTTVHLN 180
QY 181 GIGSTLTDPLTLNLTGATNTNTNNDVDEKRRASVADVNLNAGWNIKGVKPGTTASDNDVF 240
DB 181 GIGSTLTDPLTLNLTGATNTNTNNDVDEKRRASVADVNLNAGWNIKGVKPGTTASDNDVF 240
QY 241 VRTYDVEFLSADTKTTTVNVEKSKDKRTVEKIGAKTSVKEKDKLVTKDKGENSS 221
DB 241 VRTYDVEFLSADTKTTTVNVEKSKDKRTVEKIGAKTSVKEKDKLVTKDKGENSS 221
QY 222 TDEGEGLVTAKEVIDAVNKAWRMKTNTANQOTGADKFEYVTSNTTFFASGKGTATV 281
DB 222 TDEGEGLVTAKEVIDAVNKAWRMKTNTANQOTGADKFEYVTSNTTFFASGKGTATV 281
QY 301 TDEGEGLVTAKEVIDAVNKAWRMKTNTANQOTGADKFEYVTSNTTFFASGKGTATV 360
DB 301 TDEGEGLVTAKEVIDAVNKAWRMKTNTANQOTGADKFEYVTSNTTFFASGKGTATV 360
QY 361 SKDDGNTTVMYDVAVGDAVLNVNOLONGSMNLDSRAVAGSSGKVTSGNVSPSKGMDFTVIN 420
DB 361 SKDDGNTTVMYDVAVGDAVLNVNOLONGSMNLDSRAVAGSSGKVTSGNVSPSKGMDFTVIN 420


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Db      361 SKDDGNTITVMYDVNVDGALNVQNLONGSGMNLDSKAVAGSSGKVIISGNVSPSKGKMDERY 420
QY      342 NINAGNNIETTRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDGALNVGSKDKKPYR 401
Db      421 NINAGNNIETTRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDGALNVGSKDKKPYR 480
QY      402 ITNVAPGVEGCVTNTVAOLKGVANLNRRIDNVGNARAGIAOAIATAGLVQAYLPGKSM 461
Db      481 ITNVAPGVEGCVTNTVAOLKGVANLNRRIDNVGNARAGIAOAIATAGLVQAYLPGKSM 540
QY      462 MAIGGTYRGEAGYALGYSISIDGNNIIGTASGSRGHFGASASVGYQW 512
Db      541 MAIGGTYRGEAGYALGYSISIDGNNIIGTASGSRGHFGASASVGYQW 591

RESULT 3
AA23746
ID      AA23746 standard; protein; 591 AA.
XX
AC      AA23746;
XX
DT      08-SEP-1999 (first entry)
XX
DE      A surface protein of Neisseria meningitidis.
XX
KW      Surface protein; surface glycoprotein; infection; vaccine;
XX      immunoreactive peptide.
XX      Neisseria meningitidis.
XX      OS
XX      PN      W0931132-A1.
XX      PD      24-JUN-1999.
XX      PF      14-DEC-1998; 98WO-AU01031.
XX      PR      12-DEC-1997; 97GB-0026398.
XX      PA      (ISTS-) ISTS INNOVATION LTD.
XX      PA      (UYOU) UNIV QUEENSLAND.
XX      PI      Jennings MP, Moxon ER, Peak IRA;
XX      DR      MPI: 1999-418754/35.
XX      DR      N-PSDB; AAX85798.
XX
PT      Neisseria meningitidis surface proteins useful for treating N.
PT      meningitidis infections
XX
PS      Claim 1; Page 127-128; 132pp; English.
XX
CC      The present sequence represents a surface protein of Neisseria
CC      meningitidis which is approximately 62 kDa. The N. meningitidis
CC      surface glycoproteins, nucleic acids, the primers and optionally
CC      a thermostable polymerase, or antibodies are useful in a kit for
CC      the detection or diagnosis of N. meningitidis infection in humans.
CC      The N. meningitidis surface glycoproteins can also be used to
CC      prevent or treat N. meningitidis infection in humans, especially
CC      in the form of vaccines. The proteins and antibodies can also
CC      be used to identify immunoreactive peptides.
XX
SQ      Sequence 591 AA;

Query Match      98.1%; Score 2550.5; DB 20; Length 591;
Best Local Similarity 86.6%; Pred. No. 1.1e-150;
Matches 512; Conservative 0; Mismatches 0; Indels 79; Gaps 1;
```

```
Db      61 YLDPVORTAVAILVNSDKECTGEGKEVENSQWAVYFNEKGVLLAREITLKAGDNLKIKQ 120
QY      55 -----TDLTSGVTEKLSFSAANGKNNITSDTKGLMFAKETAGTNDOTTYHLN 101
Db      121 NGNTFTYSLKRDLDLTLTSVGETKLSFSANGKNNITSDTKGLMFAKETAGTNDOTTYHLN 180
QY      102 GIGSTLTDLTLTGATTNTVNDVTDDEKRAASVADVNLACNNINGVKRGCTASDVDF 161
Db      181 GIGSTLTDLTLTGATTNTVNDVTDDEKRAASVADVNLACNNINGVKRGCTASDVDF 240
QY      162 VRTYDVEFLSADTKTTTVNVESEKDKGKTEVKGAKTSYIKERDKLYTGKDKGENGSS 221
Db      241 VRTYDVEFLSADTKTTTVNVESEKDKGKTEVKGAKTSYIKERDKLYTGKDKGENGSS 300
QY      222 TDEGEGLVTAKKEYIDAVNKAQFMKTTTANGOTGQADKFEETVTSGTNVTFAKSGTATV 281
Db      301 TDEGEGLVTAKKEYIDAVNKAQFMKTTTANGOTGQADKFEETVTSGTNVTFAKSGTATV 360
QY      282 SKDDGNTITVMYDVNVDGALNVQNLONGSGMNLDSKAVAGSSGKVIISGNVSPSKGKMDERY 341
Db      361 SKDDGNTITVMYDVNVDGALNVQNLONGSGMNLDSKAVAGSSGKVIISGNVSPSKGKMDERY 420
QY      342 NINAGNNIETTRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDGALNVGSKDKKPYR 401
Db      421 NINAGNNIETTRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDGALNVGSKDKKPYR 480
QY      402 ITNVAPGVEGCVTNTVAOLKGVANLNRRIDNVGNARAGIAOAIATAGLVQAYLPGKSM 461
Db      481 ITNVAPGVEGCVTNTVAOLKGVANLNRRIDNVGNARAGIAOAIATAGLVQAYLPGKSM 540
QY      462 MAIGGTYRGEAGYALGYSISIDGNNIIGTASGSRGHFGASASVGYQW 512
Db      541 MAIGGTYRGEAGYALGYSISIDGNNIIGTASGSRGHFGASASVGYQW 591

RESULT 4
AAU06171
ID      AAU06171 standard; protein; 591 AA.
XX
AC      AAU06171;
XX
DT      24-OCT-2001 (first entry)
XX
DE      N. meningitidis PMC21 surface antigen NhhA polypeptide sequence.
XX      Surface antigen NhhA; meningococcal disease; meningitis vaccine.
XX      OS
XX      Neisseria meningitidis strain PMC21.
XX
PH      key
PT      Peptide
XX      Location/Qualifiers
XX      1..51
XX      /label= signal_peptide
XX      1..50
XX      /label= C1
XX      /note= "Conserved region 1"
XX      51..108
XX      /label= V1
XX      /note= "Variable region 1"
XX      52..591
XX      /label= Mature_NhhA
XX      /note= "predicted mature protein, specifically
XX      claimed in claim 12"
XX      109..120
XX      /label= C2
XX      /note= "Conserved region 2"
XX      121..124
XX      /label= V2
XX      /note= "Variable region 2"
XX      125..188
XX      /label= C3
XX      /note= "Conserved region 3"
XX      189..210

Region
Region
Region
Region
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FT      /label= V3
FT      /note= "Variable region 3"
FT      211..229
FT      Region
FT      /label= C4
FT      /note= "Conserved region 4"
FT      230..236
FT      Region
FT      /label= V4
FT      /note= "Variable region 4"
FT      237..591
FT      /label= C5
FT      /note= "Conserved region 5"
PN      WO20015182-A1.
XX      PD
XX      02-AUG-2001.
XX      25-JAN-2001; 2001WO-AU00069.
XX      PR
XX      25-JAN-2000; 2000US-0177917.
XX      PA
XX      (UYQU ) UNIV QUEENSLAND.
XX      PI
XX      Peak IRA, Jennings MP;
XX      WPI; 2001-488774/53.
XX      DR
XX      N-PSDB; AAS09161.
PT      New Nhha surface antigen polypeptides and polynucleotides from
PT      Neisseria meningitidis, useful in producing vaccines for treating or
PT      preventing broad spectrum of Neisseria meningitidis .
XX      PS
XX      Claim 9; Fig 1; 91pp; English.
CC      The present invention relates to the isolation of novel Neisseria
CC      meningitidis mutant polypeptides of the surface antigen Nhha
CC      (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC      characterised by deletions of non-conserved amino acids, particularly
CC      the deletion of variable regions. The deletion mutants are useful in
CC      diagnostics, therapeutic and prophylactic vaccines against a broader
CC      spectrum of N. meningitidis, and in designing and/or screening of
CC      medicaments. The mutant proteins when used as a vaccine can effectively
CC      immunise against a broader spectrum of N. meningitidis strains than
CC      would be expected from a corresponding wild-type surface antigen.
CC      The present sequence representing the wild type surface antigen Nhha
CC      from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences
CC      (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC      the present invention.
XX      SQ
XX      Sequence 591 AA:
SQ      Query Match      98.1%; Score 2550.5; DB 22; Length 591;
SQ      Best Local Similarity 86.6%; Pred. No. 1.1e-150;
SQ      Matches 512; Conservative 0; Mismatches 0; Indels 79; Gaps 1;
OY      1 MNKIYRIIWSNLSALNMAVYVSELTNRHTRKASATVAVLATLLFAVQASANNE----- 54
OY      1 MNKIYRIIWSNLSALNMAVYVSELTNRHTRKASATVAVLATLLFAVQASANNEQEDL 60
DB      1 MNKIYRIIWSNLSALNMAVYVSELTNRHTRKASATVAVLATLLFAVQASANNEQEDL 60
OY      55 ----- 54
DB      61 YLDPVQRTVAVLIVNSDEKTEGEKKEVEENSDMAVYFNEKGVLTAREITLKAGDNLIKIQ 120
OY      55 ----- 54
DB      121 NGTNTFYSLKQDLTDLTSTVGEKLSFSANGNKVNITSDPKGNLFAKETAAGTGDTHLN 180
OY      102 GIGSTLTPTLNTGATNTVNDNTDDEKRAASVYKVDVLAAGWNLKGVKPGTTASDNVDF 161
DB      181 GIGSTLTPTLNTGATNTVNDNTDDEKRAASVYKVDVLAAGWNLKGVKPGTTASDNVDF 240
OY      162 VRTYTVTEFLADTITTYVNVASKNGKKEVYKAKTSVIEKEKGKLVTKGDKGENSS 221
DB      241 VRTYTVTEFLADTITTYVNVASKNGKKEVYKAKTSVIEKEKGKLVTKGDKGENSS 300

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OY      222 TDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGQADFEFTVTSSTNTVFSAGKGTATV 281
DB      301 TDEGBGLYTAKEVIDAVNKAQRMKTTTANGOTGQADFEFTVTSSTNTVFSAGKGTATV 360
OY      282 SKDDGNITVTVYDVNVGDALNVNOLQNSGMWLSKAVAGSSGKVIISGVNPSFKGMDET 341
DB      361 SKDDGNITVTVYDVNVGDALNVNOLQNSGMWLSKAVAGSSGKVIISGVNPSFKGMDET 420
OY      342 NINAGNNIEITRNKGNIDTATSMTPQFSSVSLGAGADAPTISVDBDALNVSSKKDNKPYR 401
DB      421 NINAGNNIEITRNKGNIDTATSMTPQFSSVSLGAGADAPTISVDBDALNVSSKKDNKPYR 480
OY      402 ITNVAFGYKEGDVTVNAQLKGYAQNLRNIDNVGNARAGIAQATATAGLYOAYLPGKSM 461
DB      481 ITNVAFGYKEGDVTVNAQLKGYAQNLRNIDNVGNARAGIAQATATAGLYOAYLPGKSM 540
OY      462 MAIGGTYRGEAGYAIYSSISDGGNWIITKGTASNSRGRHFGASASVGYQW 512
DB      541 MAIGGTYRGEAGYAIYSSISDGGNWIITKGTASNSRGRHFGASASVGYQW 591

RESULT 5
AAV23737
ID      AAV23737 standard; Protein: 592 AA.
XX      AC
XX      AAV23737;
XX      DT
XX      08-SEP-1999 (first entry)
XX      DE
XX      A surface protein of Neisseria meningitidis.
XX      KW
XX      Surface protein; surface glycoprotein; infection; vaccine;
XX      immunoreactive peptide.
XX      OS
XX      Neisseria meningitidis.
XX      PN
XX      WO9931132-A1.
XX      PD
XX      24-JUN-1999.
XX      PF
XX      14-DEC-1998; 98WO-AU01031.
XX      PR
XX      12-DEC-1997; 97GB-0026398.
XX      PA
XX      (ISTS-) ISIS INNOVATION LTD.
XX      PA
XX      (UYQU ) UNIV QUEENSLAND.
XX      PI
XX      Jennings MP, Moxon ER, Peak IRA;
XX      DR
XX      WPI; 1999-418754/35.
XX      DR
XX      N-PSDB; AAX85788.
PT      Neisseria meningitidis surface proteins useful for treating N.
PT      meningitidis infections
XX      PS
XX      Claim 1; Page 86-87; 132pp; English.
CC      The present sequence represents a surface protein of Neisseria
CC      meningitidis which is approximately 62 kDa. The N. meningitidis
CC      surface glycoproteins, nucleic acids, the primers and optionally
CC      a thermostable polymerase, or antibodies are useful in a kit for
CC      the detection or diagnosis of N. meningitidis infection in humans.
CC      The N. meningitidis surface glycoproteins can also be used to
CC      prevent or treat N. meningitidis infection in humans, especially
CC      in the form of vaccines. The proteins and antibodies can also
CC      be used to identify immunoreactive peptides.
XX      SQ
XX      Sequence 592 AA:
SQ      Query Match      97.9%; Score 2546; DB 20; Length 592;
SQ      Best Local Similarity 86.3%; Pred. No. 2.1e-150;
SQ      Matches 511; Conservative 0; Mismatches 1; Indels 80; Gaps 1;

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QY 1 MNKIRIIMNSALNAAWVVSSELTNRHTRKASATYKTAVALTLFATYQASANNE----- 54
DQ 1 MNKIRIIMNSALNAAWVVSSELTNRHTRKASATYKTAVALTLFATYQASANNEPRKKD 60
QY 55 ----- 54
DQ 61 YLDPVQRTVAVLIVNSDEKTEGTEKEVEENSDMAVVFENEKGVLTAREITLKAGDNLKIR 120
QY 55 -----TDLTSVTEKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVHL 100
DQ 121 QNGTNFTYSLKKDLTDLTSVTEKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVHL 180
QY 101 NGIGSTLDTLNTGATNTVNDVNDDEKRRASAVDVNLNAGNIGVPCGTASDNVD 160
DQ 181 NGIGSTLDTLNTGATNTVNDVNDDEKRRASAVDVNLNAGNIGVPCGTASDNVD 240
QY 161 FVRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSYKEKDKLVTGKDKGENGS 220
DQ 241 FVRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSYKEKDKLVTGKDKGENGS 300
QY 221 STDEGELVTAKEVIDAVNKGARMKTTTANGOTGAADKEETVSGTNVTFASGKGTAT 280
DQ 301 STDEGELVTAKEVIDAVNKGARMKTTTANGOTGAADKEETVSGTNVTFASGKGTAT 360
QY 281 VSKDQGNITVMYDVNVDALNVNQLQNSGNLDSKAVASGSGKVISGNTSPSKGKMDT 340
DQ 361 VSKDQGNITVMYDVNVDALNVNQLQNSGNLDSKAVASGSGKVISGNTSPSKGKMDT 420
QY 341 VNINAGNNIEITRNGKNIDIAITSMTPQSSVSLGAGADAPTLVSDGALNVGSKDKNPV 400
DQ 421 VNINAGNNIEITRNGKNIDIAITSMTPQSSVSLGAGADAPTLVSDGALNVGSKDKNPV 480
QY 401 RITNVAGVNEGDTVNTAQLKGVANLNRRIDNDVNGARAGIAQAITAGLVQAYLDEGS 460
DQ 481 RITNVAGVNEGDTVNTAQLKGVANLNRRIDNDVNGARAGIAQAITAGLVQAYLDEGS 540
QY 461 MMAIGGTYGEGAGYGAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOM 512
DQ 541 MMAIGGTYGEGAGYGAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOM 592

RESULT 6
AAV57045
ID AAV57045 standard; Protein: 591 AA.
XX
AC AAV57045;
XX
DT 21-FEB-2000 (first entry)
XX
DE BASB029 amino acid sequence from N. meningitidis strain H44/76.
XX
KW BASB029; Neisseria meningitidis; surface fibril protein; HSF; diagnosis;
KW infection; treatment; prevent; antibacterial drug.
XX
OS Neisseria meningitidis.
XX
FH key location/qualifiers
FT Misc-difference 90
FT Misc-difference 92 /note= "Encoded by AAT"
FT Misc-difference 98 /note= "Encoded by GAT"
FT Misc-difference 98 /note= "Encoded by AAC"
FT Misc-difference 108 /note= "Encoded by AATC"
FT Misc-difference 123 /note= "Encoded by ACA"
FT Misc-difference 269 /note= "Encoded by AAA"
FT Misc-difference 389 /note= "Encoded by CGT"
XX
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PN WO958683-A2.
XX
PD 18-NOV-1999.
XX
PE 07-MAY-1999; 99WO-EP03255.
XX
PR 13-MAY-1998; 98GB-0010276.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Ruelle J;
XX
XX WPI: 2000-053103/04.
XX N-PDSB: AA239865.
PT New polypeptide from neisseria meningitidis useful for diagnosis,
PT treatment or prevention of bacterial infections in mammal
XX
PS Claim 4; Fig 2; 74pp; English.
XX
CC This is the Neisseria meningitidis BASB029 amino acid sequence from
CC serogroup B strain H44/76. The BASB029 protein is homologous to the
CC Haemophilus influenzae surface fibril (HSF) protein. The invention
CC relates to BASB029 polynucleotide sequences (AA239864-239865) and
CC polypeptide sequences (AAV57044-Y57045) and their immunogenic fragments.
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria
CC meningitidis infection in a mammal. Compositions containing BASB029
CC polynucleotides and polypeptides are useful for generating an immune
CC response in an animal. A therapeutic composition comprising an antibody
CC directed against BASB029 is useful in treating humans with Neisseria
CC meningitidis disease. The polynucleotide is useful in the diagnosis of
CC the stage of infection, type of infection, susceptibility to an
CC infection which results from increased or decreased expression of the
CC polynucleotide, and for therapeutic or prophylactic purposes,
CC particularly genetic immunisation. Antibodies against BASB029
CC polynucleotides and polypeptides are also useful for treating infections
CC particularly bacterial infections. The protein is useful in the
CC screening and development of antibacterial drugs. Fused recombinant
CC protein is useful for the stimulation of the immune system of an organism
CC receiving the protein.
XX
SQ Sequence 591 AA;
XX
Query Match 97.8%; Score 2543.5; DB 21; Length 591;
Best Local Similarity 86.3%; Pred. No. 3e-150;
Matches 510; Conservative 1; Mismatches 1; Indels 79; Gaps 1;
QY 1 MNKIRIIMNSALNAAWVVSSELTNRHTRKASATYKTAVALTLFATYQASANNE----- 54
DQ 1 MNKIRIIMNSALNAAWVVSSELTNRHTRKASATYKTAVALTLFATYQASANNEQEDL 60
QY 55 ----- 54
DQ 61 YLDPVQRTVAVLIVNSDEKTEGTEKEVEENSDMAVVFENEKGVLTAREITLKAGDNLKIR 120
QY 55 -----TDLTSVTEKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVHL 101
DQ 121 NGSNFTYSLKKDLTDLTSVTEKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVHL 180
QY 102 GIGSTLDTLNTGATNTVNDVNDDEKRRASAVDVNLNAGNIGVPCGTASDNVD 161
DQ 181 GIGSTLDTLNTGATNTVNDVNDDEKRRASAVDVNLNAGNIGVPCGTASDNVD 240
QY 162 VRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSYKEKDKLVTGKDKGENGS 221
DQ 241 VRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSYKEKDKLVTGKDKGENGS 300
QY 222 TDEGEGLVTAKEVIDAVNKGARMKTTTANGOTGAADKEETVSGTNVTFASGKGTAT 281
DQ 301 TDEGEGLVTAKEVIDAVNKGARMKTTTANGOTGAADKEETVSGTNVTFASGKGTAT 360
QY 282 SKDQGNITVMYDVNVDALNVNQLQNSGNLDSKAVASGSGKVISGNTSPSKGKMDT 341
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Db 361 SKDDGNTITVMYDVNVGDALNVNQLONSGMNLDSKAVAGSSGKVIISGNVSPSKGKMDFTV 420
 QY 342 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKKPYR 401
 Db 421 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKKPYR 480
 QY 402 ITNVAVGKEGDTVNTVAOLKGYAQNLRIDNVGNARAGIAQAIAATAGLVQAYLPKGSX 461
 Db 481 ITNVAVGKEGDTVNTVAOLKGYAQNLRIDNVGNARAGIAQAIAATAGLVQAYLPKGSX 540
 QY 462 MAIGGTTRGEGAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 512
 Db 541 MAIGGTTRGEGAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 591

RESULT 7
 AAY23741 standard; protein; 591 AA.

XX AAY23741;

DT 08-SEP-1999 (first entry)

DE A surface protein of Neisseria meningitidis.

KW Surface protein; surface glycoprotein; infection; vaccine;

KM Immunoreactive peptide.

XX Neisseria meningitidis.

XX WO931132-A1.

XX 24-JUN-1999.

PF 14-DEC-1998; 98MO-AU01031.

PR 12-DEC-1997; 97GB-0026398.

PA (ISIS-) ISIS INNOVATION LTD.

XX (UYOU) UNIV QUEENSLAND.

PI Jennings MP, Moxon ER, Peak IRA;

XX WPI; 1999-418754/35.

DR N-PSDB; AAX85793.

XX Neisseria meningitidis surface proteins useful for treating N.

PT meningitidis infections

XX Claim 1; Page 104-106; 132pp; English.

XX The present sequence represents a surface protein of Neisseria
 CC meningitidis which is approximately 62 kDa. The N. meningitidis
 CC surface glycoproteins, nucleic acids, the primers and optionally
 CC a thermostable polymerase, or antibodies are useful in a kit for
 CC the detection or diagnosis of N. meningitidis infection in humans.
 CC The N. meningitidis surface glycoproteins can also be used to
 CC prevent or treat N. meningitidis infection in humans, especially
 CC in the form of vaccines. The proteins and antibodies can also
 CC be used to identify immunoreactive peptides.

XX Sequence 591 AA;

Query Match 97.6%; Score 2538.5; DB 20; Length 591;

Best Local Similarity 86.3%; Pred. No. 6,2e-150;

Matches 510; Conservative 1; Mismatches 1; Indels 79; Gaps 1;

QY 1 MNKIVRIINNSALNAVWVSELTRNHTKRASATVKTAVLATLLFATVQASANNE----- 54

Db 1 MNEIIRIINNSALNAVWVSELTRNHTKRASATVKTAVLATLLFATVQASANNEDEEDL 60

QY 55 ----- 54

Db 61 YLDPVLRTVAVLITNSDKEGTGEKEVEENSQWAVYFNEKGVLTAAREITLKAGDNLKIKO 120
 QY 55 -----TDLTSVGTETKLSFANGKNVNTSDTKGLNFAKETAGTNGDTVHLN 101
 Db 121 NGTNFTYSLKDLTDLTSTGTEKLSFANGKNVNTSDTKGLNFAKETAGTNGDTVHLN 180
 QY 102 GIGSTLITDLTLNTGATTTNTNDVTDDEKRRASVYKDVNLNAGNNIKGVKPGTTASDNVDF 161
 Db 181 GIGSTLITDLTLNTGATTTNTNDVTDDEKRRASVYKDVNLNAGNNIKGVKPGTTASDNVDF 240
 QY 162 VRTYDVEFLSADFTKTTTVNVEKNGKTEYKIGAKTSVIEKDDKLVTKGDKGENSS 221
 Db 241 VRTYDVEFLSADFTKTTTVNVEKNGKTEYKIGAKTSVIEKDDKLVTKGDKGENSS 300
 QY 222 TDEGEGLYAKFVIDAVNKGMRKTTTANGOTGADKFEFTYSGTNVTFASGKGTATV 281
 Db 301 TDEGEGLYAKFVIDAVNKGMRKTTTANGOTGADKFEFTYSGTNVTFASGKGTATV 360
 QY 282 SKDDGNTITVMYDVNVGDALNVNQLONSGMNLDSKAVAGSSGKVIISGNVSPSKGKMDFTV 341
 Db 361 SKDDGNTITVMYDVNVGDALNVNQLONSGMNLDSKAVAGSSGKVIISGNVSPSKGKMDFTV 420
 QY 342 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKKPYR 401
 Db 421 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKKPYR 480
 QY 402 ITNVAVGKEGDTVNTVAOLKGYAQNLRIDNVGNARAGIAQAIAATAGLVQAYLPKGSX 461
 Db 481 ITNVAVGKEGDTVNTVAOLKGYAQNLRIDNVGNARAGIAQAIAATAGLVQAYLPKGSX 540
 QY 462 MAIGGTTRGEGAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 512
 Db 541 MAIGGTTRGEGAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 591

RESULT 8

AAU06175 standard; protein; 591 AA.

XX AAU06175;

DT 24-OCT-2001 (first entry)

DE N. meningitidis EG329 surface antigen NhaA polypeptide sequence.

XX Surface antigen NhaA; meningococcal disease; meningitis vaccine.

XX Neisseria meningitidis strain EG329.

OS Neisseria meningitidis

XX Location/Qualifiers

FT 1..50 /label= C1

FT /note= "Conserved region 1"

FT 51..108 /label= V1

FT /note= "Variable region 1"

FT 109..120 /label= C2

FT /note= "Conserved region 2"

FT 121..124 /label= V2

FT /note= "Variable region 2"

FT 125..188 /label= C3

FT /note= "Conserved region 3"

FT 189..210 /label= V3

FT /note= "Variable region 3"

FT 211..229 /label= C4

FT /note= "Conserved region 4"

FT 230..236 /label= V4

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FT      /note="Variable region 4"
FT      Region      237..591
FT      /label=C5
FT      /note="Conserved region 5"
XX      WO200155182-A1.
XX      02-AUG-2001.
XX      25-JAN-2001; 2001WO-AU00069.
XX      25-JAN-2000; 2000US-0177917.
XX      (UYOU ) UNIV QUEENSLAND.
XX      Peak IRA, Jennings MP;
XX      WPI; 2001-488774/53.
XX      DR      N-PSDB; AAS09165.
XX      PT      New Nhba surface antigen polypeptides and polynucleotides from
XX      PT      Neisseria meningitidis, useful in producing vaccines for treating or
XX      PT      preventing broad spectrum of Neisseria meningitidis -
XX      PS      Claim 9; Fig 1; 91pp; English.
XX      CC      The present invention relates to the isolation of novel Neisseria
XX      CC      meningitidis mutant polypeptides of the surface antigen Nhba
XX      CC      (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are
XX      CC      characterised by deletions of non-conserved amino acids, particularly
XX      CC      the deletion of variable regions. The deletion mutants are useful in
XX      CC      diagnostics, therapeutic and prophylactic vaccines against a broader
XX      CC      spectrum of N. meningitidis, and in designing and/or screening of
XX      CC      medicaments. The mutant proteins when used as a vaccine can effectively
XX      CC      immunise against a broader spectrum of N. meningitidis strains than
XX      CC      would be expected from a corresponding wild-type surface antigen.
XX      CC      The present sequence representing the wild type surface antigen Nhba
XX      CC      from N. meningitidis strain EG329 is 1 of 10 Nhba polypeptide sequences
XX      CC      (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX      CC      the present invention.
XX      SQ      Sequence 591 AA;
XX
Query Match      97.6%; Score 2538.5; DB 22; Length 591;
Best Local Similarity 86.3%; Pred. No 6.2e-150;
Matches 510; Conservative 1; Mismatches 1; Indels 79; Gaps 1;
XX
QY      1 MNRIRIIMVSALNANWVSELTRNHTKRASATVKTAVLATLLFATVQASANNE----- 54
DB      1 MNEILRIIMVSALNANWVSELTRNHTKRASATVKTAVLATLLFATVQASANNEQEDL 60
XX
QY      55 ----- 54
DB      61 YLDPVLTAVAVLIIVNSDEKGTGEKEVEENSDMAVFNENKGVLTAREITLKAGDNLIKQ 120
XX
QY      55 -----TDLTSVGTETKLSFSGANGKNYITSDTGKLNPAKTAGTNGDTYHLN 101
DB      121 NGTINFTYSLKKDLTDLTSVGTETKLSFSGANGKNYITSDTGKLNPAKTAGTNGDTYHLN 180
XX
QY      102 GIGSTLITDILLNGATTNVTNDVYTDDEKRAASVKVDYLNAGNNIKVCKGTATASDNVDF 161
DB      181 GIGSTLITDILLNGATTNVTNDVYTDDEKRAASVKVDYLNAGNNIKVCKGTATASDNVDF 240
XX
QY      162 VRTYDYVEFISADTKTTTAVVESKDKGKTEVKIGATSVYIKEDGKLVYGGKDGENGSS 221
DB      241 VRTYDYVEFISADTKTTTAVVESKDKGKTEVKIGATSVYIKEDGKLVYGGKDGENGSS 300
XX
QY      222 TDEGEGLVTAKEVIDAVNKAQMKRTTANGOTGOADKFEVTSCTNVTAFASGKGTATV 281
DB      301 TDEGEGLVTAKEVIDAVNKAQMKRTTANGOTGOADKFEVTSCTNVTAFASGKGTATV 360
XX
QY      282 SKDDGNTVYVDVNGDALNVNOLQNSGNLDSKAVAGSSGKVYISGNVSPSKGMDETV 341
XX

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DB      361 SKDDGNTVYVDVNGDALNVNOLQNSGNLDSKAVAGSSGKVYISGNVSPSKGMDETV 420
QY      342 NINAGNNIETBRNGKNIDTATSMPPSSVSLGAGADAPTLSDGDLANSGSKDKNPKVR 401
DB      421 NINAGNNIETBRNGKNIDTATSMPPSSVSLGAGADAPTLSDGDLANSGSKDKNPKVR 480
QY      402 ITNVAPGKRGADVTNNVQOLKGVQNLNNRIDNDVGNARAGIAQAIATAGLVQAVLPCKSM 461
DB      481 ITNVAPGKRGADVTNNVQOLKGVQNLNNRIDNDVGNARAGIAQAIATAGLVQAVLPCKSM 540
QY      462 MAIGGTYRGEAGYAIQYSSISDGNMIIKGTASGNSRGHFGASASVGYOM 512
DB      541 MAIGGTYRGEAGYAIQYSSISDGNMIIKGTASGNSRGHFGASASVGYOM 591
XX
RESULT 9
AAU06183
ID      AAU06183 standard; Protein: 513 AA.
XX
AC      AAU06183;
XX
DT      24-OCT-2001 (first entry)
XX
DE      N. meningitidis H41 Nhba deletion mutant.
XX
KW      Surface antigen Nhba; meningococcal disease; meningitis vaccine;
XX      mutant; muten.
XX
OS      Neisseria meningitidis strain H41.
XX
FH      Key      Location/Qualifiers
FT      Peptide 1..51
FT      Protein 52..513
FT      /label= "Mature_Nhba_deletion_mutant
FT      /note= "Predicted mature protein, specifically
FT      claimed in claim 12"
XX
PN      WO200155182-A1.
XX
PD      02-AUG-2001.
XX
PE      25-JAN-2001; 2001WO-AU00069.
XX
PR      25-JAN-2000; 2000US-0177917.
XX
PA      (UYOU ) UNIV QUEENSLAND.
XX
PI      Peak IRA, Jennings MP;
XX      WPI; 2001-488774/53.
XX      DR      N-PSDB; AAS09173.
XX
PT      New Nhba surface antigen polypeptides and polynucleotides from
PT      Neisseria meningitidis, useful in producing vaccines for treating or
PT      preventing broad spectrum of Neisseria meningitidis -
XX
PS      Claim 12; Fig 6; 91pp; English.
XX
CC      The present invention relates to the isolation of novel Neisseria
CC      meningitidis mutant polypeptides of the surface antigen Nhba
CC      (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are
CC      characterised by deletions of non-conserved amino acids, particularly
CC      the deletion of variable regions. The deletion mutants are useful in
CC      diagnostics, therapeutic and prophylactic vaccines against a broader
CC      spectrum of N. meningitidis, and in designing and/or screening of
CC      medicaments. The mutant proteins when used as a vaccine can effectively
CC      immunise against a broader spectrum of N. meningitidis strains than
CC      would be expected from a corresponding wild-type surface antigen.
CC      The present sequence represents N. meningitidis strain H41 surface
CC      antigen Nhba deletion mutant.
XX

```

SQ Sequence 513 AA;
Query Match 94.5%; Score 2456.5; DB 22; Length 513;
Best Local Similarity 95.3%; Pred. No. 6-145;
Matches 489; Conservative 5; Mismatches 18; Indels 1; Gaps 1;

QY 1 MKKIRIINWSALNMAVYSELTRNHTKASATVKTAVLATLLFATVOASANNEDLTSV 60
DB 1 MKKIRIINWSALNMAVASELTRNHTKASATVKTAVLATLLFATVOANATDEDEEL 60
QY 61 GTEKISFSGANGKVNITSDTKGINPAKETAGTNGDTVHLNGISLTTLMLNTGATTV 120
DB 61 ETEKISFSGANGKVNITSDTKGINPAKETAGTNGDTVHLNGISLTTLMLNTGATTV 120
QY 121 TNDNVTDEKKRAASVDVNLNAGWNKGVKPGTTASDNDVFRITYDTVEFLSADTKTV 180
DB 121 TNDNVTDEKKRAASVDVNLNAGWNKGVKPGTTASDNDVFRITYDTVEFLSADTKTV 180
QY 181 NVESKDNCKKTEVKIGAKTSVIEKDKLVTSKDKENGSSFDEGGLVTAKEVDAVK 240
DB 181 NVESKDNCKKTEVKIGAKTSVIEKDKLVTSKDKENGSSFDEGGLVTAKEVDAVK 240
QY 241 AGMRKTTTANGOTGADKFEVTSTNTVPSAGKTTATVSKDOGNTVATDVAVGA 300
DB 241 AGMRKTTTANGOTGADKFEVTSTNTVPSAGKTTATVSKDOGNTVATDVAVGA 300
QY 301 LNVNOLONGSMNLDKSAVAGSSGKVTSGNVSPSKGMDETVNNAGNNIEITRNGKNIDI 360
DB 301 LNVNOLONGSMNLDKSAVAGSSGKVTSGNVSPSKGMDETVNNAGNNIEITRNGKNIDI 360
QY 361 ATSMPTPOFSSVSLGAGADAPTLSDVDG-ALNVGSKKDNKPVRTTNVAPGVKEGDTVNAQ 419
DB 361 ATSMPTPOFSSVSLGAGADAPTLSDVDGALNVGSKKDNKPVRTTNVAPGVKEGDTVNAQ 420
QY 420 LKGVQNLNRRIDNDVGNARAGIAQAIATAGLVQATLPGKSMAIGCGYRGAGATGY 479
DB 421 LKGVQNLNRRIDNDVGNARAGIAQAIATAGLVQATLPGKSMAIGCGYRGAGATGY 480
QY 480 SSISDGNWIIKGTASGNSRGHFASASVGYOM 512
DB 481 SSISAGGNWIIKGTASGNSRGHFASASVGYOM 513

RESULT 10
AA23743
ID AA23743 standard; Protein; 599 AA.
XX
AC AA23743;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
XX
KW Immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN MO9931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PA (UYOU) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX
DR WPI; 1999-418754/35.
DR N-PSDB; AAX85795.

XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
PS Claim 1; Page 114-115; 132pp: English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.

SQ Sequence 599 AA;
Query Match 94.4%; Score 2453.5; DB 20; Length 599;
Best Local Similarity 83.0%; Pred. No. 1-2e-144;
Matches 497; Conservative 4; Mismatches 11; Indels 87; Gaps 2;

QY 1 MKKIRIINWSALNMAVYSELTRNHTKASATVKTAVLATLLFATVOASANNE----- 54
DB 1 MKKIRIINWSALNMAVASELTRNHTKASATVKTAVLATLLFATVOANATDEDEEEL 60
QY 55 -----
DB 61 EPPVNSALVLPQIMIDKEGNGENESTGNIGMSIYYDNHNTLHGATVTLKAGDLKIKONTN 120
QY 55 -----
DB 121 KMTNENTNDSSEFYSLSKKDLTDLTSVETKLSFGANGKNVNTSDTKGINFAKETAGTNG 180
QY 95 DPTVHLNGISLTTLTLNTGATNTNNDVNDDEKKRAASVDVNLNAGWNKGVKPGTT 154
DB 181 DPTVHLNGISLTTLTLNTGATNTNNDVNDDEKKRAASVDVNLNAGWNKGVKPGTT 240
QY 155 ASDNDVFRITYDTVEFLSADTKTNTVNVESKDNCKKTEVKIGAKTSVIEKDKLVTSKDK 214
DB 241 ASDNDVFRITYDTVEFLSADTKTNTVNVESKDNCKKTEVKIGAKTSVIEKDKLVTSKDK 300
QY 215 KGENSSFDEGGLVTAKEVDAVNAKGRMKTTTANGOTGADKFEVTSTNTVPSAG 274
DB 301 KGENSSFDEGGLVTAKEVDAVNAKGRMKTTTANGOTGADKFEVTSTNTVPSAG 360
QY 275 KGTATVSKDOGNTVATDVAVGALNVOLONSGMNLDKSAVAGSSGKVTSGNVSPSK 334
DB 361 KGTATVSKDOGNTVATDVAVGALNVOLONSGMNLDKSAVAGSSGKVTSGNVSPSK 420
QY 335 GRMDETVNNAGNNIEITRNGKNIDIATSMPTPOFSSVSLGAGADAPTLSDVDG-DALNVGS 393
DB 421 GRMDETVNNAGNNIEITRNGKNIDIATSMPTPOFSSVSLGAGADAPTLSDVDGKALNVGS 480
QY 394 KDKNKPVRITTNVAPGVKEGDTVNAQVKVAONLNNRIDNDVGNARAGIAQAIATAGLVQ 453
DB 481 KDKNKPVRITTNVAPGVKEGDTVNAQVKVAONLNNRIDNDVGNARAGIAQAIATAGLVQ 540
QY 454 ATLPKSMMAIGCGYRGAGATGYSSISDGNWIIKGTASGNSRGHFASASVGYOM 512
DB 541 ATLPKSMMAIGCGYRGAGATGYSSISDGNWIIKGTASGNSRGHFASASVGYOM 599

RESULT 11
AAU06176
ID AAU06176 standard; Protein; 599 AA.
XX
AC AAU06176;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis H38 surface antigen NhaA polypeptide sequence.

Matches	497;	Conservative	4;	Mismatches	11;	Indels	87;	Gaps	2;
QY	1	NKKIRRIIWN	SALNMAVVS	SELT	RRHTRKASAT	YKTAVALATLL	FAFYAOSANNE	-----	54
Db	1	NKKIRRIIWN	SALNMAVVS	SELT	RRHTRKASAT	YKTAVALATLL	FAFYAOSANNE	DEDEBEL	60
QY	55	-----	-----	-----	-----	-----	-----	-----	54
Db	61	EPVRSALVLQ	EMIDKEG	NESTGNIG	WSIYYDNHNT	LHGATVTLKAGDNLK	IKOMTN		120
QY	55	-----	-----	-----	-----	-----	-----	-----	94
Db	121	KNTNENTNDS	SEFYSY	LKCOLD	TLDTSETEK	LSFGANGKRN	VNTSDPTKGLN	FAKEATGAG	180
QY	95	DTTVHLNGIS	TLDTTLNTG	ATTWTDND	NTDDEK	KKRAASYKDV	LNLGAMN	KGPKPGTT	154
Db	181	DTTVHLNGIS	TLDTTLNTG	ATTWTDND	NTDDEK	KKRAASYKDV	LNLGAMN	KGPKPGTT	240
QY	155	ASDNVDFV	RTDYTFE	LSADTKTT	TVNYESK	DKNGKTEV	KIGAKTSV	IKENDGLV	214
Db	241	ASDNVDFV	RTDYTFE	LSADTKTT	TVNYESK	DKNGKTEV	KIGAKTSV	IKENDGLV	300
QY	215	KGENSSST	DEGEGLY	TAKEVIDA	VNAKAG	RMAKTTTAN	OTGQADK	FEVTSGTNT	274
Db	301	KGENSSST	DEGEGLY	TAKEVIDA	VNAKAG	RMAKTTTAN	OTGQADK	FEVTSGTNT	360
QY	275	KGTTATVSK	DDOGNTT	WVDVNG	ALVNO	LNSGMM	LDKRAV	GSSGKVT	334
Db	361	KGTTATVSK	DDOGNTT	WVDVNG	ALVNO	LNSGMM	LDKRAV	GSSGKVT	420
QY	335	GKMDETVIN	INAGNNIE	ITRNGKN	IDIATSM	TPQSFSSV	SLGAGADA	P	393
Db	421	GKMDETVIN	INAGNNIE	ITRNGKN	IDIATSM	TPQSFSSV	SLGAGADA	P	480
QY	394	KKDNK	PVRITN	VAPEVKG	BDVTNNA	QLKGA	ONLNN	RIDNDG	512
Db	481	KDNK	PVRITN	VAPEVKG	BDVTNNA	QLKGA	ONLNN	RIDNDG	540
QY	454	AYLPKSSMA	ATGCGT	YRGEAG	ATGCGSS	ISOGMM	ITIGTAS	GNRGH	512
Db	541	AYLPKSSMA	ATGCGT	YRGEAG	ATGCGSS	ISOGMM	ITIGTAS	GNRGH	599
RESULT 12									
AAV23740									
ID	AAV23740 standard; Protein; 594 AA.								
XX	AAV23740;								
AC	AAV23740;								
XX	08-SEP-1999 (first entry)								
DT	A surface protein of Neisseria meningitidis.								
XX	Surface protein; surface glycoprotein; infection; vaccine;								
KW	immunoreactive peptide.								
XX	Neisseria meningitidis.								
OS	Neisseria meningitidis.								
PN	W09931132-A1.								
XX	24-JUN-1999.								
PD	14-DEC-1998; 98WO-AU01031.								
PF	12-DEC-1997; 97GB-0026398.								
XX	(ISIS-) ISIS INNOVATION LTD.								
PA	(UYOU) UNIT QUEENSLAND.								
XX	Jennings MP, Moxon ER, Peak IRA.								

XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX

PS Claim 1; Page 100-101; 132pp; English.

XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX

Sequence 594 AA;

Query Match 94.2%; Score 2449; DB 20; Length 594;
Best Local Similarity 83.3%; Pred. No. 2.3e-144;
Matches 495; Conservative 6; Mismatches 11; Indels 82; Gaps 2;

```

OY 1 MNKIRIIRIWNNSALNMAVAVVSELTRNHTKRASATVAVLALFLFATVQASANNE----- 54
    |||||||
DB 1 MNKIRIIRIWNNSALNMAVAVVSELTRNHTKRASATVAVLALFLFATVQASSTDDDDLYLE 60
    |||||||
OY 55 ----- 54
DB 61 PVQRTAVVLSFRSDEKTEGKEVEEDSNMGVYFDKKGVLTAGTTTLKAGDNLIKONTNE 120
OY 55 -----TDLTSVTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTVH 99
    |||||||
DB 121 NTNASSFTYSLKKDLTDLTSVTEKLSFSANSNKVNITSDTKGLNFAKTAETNGDTVH 180
OY 100 LNGIGSTLDTLTLNLTGATNTVNDVTDDEKKRAASVDVNLNAGNNIGVKGPGTASDNV 159
    |||||||
DB 181 LNGIGSTLDTLTLNLTGATNTVNDVTDDEKKRAASVDVNLNAGNNIGVKGPGTASDNV 240
OY 160 DVRTYDIVEFLSADTKTTTVNVEESKDKGKTEVKGATSVYKEKDKLVTGKDKENG 219
    |||||||
DB 241 DVRTYDIVEFLSADTKTTTVNVEESKDKGKTEVKGATSVYKEKDKLVTGKDKENG 300
OY 220 SSTDEGECVLTAKEVIDAVNKAQWPKTTTANGOTGQADKEFTVTSCTNVTFASGKGTGA 279
    |||||||
DB 301 SSTDEGECVLTAKEVIDAVNKAQWPKTTTANGOTGQADKEFTVTSCTNVTFASGKGTGA 360
OY 280 TVSKDQGNITVMYVNVNVDALNVNQLNSGNLDSKAVAGSSGVISGNNVSPSKGKMD 339
    |||||||
DB 361 TVSKDQGNITVMYVNVNVDALNVNQLNSGNLDSKAVAGSSGVISGNNVSPSKGKMD 420
OY 340 TVNINAGNNIETTRNGKNIDTATSMTPOFSSVSLGAGADAPTLISVDCD-ALNVSGSKKNK 398
    |||||||
DB 421 TVNINAGNNIETTRNGKNIDTATSMTPOFSSVSLGAGADAPTLISVDCD-ALNVSGSKKNK 480
OY 399 PVRTITNAPGVKESGDVTNVAOLKGYAONLNNRIDVNDGNARAGIAOAIATAGLVQAYLP 458
    |||||||
DB 481 PVRTITNAPGVKESGDVTNVAOLKGYAONLNNRIDVNDGNARAGIAOAIATAGLVQAYLP 540
OY 459 KSMMAIGGCTYRGEAGYALIGYSSISDGGNMIITKGASGNSRCHPEASASVGVQW 512
    |||||||
DB 541 KSMMAIGGCTYRGEAGYALIGYSSISDGGNMIITKGASGNSRCHPEASASVGVQW 594

```

RESULT 13

AA57044 ID AA57044 standard; Protein; 594 AA.

AC AA57044;

XX 21-FEB-2000 (first entry)

DE BASB029 amino acid sequence from N. meningitidis strain ATCC13090.

KW BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis;
KW infection; treatment; prevent; antibacterial drug.
XX

XX Neisseria meningitidis.

EH Key Location/Qualifiers
FT Misc-difference 104
PT /note= "Encoded by AATC"

MO958683-A2.

18-NOV-1999.

07-MAY-1999; 99WO-EP03255.

13-MAY-1998; 98GB-0010276.

(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

Ruelle J;

WPI; 2000-053103/04.

N-PSDB; AAZ39864.

New polypeptide from neisseria meningitidis useful for diagnosis,
PT treatment or prevention of bacterial infections in mammal

PS Claim 4; Fig 2; 74pp; English.

XX This is the Nisseria meningitidis BASB029 amino acid sequence from
CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the
CC Haemophilus influenzae surface fibril (HSF) protein. The invention
CC relates to BASB029 polynucleotide sequences (AAZ39864-239865) and
CC polypeptide sequences (AA57044-Y57045) and their immunogenic fragments.
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria
CC meningitidis infection in a mammal. Compositions containing BASB029
CC polynucleotides and polypeptides are useful for generating an immune
CC response in an animal. A therapeutic composition comprising an antibody
CC directed against BASB029 is useful in treating humans with Neisseria
CC meningitidis disease. The polynucleotide is useful in the diagnosis of
CC the stage of infection, type of infection, susceptibility to an
CC infection which results from increased or decreased expression of the
CC polynucleotide, and for therapeutic or prophylactic purposes.
CC particularly genetic immunisation. Antibodies against BASB029
CC polynucleotides and polypeptides are also useful for treating infections
CC particularly bacterial infections. The protein is useful in the
CC screening and development of antibacterial drugs. Fused recombinant
CC protein is useful for the stimulation of the immune system of an organism
XX receiving the protein.

Sequence 594 AA;

Query Match 94.2%; Score 2449; DB 21; Length 594;
Best Local Similarity 83.3%; Pred. No. 2.3e-144;
Matches 495; Conservative 6; Mismatches 11; Indels 82; Gaps 2;

```

OY 1 MNKIRIIRIWNNSALNMAVAVVSELTRNHTKRASATVAVLALFLFATVQASANNE----- 54
    |||||||
DB 1 MNKIRIIRIWNNSALNMAVAVVSELTRNHTKRASATVAVLALFLFATVQASSTDDDDLYLE 60
    |||||||
OY 55 ----- 54
DB 61 PVQRTAVVLSFRSDEKTEGKEVEEDSNMGVYFDKKGVLTAGTTTLKAGDNLIKONTNE 120
OY 55 -----TDLTSVTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTVH 99
    |||||||
DB 121 NTNASSFTYSLKKDLTDLTSVTEKLSFSANSNKVNITSDTKGLNFAKTAETNGDTVH 180
OY 100 LNGIGSTLDTLTLNLTGATNTVNDVTDDEKKRAASVDVNLNAGNNIGVKGPGTASDNV 159
    |||||||
DB 181 LNGIGSTLDTLTLNLTGATNTVNDVTDDEKKRAASVDVNLNAGNNIGVKGPGTASDNV 240
OY 160 DVRTYDIVEFLSADTKTTTVNVEESKDKGKTEVKGATSVYKEKDKLVTGKDKENG 219

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Db      241 DEVRITDVEEFLSADTKTTTVNVESEKNGKRETEVKIGAKTSVIREKDGKLVTKDGKEND 300
QY      220 SSTDEBGLVTAKEVIDAVNKKAGMRKTTTANGOTGOAKFEVTVSGTNTFASGKGT 279
Db      301 SSTDKGEGLVTAKEVIDAVNKKAGMRKTTTANGOTGOAKFEVTVSGTNTFASGKGT 360
QY      280 TVSKDQGNITVYDVNVDALNVNOLONGSNGLDSKAVAGSSGKVISGNSVPSKGMDE 339
Db      361 TVSKDQGNITVYDVNVDALNVNOLONGSNGLDSKAVAGSSGKVISGNSVPSKGMDE 420
QY      340 TVNINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKDKN 398
Db      421 TVNINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKDKN 480
QY      399 PVKITVAPGVKRGDVTNVAOLKGVANLNINRDNDVGNARAGIAQAIATAGLVQAYLPG 458
Db      481 PVKITVAPGVKRGDVTNVAOLKGVANLNINRDNDVGNARAGIAQAIATAGLVQAYLPG 540
QY      459 KSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 512
Db      541 KSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 594

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RESULT 14

AAU06174 standard; Protein: 594 AA.

AAU06174:

24-OCT-2001 (first entry)

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DE      N. meningitidis EG327 surface antigen Nhma polypeptide sequence.
XX      Surface antigen Nhma: meningococcal disease; meningitis vaccine.
XX      Neisseria meningitidis strain EG327.
XX      Location/Qualifiers
FH      1..50
FT      /label= C1
FT      /note= "Conserved region 1"
FT      /label= V1
FT      /note= "Variable region 1"
FT      /label= C2
FT      /note= "Conserved region 2"
FT      /label= V2
FT      /note= "Variable region 2"
FT      /label= C3
FT      /note= "Conserved region 3"
FT      /label= V3
FT      /note= "Variable region 3"
FT      /label= C4
FT      /note= "Conserved region 4"
FT      /label= V4
FT      /note= "Variable region 4"
FT      /label= C5
FT      /note= "Conserved region 5"

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02-AUG-2001.
25-JAN-2001: 2001WO-AU00069.

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PR      25-JAN-2000: 2000US-0177917.
XX      (UYOU ) UNIV QUEENSLAND.
XX      Peak IRA, Jennings MP;
XX      WPI: 2001-488774/53.
XX      DR N-FSDB: AAS09164.
XX      New Nhma surface antigen polypeptides and polynucleotides from
XX      PT Neisseria meningitidis, useful in producing vaccines for treating or
XX      PS preventing broad spectrum of Neisseria meningitidis -
XX      Claim 9; Fig 1; 91pp; English.
XX      The present invention relates to the isolation of novel Neisseria
XX      CC meningitidis mutant polypeptides of the surface antigen Nhma
XX      CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are
XX      CC characterised by deletions of non-conserved amino acids, particularly
XX      CC the deletion of variable regions. The deletion mutants are useful in
XX      CC diagnostics, therapeutic and prophylactic vaccines against a broader
XX      CC spectrum of N. meningitidis, and in designing and/or screening of
XX      CC medicaments. The mutant proteins when used as a vaccine can effectively
XX      CC immunise against a broader spectrum of N. meningitidis strains than
XX      CC would be expected from a corresponding wild-type surface antigen.
XX      CC The present sequence representing the wild type surface antigen Nhma
XX      CC from N. meningitidis strain EG327 is 1 of 10 Nhma polypeptide sequences
XX      CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX      CC the present invention.
SQ      Sequence 594 AA:

```

Query Match 94.2%; Score 2449; DB 22; Length 594;

Best Local Similarity 83.3%; Pred. No. 2, 3e-144;

Matches 495; Conservative 6; Mismatches 11; Indels 82; Gaps 2;

```

QY      1 MKKIYIINNSALNAVWVSELTNRHTKRASATVTRAVATLLEFATVOASNE----- 54
Db      1 MKKIYIINNSALNAVWVSELTNRHTKRASATVTRAVATLLEFATVOASTDDDDLYLE 60
QY      55 ----- 54
Db      61 PVQRTAVLSFRSDKRGTEKEVEYEDSNMGVYFDKKGVLTAGTITLKADNLKIKONTNE 120
QY      55 ----- 54
Db      55 ----- 54
QY      121 NTNASSFTYSLKDLTDLTLSVGTKEKLSFANSRKVITSDTGLNFAKKTAEFTNGDTTVA 180
Db      121 LNCIGSTLTDTLLNTGATNTNTNDVYTDDEKRAASVKDYLVNAGNMIKGVKPGTASDNY 159
QY      100 LNCIGSTLTDTLLNTGATNTNTNDVYTDDEKRAASVKDYLVNAGNMIKGVKPGTASDNY 159
Db      181 LNCIGSTLTDTLLNTGATNTNTNDVYTDDEKRAASVKDYLVNAGNMIKGVKPGTASDNY 240
QY      160 DEVRITDVEEFLSADTKTTTVNVESEKNGKRETEVKIGAKTSVIREKDGKLVTKDGKENG 219
Db      241 DEVRITDVEEFLSADTKTTTVNVESEKNGKRETEVKIGAKTSVIREKDGKLVTKDGKEND 300
QY      220 SSTDEBGLVTAKEVIDAVNKKAGMRKTTTANGOTGOAKFEVTVSGTNTFASGKGT 279
Db      301 SSTDKGEGLVTAKEVIDAVNKKAGMRKTTTANGOTGOAKFEVTVSGTNTFASGKGT 360
QY      280 TVSKDQGNITVYDVNVDALNVNOLONGSNGLDSKAVAGSSGKVISGNSVPSKGMDE 339
Db      361 TVSKDQGNITVYDVNVDALNVNOLONGSNGLDSKAVAGSSGKVISGNSVPSKGMDE 420
QY      340 TVNINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKDKN 398
Db      421 TVNINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKDKN 480
QY      399 PVKITVAPGVKRGDVTNVAOLKGVANLNINRDNDVGNARAGIAQAIATAGLVQAYLPG 458
Db      481 PVKITVAPGVKRGDVTNVAOLKGVANLNINRDNDVGNARAGIAQAIATAGLVQAYLPG 540
QY      459 KSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOM 512

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:14:45 : Search time 13.6919 Seconds
(without alignments)
1582.188 Million cell updates/sec

Title: US-09-771-382-23
Perfect score: 2600
Sequence: 1 MNKIYRIINNSALNMAVYVS.....TASGNSRGHFGASAGYQW 512

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2550.5	98.1	591	US-09-377-155-21	Sequence 21, Appl
2	2550.5	98.1	591	US-09-669-974-21	Sequence 21, Appl
3	2546	97.9	592	US-09-377-155-2	Sequence 2, Appl
4	2546	97.9	592	US-09-669-974-2	Sequence 2, Appl
5	2538.5	97.6	591	US-09-377-155-11	Sequence 11, Appl
6	2538.5	97.6	591	US-09-669-974-11	Sequence 11, Appl
7	2453.5	94.4	599	US-09-377-155-15	Sequence 15, Appl
8	2453.5	94.4	599	US-09-669-974-15	Sequence 15, Appl
9	2449	94.2	594	US-09-377-155-9	Sequence 9, Appl
10	2449	94.2	594	US-09-669-974-9	Sequence 9, Appl
11	2442	93.9	594	US-09-377-155-7	Sequence 7, Appl
12	2442	93.9	594	US-09-669-974-7	Sequence 7, Appl
13	2427	93.3	598	US-09-377-155-13	Sequence 13, Appl
14	2427	93.3	598	US-09-669-974-13	Sequence 13, Appl
15	2418	93.0	598	US-09-377-155-5	Sequence 5, Appl
16	2418	93.0	598	US-09-669-974-5	Sequence 5, Appl
17	2407	92.6	592	US-09-377-155-17	Sequence 17, Appl
18	2407	92.6	592	US-09-669-974-17	Sequence 17, Appl
19	2234.5	86.7	589	US-09-377-155-19	Sequence 19, Appl
20	2234.5	86.7	589	US-09-669-974-19	Sequence 19, Appl
21	991	38.1	1094	US-09-268-347-32	Sequence 32, Appl
22	991	38.1	1098	US-08-409-995-2	Sequence 2, Appl
23	991	38.1	1098	US-08-685-467-2	Sequence 2, Appl
24	991	38.1	1098	US-09-377-155-32	Sequence 32, Appl
25	991	38.1	1098	US-08-913-942-2	Sequence 2, Appl
26	991	38.1	1098	US-09-669-974-32	Sequence 32, Appl
27	991	38.1	1098	US-09-268-347-44	Sequence 44, Appl

28	973	37.4	658	1	US-08-409-995-5	Sequence 5, Appl
29	973	37.4	658	3	US-08-685-467-5	Sequence 5, Appl
30	973	37.4	658	3	US-08-913-942-5	Sequence 5, Appl
31	956.5	36.8	2411	4	US-09-268-347-36	Sequence 36, Appl
32	954.5	36.7	2353	3	US-09-377-155-33	Sequence 33, Appl
33	954.5	36.7	2353	3	US-08-913-942-4	Sequence 4, Appl
34	954.5	36.7	2353	4	US-09-669-974-33	Sequence 33, Appl
35	953.5	36.7	2354	4	US-09-268-347-47	Sequence 47, Appl
36	897	34.5	607	1	US-08-409-995-6	Sequence 6, Appl
37	897	34.5	607	3	US-08-685-467-6	Sequence 6, Appl
38	897	34.5	607	3	US-08-913-942-6	Sequence 6, Appl
39	897	34.5	1912	1	US-08-409-995-4	Sequence 4, Appl
40	897	34.5	1912	3	US-08-685-467-4	Sequence 4, Appl
41	789.5	30.4	679	3	US-08-913-942-15	Sequence 15, Appl
42	789.5	30.4	679	4	US-09-268-347-26	Sequence 26, Appl
43	683	26.3	1004	4	US-09-268-347-30	Sequence 30, Appl
44	679	26.1	1002	4	US-09-268-347-24	Sequence 24, Appl
45	573	22.0	1104	4	US-09-268-347-28	Sequence 28, Appl

ALIGNMENTS

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RESULT 1
US-09-377-155-21
; Sequence 21, Application US/09377155
; Patent No. 6197312
;
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO: 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-21
Query Match      98.1%; Score 2550.5; DB 3; Length 591;
Best Local Similarity 86.6%; Pred. No. 2.4e-197;
Matches 512; Conservative 0; Mismatches 0; Indels 79; Gaps 1;

QY      1 MNKIYRIINNSALNMAVYVSELTNRNITKRSATVKAVALATLTFATVOASANNE----- 54
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DB      1 MNKIYRIINNSALNMAVYVSELTNRNITKRSATVKAVALATLTFATVOASANNEDEDL 60
QY      55 ----- 54
DB      61 YLDPVORTAVLIVNSDKRGTEKEVENSMDAVFNEKCVLTAREITLKKADNLKIQO 120
QY      55 ----- 54
DB      121 NGNFTYSIAKKDLDLTSVGETKLSFSAANGKNKINISDKLGNFAFETAGTNGDITVHLN 180
QY      102 GIGSTLTDLTLNLTGATTNTVNDVYDEKKRAASVADVLNAGNINIGVPGRTASDNVDF 161
        |||||||
DB      181 GIGSTLTDLTLNLTGATTNTVNDVYDEKKRAASVADVLNAGNINIGVPGRTASDNVDF 240
QY      162 VRTYDVEFLSADTKTTTVNVSCKGKTEVKGKTSVIREKDKLVTGKDKGNGSS 221
        |||||||
DB      241 VRTYDVEFLSADTKTTTVNVSCKGKTEVKGKTSVIREKDKLVTGKDKGNGSS 300
QY      222 TDEGEGLVTAKEVIDAVNKRAGRMKTTTNGGTGQADKFEVYSGTNTVPASGKGTATV 281
        |||||||
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Db 301 TDEGEGLVTAKEVIDAVNKAQWRMKTTTANGOTGOADKFEVTSGTNTVFASGKGTATV 360
QY 282 SKDOGNITVWYDVNVGDALNVNOLONGMNLDSKAVAGSSGKVIISGNVSPSKGMDFTV 341
Db 361 SKDOGNITVWYDVNVGDALNVNOLONGMNLDSKAVAGSSGKVIISGNVSPSKGMDFTV 420
QY 342 NINAGNNIETIRNKNKIDDIATSMTPPOFSSVSLGAGADAPTLISVGDALNVSSKDKNRPVR 401
Db 421 NINAGNNIETIRNKNKIDDIATSMTPPOFSSVSLGAGADAPTLISVGDALNVSSKDKNRPVR 480
QY 402 ITNAPGVKEGDVTNNVAOLKGVQAOVLNNRINDVGNARAGIAQAIATATGLVQAYLPGKSM 461
Db 481 ITNAPGVKEGDVTNNVAOLKGVQAOVLNNRINDVGNARAGIAQAIATATGLVQAYLPGKSM 540
QY 462 MAIGGTYRGEAGYAIIGYSSISDGGNMIITKGTASGNSGHHFGASASVGYQW 512
Db 541 MAIGGTYRGEAGYAIIGYSSISDGGNMIITKGTASGNSGHHFGASASVGYQW 591

RESULT 2

US-09-669-974-21
; Sequence 21, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-21

Query Match 98.1%; Score 2550.5; DB 4; Length 591;
Best Local Similarity 86.6%; Pred. No. 2.4e-197;
Matches 512; Conservative 0; Mismatches 0; Indels 79; Gaps 1;

QY 1 MNKIYRIIWSALNANMYYVSELTRNHTKRASATVTAVALTLLEFATVOASANNE----- 54
Db 1 MNKIYRIIWSALNANMYYVSELTRNHTKRASATVTAVALTLLEFATVOASANNEEQEDDL 60
QY 55 ----- 54
Db 61 YLDPVQRTAVAVLIYNSDKEGTGEKEVEENSDMAVYFNEKGVLTAAREITLKAGDNLKIK 120
QY 55 ----- 54
Db 121 NGTNTFTYSLKRDLDLTLSVGTETKLSFSANGKNKVNITSDTGKLNFAKKTAGTNGDTTVALN 101
QY 121 NGTNTFTYSLKRDLDLTLSVGTETKLSFSANGKNKVNITSDTGKLNFAKKTAGTNGDTTVALN 180
QY 102 GIGSTLDITLNTGATNTVNDNTVDDEKKRAASVADVLANAGWNIKGVKPGTTASDNVDF 161
Db 181 GIGSTLDITLNTGATNTVNDNTVDDEKKRAASVADVLANAGWNIKGVKPGTTASDNVDF 240
QY 162 VRTDYVTEFLSADTKTTTVNVEESKDNKKTEVKGATSVIKKEKDKGLVTKDKGNGSS 221
Db 241 VRTDYVTEFLSADTKTTTVNVEESKDNKKTEVKGATSVIKKEKDKGLVTKDKGNGSS 300
QY 222 TDEGEGLVTAKEVIDAVNKAQWRMKTTTANGOTGOADKFEVTSGTNTVFASGKGTATV 281
Db 301 TDEGEGLVTAKEVIDAVNKAQWRMKTTTANGOTGOADKFEVTSGTNTVFASGKGTATV 360

QY 282 SKDOGNITVWYDVNVGDALNVNOLONGMNLDSKAVAGSSGKVIISGNVSPSKGMDFTV 341
Db 361 SKDOGNITVWYDVNVGDALNVNOLONGMNLDSKAVAGSSGKVIISGNVSPSKGMDFTV 420
QY 342 NINAGNNIETIRNKNKIDDIATSMTPPOFSSVSLGAGADAPTLISVGDALNVSSKDKNRPVR 401
Db 421 NINAGNNIETIRNKNKIDDIATSMTPPOFSSVSLGAGADAPTLISVGDALNVSSKDKNRPVR 480
QY 402 ITNAPGVKEGDVTNNVAOLKGVQAOVLNNRINDVGNARAGIAQAIATATGLVQAYLPGKSM 461
Db 481 ITNAPGVKEGDVTNNVAOLKGVQAOVLNNRINDVGNARAGIAQAIATATGLVQAYLPGKSM 540
QY 462 MAIGGTYRGEAGYAIIGYSSISDGGNMIITKGTASGNSGHHFGASASVGYQW 512
Db 541 MAIGGTYRGEAGYAIIGYSSISDGGNMIITKGTASGNSGHHFGASASVGYQW 591

RESULT 3

US-09-377-155-2
; Sequence 2, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-2

Query Match 97.9%; Score 2546; DB 3; Length 592;
Best Local Similarity 86.3%; Pred. No. 5.4e-197;
Matches 511; Conservative 0; Mismatches 1; Indels 80; Gaps 1;

QY 1 MNKIYRIIWSALNANMYYVSELTRNHTKRASATVTAVALTLLEFATVOASANNE----- 54
Db 1 MNKIYRIIWSALNANMYYVSELTRNHTKRASATVTAVALTLLEFATVOASANNEPRKKD 60
QY 55 ----- 54
Db 61 YLDPVQRTAVAVLIYNSDKEGTGEKEVEENSDMAVYFNEKGVLTAAREITLKAGDNLKIK 120
QY 55 ----- 54
Db 121 QNGTNTFTYSLKRDLDLTLSVGTETKLSFSANGKNKVNITSDTGKLNFAKKTAGTNGDTTVALN 180
QY 101 NGIGSTLDITLNTGATNTVNDNTVDDEKKRAASVADVLANAGWNIKGVKPGTTASDNVDF 160
Db 181 NGIGSTLDITLNTGATNTVNDNTVDDEKKRAASVADVLANAGWNIKGVKPGTTASDNVDF 240
QY 161 FVRTDYVTEFLSADTKTTTVNVEESKDNKKTEVKGATSVIKKEKDKGLVTKDKGNGSS 220
Db 241 FVRTDYVTEFLSADTKTTTVNVEESKDNKKTEVKGATSVIKKEKDKGLVTKDKGNGSS 300
QY 221 STDEGEGLVTAKEVIDAVNKAQWRMKTTTANGOTGOADKFEVTSGTNTVFASGKGTATV 280
Db 301 STDEGEGLVTAKEVIDAVNKAQWRMKTTTANGOTGOADKFEVTSGTNTVFASGKGTATV 360
QY 281 VSKDOGNITVWYDVNVGDALNVNOLONGMNLDSKAVAGSSGKVIISGNVSPSKGMDFT 340
Db 361 VSKDOGNITVWYDVNVGDALNVNOLONGMNLDSKAVAGSSGKVIISGNVSPSKGMDFT 420

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Db	421	VNANNGNIEITRRNKNIDIASMTPOESSVSLGAGADAPTLSVSDDALNYSKKONKPY	480
OY	401	RITNVPVKKEDVYNVAOLKGVANLNRRIDNVGNARAGIAQATATAGIYVAYLPGRS	460
Db	481	RITNVPVKKEDVYNVAOLKGVANLNRRIDNVGNARAGIAQATATAGIYVAYLPGRS	540
OY	461	MMAIIGGGRGDEAGYAIGYSSISDGGNMWIKGTASGNSRGHGASASVYGOW	512
Db	541	MMAIIGGGRGDEAGYAIGYSSISDGGNMWIKGTASGNSRGHGASASVYGOW	592

RESULT 4
 US-09-669-974-2
 : Sequence 2, Application US/09669974
 : Patent No. 633173
 : GENERAL INFORMATION:
 : APPLICANT: PEAK, Ian Richard Anselm
 : APPLICANT: JENNINGS, Michael Paul
 : APPLICANT: MOXON, E. Richard
 : TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
 : FILE REFERENCE: 065064/0128
 : CURRENT APPLICATION NUMBER: US/09/669, 974
 : CURRENT FILING DATE: 2000-09-26
 : PRIOR APPLICATION NUMBER: US 09/377, 155
 : PRIOR FILING DATE: 1999-08-19
 : PRIOR APPLICATION NUMBER: PCT/AU98/01031
 : PRIOR FILING DATE: 1998-12-14
 : PRIOR APPLICATION NUMBER: GB 9726398.2
 : PRIOR FILING DATE: 1997-12-12
 : NUMBER OF SEQ ID NOS: 33
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 2
 : LENGTH: 592
 : TYPE: PRT
 : ORGANISM: *Neisseria meningitidis*
 US-09-669-974-2

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Qy	401	RITNAPGVKEDDYNVAOLKGVADNNINRINDNNGNAAGATPOALTATGIVQATYIPGS	460
Db	481	RITNAPGVKEDDYNVAOLKGVADNNINRINDNNGNAAGATPOALTATGIVQATYIPGS	540
Qy	461	MMALIGGGYRGAGYAIGYSTISDGGNNIIKTGTASGNSKGHFGASASVYGW	512
Db	541	MMALIGGGYRGAGYAIGYSTISDGGNNIIKTGTASGNSKGHFGASASVYGW	592

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RESULT 5
US-09-377-155-11
: Sequence 11, Application US/09377155
: Patent No. 6197312
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/377, 155
: CURRENT FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 11
: LENGTH: 591
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-377-155-11

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	Query Match	97.6%	Score 2538.5;	DB: 3;	Length 591;
	Best Local Similarity	86.3%;	Pred. No. 2.2e-196;		
	Matches 510;	Conservative 1;	Mismatches 1;	Indels 79;	Gaps 1
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QY	55 -----	54			
Dd	61 YLDPYLRTAVALIYNDSKEGTEGEKEVEBNSDMAYTFENEKGVLTAIREITLKAGDNLIKIQ	120			
QY	55 -----TDLTISVGTEKESFSANGKNVNITSPTDKGLNFAKETAGNGDPTVHLN	101			
Dd	121 NGINFTYSLKKDLDLDTISVGTREKLFSFANGKNVNITSPTDKGLNFAKETAGNGDPTVHLN	180			
QY	102 GIGSTLDTDLINTGATTNTNDNTVDDEKKRAASYKDVNLNAGWINIKGVPGTTASDNDF	161			
Dd	181 GIGSTLDTDLINTGATTNTNDNTVDDEKKRAASYKDVNLNAGWINIKGVPGTTASDNDF	240			
QY	162 VRFTDYVEFLSADPRTTNTVESKONGKKTTEVIKGAFTSVIKERKGLVTGDKDENSS	221			
Dd	241 VRFTDYVEFLSADPRTTNTVESKONGKKTTEVIKGAFTSVIKERKGLVTGDKDENSS	300			
QY	222 TDESEGILTAKEVIDAIVNKAGMRMKTTHANGOTGOADRFEVTVSGTNVTFASGKCTATV	281			
Dd	301 TDESEGILTAKEVIDAIVNKAGMRMKTTHANGOTGOADRFEVTVSGTNVTFASGKCTATV	360			
QY	282 SKDDOGNTTWYDVNVGDALVNOLONSGMULDRAVNGSSGKVTSIGNVSPBKGMDETIV	341			
Dd	361 SKDDOGNTTWYDVNVGDALVNOLONSGMULDRAVNGSSGKVTSIGNVSPBKGMDETIV	420			
QY	342 NINAGNNIEIRNRGNIDIAISMTPOFFSSVSLGAGADAPTLSVGDALANVSKKKNKPEVR	401			
Dd	421 NINAGNNIEIRNRGNIDIAISMTPOFFSSVSLGAGADAPTLSVGDALANVSKKKNKPEVR	480			
QY	402 ITNVAPEGVEDVTNVAOIKGYAONLNRRINDVGNARAGTAQAATATAGLYOATPLPKASM	461			

Db 481 ITTNVAPGVKEGDTVTVADLKGVAQNINNRIDVDGARRAGIAQALITAGLVQAYLEFGSM 540

QY 462 MAIGGCTYRGAGYAIGYSSISDGGNWIITKGTASGSRBHFAGSASVGYQM 512
 |||||
 541 MAIGGCTYRGAGYAIGYSSISDGGNWIITKGTASGSRBHFAGSASVGYQM 591

RESULT 6
US-09-669-974-11
; Sequence 11, Application US/09669974

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1  GENERAL INFORMATION:
2  APPLICANT:  PEAK, Ian Richard Anselm
3  APPLICANT:  JENNINGS, Michael Paul
4  APPLICANT:  MOXON, E. Richard
5  TITLE OF INVENTION:  NOVEL SURFACE ANTIGEN
6  FILE REFERENCE:  065064/0128
7  CURRENT APPLICATION NUMBER:  US/09/669,974
8  CURRENT FILING DATE:  2000-09-26
9  PRIOR APPLICATION NUMBER:  US 09/377,155
10 PRIOR FILING DATE:  1999-08-19
11 PRIOR APPLICATION NUMBER:  PCT/AU99/01031
12 PRIOR FILING DATE:  1998-12-14
13 PRIOR APPLICATION NUMBER:  GB 9726398.2
14 PRIOR FILING DATE:  1997-12-12
15 NUMBER OF SEQ ID NOS:  33
16 SOFTWARE:  PatentIn Ver. 2.0
17 SEQ ID NO 11
18 LENGTH:  591
19 TYPE:  PRP
20 ORGAINISM:  Neisseria meningitidis
21 US-09-669,974-11

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Query Match	97.68%	Score 2538.5	-DB 4	Length 591
Best Local Similarity	86.38%	Pred. No. 2.2e-196		
Matches 510; Conservative	1;	Mismatches	1;	Indels 79; Gaps 1;

QY	1	MMKIRIIRIIMNSALNMVYVSELTIRNHTKASATVKAVALATLLEFAVYQASANNE----	54
Db	1	MNEILRIIRIIMNSALNMVYVSELTIRNHTKASATVKAVALATLLEFAVYQASANNEBQEDL	60
QY	55	-----	54
Db	61	YLDPLVLTVAVLIVNSDEKTEKEKEVENSBMAVYFNKRGVLTAREITLAKADNLIKIO	120
QY	55	-----TDLTSVGETEKLFSFANGKNVNIISPTKGLFARKEIAGTNDOTYHLN	101
Db	121	NGTNETYSLKKDLDLTSVGETEKLFSFANGKNVNIISPTKGLFARKEIAGTNDOTYHLN	180
QY	102	GIGSLTDLTLNTGATTNVTNDNVYTDDEKKRAASVKDVIYNAGNIIKGVKPGTTASDNVF	161
Db	181	GIGSLTDLTLNTGATTNVTNDNVYTDDEKKRAASVKDVIYNAGNIIKGVKPGTTASDNVF	240
QY	162	VRTYDVEEFLSADTETTTVTVNVESEKNGKKTEVKGAKTSVIREKDDKILVTKRDKGENGS	221
Db	241	VRTYDVEEFLSADTETTTVTVNVESEKNGKKTEVKGAKTSVIREKDDKILVTKRDKGENGS	300
QY	222	TDEBEGVLTAKEVIDAVNKAGHRMKTITTTANGOTGOADKEIETVYSGTNVTFPASKGTTAY	281
Db	301	TDEBEGVLTAKEVIDAVNKAGHRMKTITTTANGOTGOADKEIETVYSGTNVTFPASKGTTAY	360
QY	282	SKDDOGNTVMYDVAVGDLALNQNONSQMNLDSDKRAVASSSGVIGSNVSPSKGKDETV	341
Db	361	SKDDOGNTVMYDVAVGDLALNQNONSQMNLDSDKRAVASSSGVIGSNVSPSKGKDETV	420
QY	342	NIMAGNNIETIRNGKNIDIASMTPOFSSVIGAGADAETLSYDGDALNVGSKKDKPVR	401
Db	421	NIMAGNNIETIRNGKNIDIASMTPOFSSVIGAGADAETLSYDGDALNVGSKKDKPVR	480
QY	402	ITNAAPGVKEGDTVVAOLKGYAOUNLNRIIDVWDGARAAGINQALITAGIYQAYLYLGKSM	461
Db	481	ITNAAPGVKEGDTVVAOLKGYAOUNLNRIIDVWDGARAAGINQALITAGIYQAYLYLGKSM	540

[illegible]

RESULT 7
US-09-377-155-15
; Sequence 15, Application US/09377155
; Patent No. 6197312

```

1 GENEKIND INFORMATION
2 APPLICANT: PEAK, Ian Richard Anselm
3 APPLICANT: JENNINGS, Michael Paul
4 APPLICANT: MOXON, E. Richard
5 TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
6 FILE REFERENCE: 065064/0128
7 CURRENT APPLICATION NUMBER: US/09/377,155
8 CURRENT FILING DATE: 1999-08-19
9 PRIOR APPLICATION NUMBER: PCT/AU98/01031
10 PRIOR FILING DATE: 1998-12-14
11 PRIOR APPLICATION NUMBER: GB 9726398.2
12 PRIOR FILING DATE: 1997-12-12
13 NUMBER OF SEQ. ID NOS: 33
14 SOFTWARE: PatentIn Ver. 2.0
15 SEQ. ID NO. 15
16 LENGTH: 599
17 TYPE: PRF
18 ORGANISM: Neisseria meningitidis
19 US-09-377-155-15

```

Query Match	94.4%;	Score	2453.5;	DB	3	Length	599;
Best Local Similarity	83.0%;	Pred. No.	1.6e-189;				
Matches	497;	Conservative	4;	Mismatches	11;	Indels	87;
						Gaps	2

OY	1	MNKIYRIIMNSALNAAVVUSELTRYHHTKRASTVYTAVALTEFTYVOASANE-----	54
Dd	1	MNKIYRIIMNSALNAAVVASELTRYHHTKRASTVYTAVALTEFTYVOANATDEBEBEL	60
OY	55	-----	54
Dd	61	EPVRSALVLOFMIDKDEGNENESTGNIGMSIYYDNHNTLHGATVTLKAGDNLKTKOMTN	120
OY	55	-----IDLISVGTBEKLSFSFSAHGKVVNTSPTKGLNPAKKEFAGTNG	94
Dd	121	KTNENTNDSFPTYSLKKDLNDELTSVEKEKLSFGANGKKNVITSTPKLNPFAKEFAGTNG	180
OY	95	DTYHLNIGSTLIDTDLTNGATTNVTNDANTYDDEKRAASVKDVLNAGWNIKGVKPGTY	154
Dd	181	DTYHLNIGSTLIDTDLTNGATTNVTNDANTYDDEKRAASVKDVLNAGWNIKGVKPGTY	240
OY	155	ASDNDVFRITYDYVEELSDATKRTTYTVNESKDNGKEKTEVKIGAKTSVIREKDKLVTKGD	214
Dd	241	ASDNDVFRITYDYVEELSDATKRTTYTVNESKDNGKEKTEVKIGAKTSVIREKDKLVTKGD	300
OY	215	KGENGSSITDEBEGLVTAKEVIDAVNKAQWRKKTITANOTQOQADFEVYTSQNTNTPASG	274
Dd	301	KGENGSSITDEBEGLVTAKEVIDAVNKAQWRKKTITANOTQOQADFEVYTSQNTNTPASG	360
OY	275	KGTATVSKDOGNITVAVDVNVGDALVWNLONGSMWLDKSAVNGSSGKTVSGNVSPSK	334
Dd	361	KGTATVSKDOGNITVAVDVNVGDALVWNLONGSMWLDKSAVNGSSGKTVSGNVSPSK	420
OY	335	GKMDETVINAANNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVG-DALNNGS	393
Dd	421	GKMDETVINAANNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDKGLNNGS	480
OY	394	KKDNKPVRITVAPGVKEGDVYTNAAQLKGVAKONLNRIDYDGNARAQIAQIAATAGLVQ	453
Dd	481	KDNKPVRITVAPGVKEGDVYTNAAQLKGVAKONLNRIDYDGNARAQIAQIAATAGLVQ	540
OY	454	AYLNGKSMALIGGGYRGEGAGYTAIGYSSISOGGWNITKGTASGNSRGHFGASASVGYOM	512
Dd	541	AYLNGKSMALIGGGYRGEGAGYTAIGYSSISOGGWNITKGTASGNSRGHFGASASVGYOM	599

RESULT 8
US-09-669-974-15
; Sequence 15, Application US/09669974
; Patent No. 6331173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-15

Query Match 94.4%; Score 2453.5; DB 4; Length 599;
Best Local Similarity 83.0%; Pred. No. 1,6e-189;
Matches 497; Conservative 4; Mismatches 11; Indels 87; Gaps 2;

QY 1 MNKIYIIMNSALNANWVSELTRNHTKRASATVATVATLTLFATVOASANNE----- 54
DB 1 MNKIYIIMNSALNANWVSELTRNHTKRASATVATVATLTLFATVOASATDEDEEEL 60
QY 55 ----- 54
DB 61 EPVRSALVLFQFIDKEGNGENESTGNIGSIYYDNHNLHGATVTLKAGDNLKIKONTN 120
QY 55 ----- 54
DB 121 KNTNENTNDSFTYSLKDLTDLTJVSGETKLSFGANGKNVITSDTKGLNFAETAGTNG 180
QY 95 DTFVHLNGISLTDLTDLTNGATTNTNDVTDDEKKRAASVADVNLNAGNINIGVPGTT 154
DB 181 DTFVHLNGISLTDLTDLTNGATTNTNDVTDDEKKRAASVADVNLNAGNINIGVPGTT 240
QY 155 ASDNVDVFTYDVEFLSADTKTTTVNVEKDKNGKTEVYKIGAKTSVKEKDKLVTKGD 214
DB 241 ASDNVDVFTYDVEFLSADTKTTTVNVEKDKNGKTEVYKIGAKTSVKEKDKLVTKGD 300
QY 215 KGENSGSTDEGELVTAKEVIDAVNKAQRMKTTTANGOTGADKFEYVSGTNVTFASG 274
DB 301 KGENSGSTDEGELVTAKEVIDAVNKAQRMKTTTANGOTGADKFEYVSGTNVTFASG 360
QY 275 KGTATVSKDDOGNITVMTDVNVDALNVNOLONGMNLDSKAVASSGKVIISGNTVSPSK 334
DB 361 KGTATVSKDDOGNITVMTDVNVDALNVNOLONGMNLDSKAVASSGKVIISGNTVSPSK 420
QY 335 GKMDFTVINAGNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLVSDG-DALNVGS 393
DB 421 GKMDFTVINAGNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLVSDG-DALNVGS 480
QY 394 KDKNKFVTRTNVAPVKEGVDYTNVAOLKGYAQNLLNRINDVNGNARAQIAIATAGLVQ 453
DB 481 KDKNKFVTRTNVAPVKEGVDYTNVAOLKGYAQNLLNRINDVNGNARAQIAIATAGLVQ 540
QY 454 AYLPKSKMAIGGGTGRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 512
DB 541 AYLPKSKMAIGGGTGRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 599

RESULT 9

US-09-377-155-9
; Sequence 9, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-9

Query Match 94.2%; Score 2449; DB 3; Length 594;
Best Local Similarity 83.3%; Pred. No. 3,6e-189;
Matches 495; Conservative 6; Mismatches 11; Indels 82; Gaps 2;

QY 1 MNKIYIIMNSALNANWVSELTRNHTKRASATVATVATLTLFATVOASANNE----- 54
DB 1 MNKIYIIMNSALNANWVSELTRNHTKRASATVATVATLTLFATVOASTDDDDLYLE 60
QY 55 ----- 54
DB 61 PVQRTAVLSFRDSEKTEGTEVTEDSNMGVYEDDKCVLTAGITTLKAGDNLKIKONTNE 120
QY 55 ----- 54
DB 121 NTNASSFTYSLKDLTDLTJVSGETKLSFGANGKNVITSDTKGLNFAETAGTNGDTTVH 180
QY 100 LNIIGSTLDTLTLNTGATTNTNDVTDDEKKRAASVADVNLNAGNINIGVPGTTASDNV 159
DB 181 LNIIGSTLDTLTLNTGATTNTNDVTDDEKKRAASVADVNLNAGNINIGVPGTTASDNV 240
QY 160 DFRYTDVTEFLSADTKTTTVNVEKDKNGKTEVYKIGAKTSVKEKDKLVTKGDKEGNG 219
DB 241 DFRYTDVTEFLSADTKTTTVNVEKDKNGKTEVYKIGAKTSVKEKDKLVTKGDKEGNG 300
QY 220 SSTDEGELVTAKEVIDAVNKAQRMKTTTANGOTGADKFEYVSGTNVTFASGKGTGA 279
DB 301 SSTDEGELVTAKEVIDAVNKAQRMKTTTANGOTGADKFEYVSGTNVTFASGKGTGA 360
QY 280 TVSKDDOGNITVMTDVNVDALNVNOLONGMNLDSKAVASSGKVIISGNTVSPSKGKMD 339
DB 361 TVSKDDOGNITVMTDVNVDALNVNOLONGMNLDSKAVASSGKVIISGNTVSPSKGKMD 420
QY 340 TVNINAGNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLVSDG-DALNVGSKDKN 398
DB 421 TVNINAGNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLVSDG-DALNVGSKDKN 480
QY 399 PVRITVNPAPVKEGVDYTNVAOLKGYAQNLLNRINDVNGNARAQIAIATAGLVQAVLP 458
DB 481 PVRITVNPAPVKEGVDYTNVAOLKGYAQNLLNRINDVNGNARAQIAIATAGLVQAVLP 540
QY 459 KSMMAIGGGTGRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 512
DB 541 KSMMAIGGGTGRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 594

RESULT 10
US-09-669-974-9
; Sequence 9, Application US/09669974
; Patent No. 6331173
; GENERAL INFORMATION:


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: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 13
: LENGTH: 598
: TYPE: PRN
: ORGANISM: Neisseria meningitidis
US-09-377-155-13

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	Query Match	93.3%;	Score 2427;	DB 33;	Length 598;	
	Best Local Similarity	82.3%;	Pred. No. 2.1e-187;			
	Matches	492;	Conservative	5;	Mismatches	15; Indels 86; Gaps 2
OY	1	MNKYYRIIWNLSALNAWVVSSELTNRNHRKRASATYKTAVALATLFLFATVOASANNE-----	54			
Db	1	MNKYYRIIWNLSALNAWVVSSELTNRNHRKRASATYKTAVALATLFLFATVOANATDDDLXLE	60	:	:	:
OY	55	-----	54			
Db	61	PVQRTAVVLSFRSKEGTGEGEGBDSMWAVYFDDEKRYLKAGALITLKGDNLUKTONTNE	120			
OY	55	-----TDLTSVGTEKLTFSSANGKNVTISDTKGLNFAPKETAGTNGD	95			
Db	121	NFNENTNDSPFTYSLLKKDLPTDLTSVEFEKLSFGANGKNVNITSPTKGLNFAKETAGTNGD	180			
OY	96	TTVHLNGIGSLTDTLLNTLGATTIVTNDNVTDDEKKRAASYKDVLNAGMNIKGVPRGTTA	155			
Db	181	PTVHLNGIGSLTDTLLNTLGATTIVTNDNVTDDEKKRAASYKDVNLNAGMNIKGVPRGTTA	240			
OY	156	SDNVDFPRTYTYVEELFSADTKTTYTNVYESKONGKKEVEIKIGAKTSVIKEKDGKLYTGDK	215			
Db	241	SDNVDFPRTYTYVEELFSADTKTTYTNVYESKONGKKEVEIKIGAKTSVIKEKDGKLYTGDK	300			
OY	216	GENGSSIDEGEGLYTAKEVIDAVNKAQRMRKTTTANGOTGOADKFETVYTSGETNVPFASG	275			
Db	301	DENGSSIDEGEGLYTAKEVIDAVNKAQRMRKTTTANGOTGOADKFETVYTSGETNVPFASG	360			
OY	276	GTTATVSKDDOGNTITVMVDVWGVALANTNOLONSGMNLDISKRVASSGKVISGANVPSKG	335			
Db	361	GTTATVSKDDOGNTITVKIDVNWGVALANTNOLONSGMNLDISKRVASSGKVISGANVPSKG	420			
OY	336	KMDPTVINAINANNIEITRNGKNIDATSMTPOFSSVSLGAGADAFTLVSDGD -ALNVGSK	394			
Db	421	KMDPTVINAINANNIEITRNGKNIDATSMTPOFSSVSLGAGADAFTLVSDDEGALNVGSK	480			
OY	395	KDNKPVRTINVAPEGVKEGDVTNVAAOLKGVAAONLNRRINDVGNARAGIAQAATATAGLYOA	454			
Db	481	DANKPVRTINVAPEGVKEGDVTNVAAOLKGVAAONLNRRINDVGNARAGIAQAATATAGLYOA	540			
OY	455	YLPEKSMMALIGGGYTRGEGAIGAIGSSISDCGNWTIKCTAGSGNSGRHGASASVGYOW	512			
Db	541	YLPEKSMMALIGGGYTRGEGAIGAIGSSISDTGMNVIKGTAGSGNSGRHGASASVGYOW	598			
	RESULT 14					
	US-09-669-974-13					
	Sequence 13, Application US/09669974					
	Patent No. 6533173					
	GENERAL INFORMATION:					
	APPLICANT: PEAK, Ian Richard Anselm					
	APPLICANT: JENNINGS, Michael Paul					
	APPLICANT: MOXON, E. Richard					
	TITLE OR INVENTION: NOVEL SURFACE ANTIGEN					
	FILE REFERENCE: 065064/0128					
	CURRENT APPLICATION NUMBER: US/09/669, 974					
	PRIOR FILING DATE: 2000-09-26					
	PRIOR FILING DATE: 1999-08-19					
	PRIOR APPLICATION NUMBER: PCT/AU98/01031					
	PRIOR FILING DATE: 1998-12-14					
	PRIOR APPLICATION NUMBER: GB 9726398.2					

;; PRIOR FILING DATE: 1997-12-12
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO 13
;; LENGTH: 598
;; TYPE: PRF
;; ORGANISM: Neisseria meningitidis
US-09-669-974-13

Query Match 93.3%; Score 2427; DB 4; Length 598;
Best Local Similarity 82.3%; Pred. No. 2,1e-187;
Matches 492; Conservative 5; Mismatches 15; Indels 86; Gaps 2;

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QY 1 MNKIRIITNSALNMAVYSELTRNHTKRASATVAVATLTLFFATVQASANNE----- 54
    |||||
DB 1 MNKIRIITNSALNMAVYSELTRNHTKRASATVAVATLTLFFATVQANATDDDDLYLE 60
    |||||

QY 55 ----- 54
DB 61 PVQRTAVVLSFRSDEKGEKTEGTEDSMVAVYFDEKRVLKAGATLTKAGDNLKIKONTNE 120
    |||||

QY 55 ----- 95
DB 121 NTNENTNDSSFTYSLKQDLTLTVEKELSGANGKNVNTISDTKGLNFAKETAGTNGD 180
    |||||

QY 96 TTVHLNGIGSTLTDLTNTGATTNTVNDVTDDEKRRASVADVNAGNINIKVAPGTGA 155
    |||||
DB 181 PTVHLNGIGSTLTDLTNTGATTNTVNDVTDDEKRRASVADVNAGNINIKVAPGTGA 240
    |||||

QY 156 SDNVDFVRYDVEFLSADTKTTTVNVEKDKGKTEVKGAKTSVIREKDKLVYTGKDK 215
    |||||
DB 241 SDNVDFVRYDVEFLSADTKTTTVNVEKDKGKTEVKGAKTSVIREKDKLVYTGKDK 300
    |||||

QY 216 GENGSSTDEGEGLVTAKEVIDAVNKAQWMTTNTANGOTGQADKFEYTSIGTNTVFAAGK 275
    |||||
DB 301 DENGSSTDEGEGLVTAKEVIDAVNKAQWMTTNTANGOTGQADKFEYTSIGTNTVFAAGK 360
    |||||

QY 276 GTTATVSKDDQGNITVMDVNVGDAALNVQLONSGMNLSKAVAGSSGKVISGNVSPSKG 335
    |||||
DB 361 GTTATVSKDDQGNITVMDVNVGDAALNVQLONSGMNLSKAVAGSSGKVISGNVSPSKG 420
    |||||

QY 336 KMDFTVINAGNNIETTRNGKNIDIAATSMTPOFSSVSLGAGADAPTLSTVDGAD-ALNVGSK 394
    |||||
DB 421 KMDFTVINAGNNIETTRNGKNIDIAATSMTPOFSSVSLGAGADAPTLSTVDGADALNVGSK 480
    |||||

QY 395 KDNKVRITTNVAPGVKEGDTNVAAOLKGYAQNLLNRRIDVNDGNARAGIAQAATATAGIYQA 454
    |||||
DB 481 DANKVRITTNVAPGVKEGDTNVAAOLKGYAQNLLNRRIDVNDGNARAGIAQAATATAGIYQA 540
    |||||

QY 455 YLPGRSMAAIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 512
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DB 541 YLPGRSMAAIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 598
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RESULT 15
US-09-377-155-5
; Sequence 5, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5

;; LENGTH: 598
;; TYPE: PRF
;; ORGANISM: Neisseria meningitidis
US-09-377-155-5

Query Match 93.0%; Score 2418; DB 3; Length 598;
Best Local Similarity 81.9%; Pred. No. 1,1e-186;
Matches 490; Conservative 6; Mismatches 16; Indels 86; Gaps 2;

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    |||||
DB 1 MNKIRIITNSALNMAVYSELTRNHTKRASATVAVATLTLFFATVQANATDDDDLYLE 60
    |||||

QY 55 ----- 54
DB 61 PVQRTAVVLSFRSDEKGEKTEGTEDSMVAVYFDEKRVLKAGATLTKAGDNLKIKONTNE 120
    |||||

QY 55 ----- 95
DB 121 NTNENTNDSSFTYSLKQDLTLTVEKELSGANGKNVNTISDTKGLNFAKETAGTNGD 180
    |||||

QY 96 TTVHLNGIGSTLTDLTNTGATTNTVNDVTDDEKRRASVADVNAGNINIKVAPGTGA 155
    |||||
DB 181 PTVHLNGIGSTLTDLTNTGATTNTVNDVTDDEKRRASVADVNAGNINIKVAPGTGA 240
    |||||

QY 156 SDNVDFVRYDVEFLSADTKTTTVNVEKDKGKTEVKGAKTSVIREKDKLVYTGKDK 215
    |||||
DB 241 SDNVDFVRYDVEFLSADTKTTTVNVEKDKGKTEVKGAKTSVIREKDKLVYTGKDK 300
    |||||

QY 216 GENGSSTDEGEGLVTAKEVIDAVNKAQWMTTNTANGOTGQADKFEYTSIGTNTVFAAGK 275
    |||||
DB 301 DENGSSTDEGEGLVTAKEVIDAVNKAQWMTTNTANGOTGQADKFEYTSIGTNTVFAAGK 360
    |||||

QY 276 GTTATVSKDDQGNITVMDVNVGDAALNVQLONSGMNLSKAVAGSSGKVISGNVSPSKG 335
    |||||
DB 361 GTTATVSKDDQGNITVMDVNVGDAALNVQLONSGMNLSKAVAGSSGKVISGNVSPSKG 420
    |||||

QY 336 KMDFTVINAGNNIETTRNGKNIDIAATSMTPOFSSVSLGAGADAPTLSTVDGAD-ALNVGSK 394
    |||||
DB 421 KMDFTVINAGNNIETTRNGKNIDIAATSMTPOFSSVSLGAGADAPTLSTVDGADALNVGSK 480
    |||||

QY 395 KDNKVRITTNVAPGVKEGDTNVAAOLKGYAQNLLNRRIDVNDGNARAGIAQAATATAGIYQA 454
    |||||
DB 481 DANKVRITTNVAPGVKEGDTNVAAOLKGYAQNLLNRRIDVNDGNARAGIAQAATATAGIYQA 540
    |||||

QY 455 YLPGRSMAAIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 512
    |||||
DB 541 YLPGRSMAAIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 598
    |||||
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Search completed: October 6, 2003, 09:35:40
Job time : 16.6919 secs

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:10 : Search time 37.6045 Seconds
(without alignments)
3513.485 Million cell updates/sec

Title: US-09-771-382-23

Perfect score: 2600

Sequence: 1 MNKIYRIINMSALNAMYVS.....TASGNSNGHGCASASVGYQW 512

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: SPREMBL_23:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_podent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacterioplasmid:*
17: sp_archaeoplasmid:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2550.5	98.1	591	09JRI8	Q9JRI8 neisseria m
2	2546.5	97.9	591	09JPS7	Q9JPS7 neisseria m
3	2546.5	97.9	591	09AOP0	Q9AOP0 neisseria m
4	2538.5	97.6	591	093QY3	Q93QY3 neisseria m
5	2488	95.7	600	09JPS6	Q9JPS6 neisseria m
6	2474	95.2	590	09JPS3	Q9JPS3 neisseria m
7	2453.5	94.4	599	09JPS8	Q9JPS8 neisseria m
8	2450	94.2	594	09JPS2	Q9JPS2 neisseria m
9	2449	94.2	594	093QY4	Q93QY4 neisseria m
10	2446	94.1	594	09JPI3	Q9JPI3 neisseria m
11	2442	93.9	592	09JPI7	Q9JPI7 neisseria m
12	2441	93.9	592	09JPS9	Q9JPS9 neisseria m
13	2440	93.8	598	09JPS9	Q9JPS9 neisseria m
14	2427	93.3	598	09JPS0	Q9JPS0 neisseria m
15	2427	93.3	598	09JPI0	Q9JPI0 neisseria m
16	2418	93.0	598	093QY5	Q93QY5 neisseria m

17	2407	92.6	592	093QY2	Q93QY2 neisseria m
18	2308.5	88.8	595	09JPI0	Q9JPI0 neisseria m
19	2305.5	88.7	595	09JPS8	Q9JPS8 neisseria m
20	2304	88.6	598	09JPI7	Q9JPI7 neisseria m
21	2296	88.3	526	09JPS4	Q9JPS4 neisseria m
22	2296	88.3	530	09JPS1	Q9JPS1 neisseria m
23	2289	88.0	592	09JQW4	Q9JQW4 neisseria m
24	2266.5	87.2	589	09JPI0	Q9JPI0 neisseria m
25	2256	86.8	600	09JPS5	Q9JPS5 neisseria m
26	2254.5	86.7	589	093QY1	Q93QY1 neisseria m
27	991	38.1	1096	048152	Q48152 haemophilus
28	990	38.1	1096	08GM79	08GM79 haemophilus
29	954.5	36.7	2353	P71401	P71401 haemophilus
30	902	34.7	1204	08GM76	08GM76 haemophilus
31	893	34.3	1210	08GM74	08GM74 haemophilus
32	885	34.0	1210	08GM75	08GM75 haemophilus
33	702	27.0	1004	08GM77	08GM77 haemophilus
34	681	26.2	1002	08GM78	08GM78 haemophilus
35	423.5	16.3	1299	09F3X6	09F3X6 pasteurella
36	364.5	14.8	2314	08KQW8	08KQW8 moraxella c
37	378	14.5	2059	09PD50	09PD50 xylella fas
38	372.5	14.3	1190	09PC04	09PC04 xylella fas
39	371.5	14.3	1107	09F2D8	09F2D8 salmonella
40	370.5	14.2	1588	08XD64	08XD64 escherichia
41	368.5	14.2	1461	08ZL64	08ZL64 salmonella
42	360	13.8	1964	08KQW9	08KQW9 moraxella c
43	358.5	13.8	1778	08FCB2	08FCB2 escherichia
44	343	13.2	2712	09F3X5	09F3X5 pasteurella
45	339.5	13.1	688	08R060	08R060 actinobacill

ALIGNMENTS

RESULT 1

ID	Q9JRI8	PRELIMINARY	PRT	591 AA.
AC	Q9JRI8:			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	Outer membrane protein GNA992 (Adhesin) (NhaA outer membrane protein).			
GN	GNA992 OR NME0992 OR NHA.			
OS	Neisseria meningitidis, and			
OS	Neisseria meningitidis (serogroup B).			
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;			
OC	Neisseriaceae; Neisseria.			
OX	NCBI_TaxID=487, 491;			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=MC58 / Serogroup B, B2169, B283, and H44/76;			
RC	MEDLINE=20175756; PubMed=10710308;			
RX	Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,			
RA	Comanducci M., Jennings G.T., Baidi L., Bartolini E., Capechi B.,			
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,			
RA	Ratelli G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,			
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,			
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,			
RA	Moynon E.R., Grandi G., Rappuoli R.;			
RT	"Identification of Vaccine Candidates Against Serogroup B			
RT	Meningococcus by Whole-Genome Sequencing.";			
RL	Science 287:1816-1820(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MC58 / Serogroup B;			
RC	STRAIN=MC58 / Serogroup B;			
RX	MEDLINE=20175755; PubMed=10710307;			
RA	Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,			
RA	Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,			
RA	Nelson W.C., Gwinn M.L., DeBoy R., Petersen J.D., Hickey E.K.,			
RA	Hait D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,			
RA	Mason T., Ciolek A., Parksey D.S., Blair E., Cillone H., Clark E.B.,			
RA	Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,			

RA Gill J., Scarlato V., Mastignani V., Pizsa M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of *Neisseria meningitidis* serogroup B strain
RT MC58";
RL Science 287:1809-1815(2000).
RN [3]
RP SOURCE FROM N.A.
RC SPECIES=*N.meningitidis*; STRAIN=PMC21;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of *Neisseria meningitidis*";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF226375; AAF42524.1; -
DR EMBL: AE002450; AAF41395.1; -
DR EMBL: AF226367; AAF42516.1; -
DR EMBL: AF226370; AAF42519.1; -
DR EMBL: AF226374; AAF42523.1; -
DR EMBL: AF157611; AAK68872.1; -
DR TIGR: NMB09922; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
KW Complete proteome.
SQ SEQUENCE 591 AA; 62112 MW; 7C22F3CAE7F73EC6 CRC64;

Query Match 98.18; Score 2550.5; DB 16; Length 591;
Best Local Similarity 86.64; Pred. No. 1.7e-100;
Matches 512; Conservative 0; Mismatches 0; Indels 79; Gaps 1;

QY 1 MNKIRIIMNSALANWVYSELTRNHTKRASATVKTAVLATLTFATVQASANNE----- 54
DB 1 MNKIRIIMNSALANWVYSELTRNHTKRASATVKTAVLATLTFATVQASANNEDEEDL 60
QY 55 ----- 54
DB 61 YLDPVORTAVLIVNSDKEGTGEKEVEENSDWAVYFENEKGVLTAREITLKAGDNLKIKQ 120
QY 55 ----- 54
DB 61 YLDPVORTAVLIVNSDKEGTGEKEVEENSDWAVYFENEKGVLTAREITLKAGDNLKIKQ 120
QY 55 ----- 54
DB 121 NGTNFTYSLKDLTDLTSLVTEKLSFSAKGNKYNITSDTKGLNFAKETAGTNDTTHLN 180
QY 102 GIGSTLDLTLNGATTNTNDVTDDEKRAASVDVLAAGNNIKGVKGTASDNVDF 161
DB 181 GIGSTLDLTLNGATTNTNDVTDDEKRAASVDVLAAGNNIKGVKGTASDNVDF 240
QY 162 VRTYDVEELSLADTKTTTVNVEESKDKGKTEVRIKAKTSYIKERDGLVYTKDKGENGSS 221
DB 241 VRTYDVEELSLADTKTTTVNVEESKDKGKTEVRIKAKTSYIKERDGLVYTKDKGENGSS 300
QY 222 TDGEGELVTAKEVIDAVNKRAGMKTTTANGOTGQADKFEFTVSGTNVTFASGKGTATV 281
DB 301 TDGEGELVTAKEVIDAVNKRAGMKTTTANGOTGQADKFEFTVSGTNVTFASGKGTATV 360
QY 282 SKDDGNTITMYDVNVGDALNVQNLQNSGNLDSKAVAGSSGKVISGNVSPSGKMDDEV 341
DB 361 SKDDGNTITMYDVNVGDALNVQNLQNSGNLDSKAVAGSSGKVISGNVSPSGKMDDEV 420
QY 342 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLVSDGALNVGSKDKKPV 401
DB 421 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLVSDGALNVGSKDKKPV 480
QY 402 ITTVAAVGEKGDVTNVAOLKGVQNLNRRIDNDVGNARAGIAQAITAGLVQAYLPKSKM 461
DB 481 ITTVAAVGEKGDVTNVAOLKGVQNLNRRIDNDVGNARAGIAQAITAGLVQAYLPKSKM 540
QY 462 MAIGGTYRGEAGYATGYSISIDGNNIITKGTASGNSRGHFGASASVGYOW 512
DB 541 MAIGGTYRGEAGYATGYSISIDGNNIITKGTASGNSRGHFGASASVGYOW 591

RESULT 2
09JPS7
AC 09JPS7; PRELIMINARY; PRT; 591 AA.

DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.

OS *Neisseria meningitidis*.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]

RP SOURCE FROM N.A.

RC STRAIN=B147;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scarlato V., Mastignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Ntli S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing";
RL Science 287:1816-1820(2000).
DR EMBL: AF226366; AAF42515.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91EIF CRC64;

Query Match 97.94; Score 2546.5; DB 2; Length 591;
Best Local Similarity 86.58; Pred. No. 2.5e-100;
Matches 511; Conservative 1; Mismatches 0; Indels 79; Gaps 1;

QY 1 MNKIRIIMNSALANWVYSELTRNHTKRASATVKTAVLATLTFATVQASANNE----- 54
DB 1 MNKIRIIMNSALANWVYSELTRNHTKRASATVKTAVLATLTFATVQASANNEDEEDL 60
QY 55 ----- 54
DB 61 YLDPVORTAVLIVNSDKEGTGEKEVEENSDWAVYFENEKGVLTAREITLKAGDNLKIKQ 120
QY 55 ----- 54
DB 121 NGTNFTYSLKDLTDLTSLVTEKLSFSAKGNKYNITSDTKGLNFAKETAGTNDTTHLN 180
QY 102 GIGSTLDLTLNGATTNTNDVTDDEKRAASVDVLAAGNNIKGVKGTASDNVDF 161
DB 181 GIGSTLDLTLNGATTNTNDVTDDEKRAASVDVLAAGNNIKGVKGTASDNVDF 240
QY 162 VRTYDVEELSLADTKTTTVNVEESKDKGKTEVRIKAKTSYIKERDGLVYTKDKGENGSS 221
DB 241 VRTYDVEELSLADTKTTTVNVEESKDKGKTEVRIKAKTSYIKERDGLVYTKDKGENGSS 300
QY 222 TDGEGELVTAKEVIDAVNKRAGMKTTTANGOTGQADKFEFTVSGTNVTFASGKGTATV 281
DB 301 TDGEGELVTAKEVIDAVNKRAGMKTTTANGOTGQADKFEFTVSGTNVTFASGKGTATV 360
QY 282 SKDDGNTITMYDVNVGDALNVQNLQNSGNLDSKAVAGSSGKVISGNVSPSGKMDDEV 341
DB 361 SKDDGNTITMYDVNVGDALNVQNLQNSGNLDSKAVAGSSGKVISGNVSPSGKMDDEV 420
QY 342 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLVSDGALNVGSKDKKPV 401
DB 421 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLVSDGALNVGSKDKKPV 480
QY 402 ITTVAAVGEKGDVTNVAOLKGVQNLNRRIDNDVGNARAGIAQAITAGLVQAYLPKSKM 461
DB 481 ITTVAAVGEKGDVTNVAOLKGVQNLNRRIDNDVGNARAGIAQAITAGLVQAYLPKSKM 540
QY 462 MAIGGTYRGEAGYATGYSISIDGNNIITKGTASGNSRGHFGASASVGYOW 512
DB 541 MAIGGTYRGEAGYATGYSISIDGNNIITKGTASGNSRGHFGASASVGYOW 591

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RESULT 3
09AOF0 PRELIMINARY: PRT: 592 AA.
AC 09AOF0:
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Outer membrane protein.
GN NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon E.R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
   membrane protein of Neisseria meningitidis.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF125375; AAK09243.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;

Query Match          97.9%; Score 2546; DB 2; Length 592;
Best Local Similarity 86.3%; Pred. No. 2.6e-100;
Matches 511; Conservative 0; Mismatches 1; Indels 80; Gaps 1;

QY 1 MNKIRIIMNSALNAWVVSSELTNRNHTKRASATVKTAVLATLTFATVQASANNE----- 54
DB 1 MNKIRIIMNSALNAWVVSSELTNRNHTKRASATVKTAVLATLTFATVQASANNEPRKKD 60
QY 55 ----- 54
DB 61 LYDPVORTVAVLIVNSDKETGEGEKEVEENSDMAVYFNEKGLTAREITLAKGDNLIK 120
QY 55 -----TDLTSVGTETKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVHL 100
DB 121 QNGNTFYSLKDLTDLTSVGTETKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVHL 180
QY 101 NGIGSTLDTLLNTGATTNVNDVTDDEKKRAASVYKDVNLNAGWNKGVKPGTTASDNVD 160
DB 181 NGIGSTLDTLLNTGATTNVNDVTDDEKKRAASVYKDVNLNAGWNKGVKPGTTASDNVD 240
QY 161 FVRITDYVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSYIKKDGKLVTKDKGENGS 220
DB 241 FVRITDYVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSYIKKDGKLVTKDKGENGS 300
QY 221 STDEGGLVTAKEVIDAVNKAQWRMKTTTANGOTGOADKFETVTSNTVTFASGKTATV 280
DB 301 STDEGGLVTAKEVIDAVNKAQWRMKTTTANGOTGOADKFETVTSNTVTFASGKTATV 360
QY 281 VSKDQGNITVYDVNVGDLNVLNQLNSGNMLDSKAVAGSSGKVIISGNVSPSKMDET 340
DB 361 VSKDQGNITVYDVNVGDLNVLNQLNSGNMLDSKAVAGSSGKVIISGNVSPSKMDET 420
QY 341 VNINAGNNIETTRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVGDALNVGSKDKNPKV 400
DB 421 VNINAGNNIETTRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVGDALNVGSKDKNPKV 480
QY 401 RITNVAQVKEGDVTNVAOLKGVNQLNLRIDNVGNAQVIAQAIATAGLVQAVLYLPGKS 460
DB 481 RITNVAQVKEGDVTNVAOLKGVNQLNLRIDNVGNAQVIAQAIATAGLVQAVLYLPGKS 540
QY 461 MAIGGTYRGEAGYALIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 512
DB 541 MAIGGTYRGEAGYALIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 592

RESULT 4
0930Y3 PRELIMINARY: PRT: 591 AA.
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AC 0930Y3;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 22, Last annotation update)
DE NHA outer membrane protein.
GN NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG329;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
   membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157606; AAK68867.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 591 AA; 62048 MW; CODC600798859C65 CRC64;

Query Match          97.6%; Score 2538.5; DB 2; Length 591;
Best Local Similarity 86.3%; Pred. No. 5.5e-100;
Matches 510; Conservative 1; Mismatches 1; Indels 79; Gaps 1;

QY 1 MNKIRIIMNSALNAWVVSSELTNRNHTKRASATVKTAVLATLTFATVQASANNE----- 54
DB 1 MNKIRIIMNSALNAWVVSSELTNRNHTKRASATVKTAVLATLTFATVQASANNEQEEDL 60
QY 55 ----- 54
DB 61 YLDPVLKRVANLIVNSDKETGEGEKEVEENSDMAVYFNEKGLTAREITLAKGDNLIK 120
QY 55 -----TDLTSVGTETKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVHL 101
DB 121 NGNTFYSLKDLTDLTSVGTETKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVHL 180
QY 102 GIGSTLDTLLNTGATTNVNDVTDDEKKRAASVYKDVNLNAGWNKGVKPGTTASDNVD 161
DB 181 GIGSTLDTLLNTGATTNVNDVTDDEKKRAASVYKDVNLNAGWNKGVKPGTTASDNVD 240
QY 162 VRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSYIKKDGKLVTKDKGENGS 221
DB 241 VRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSYIKKDGKLVTKDKGENGS 300
QY 222 TDEGGLVTAKEVIDAVNKAQWRMKTTTANGOTGOADKFETVTSNTVTFASGKTATV 281
DB 301 TDEGGLVTAKEVIDAVNKAQWRMKTTTANGOTGOADKFETVTSNTVTFASGKTATV 360
QY 282 SKDQGNITVYDVNVGDLNVLNQLNSGNMLDSKAVAGSSGKVIISGNVSPSKMDETV 341
DB 361 SKDQGNITVYDVNVGDLNVLNQLNSGNMLDSKAVAGSSGKVIISGNVSPSKMDETV 420
QY 342 NINAGNNIETTRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVGDALNVGSKDKNPKV 401
DB 421 NINAGNNIETTRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVGDALNVGSKDKNPKV 480
QY 402 ITNVAQVKEGDVTNVAOLKGVNQLNLRIDNVGNAQVIAQAIATAGLVQAVLYLPGKS 461
DB 481 ITNVAQVKEGDVTNVAOLKGVNQLNLRIDNVGNAQVIAQAIATAGLVQAVLYLPGKS 540
QY 462 MAIGGTYRGEAGYALIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 512
DB 541 MAIGGTYRGEAGYALIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 591

RESULT 5
09JPB6 PRELIMINARY: PRT: 600 AA.
AC 09JPB6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
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DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria: Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
NCBI_TaxID=487;
RX SEQUENCE FROM N.A.
RC STRAIN=NE26;
MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappunli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
EMBL: AF226371; AAF42520.1; --
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;

Query Match 95.7%; Score 2488; DB 2; Length 600;
Best Local Similarity 83.7%; Pred. No. 7, 6e-98;
Matches 502; Conservative 2; Mismatches 8; Indels 88; Gaps 1;

QY 1 MNKIRIINNSALNAVAVVSELTRNHTKRASATVKTAVLATLLFAVQASANNE----- 54
DB 1 MNKIRIINNSALNAVAVVSELTRNHTKRASATVKTAVLATLLFAVQASADN 60
QY 55 ----- 54
DB 61 EEEETLEPVYRTAPVLSFYSDAEDFGEKEVENTNNGIYFDKNGVIRKAGTITIKAGDNK 120
QY 55 ----- 54
DB 121 IKONTDEBNTNASSFTYSLKKELEFDTLSVGTSEKLSFGANGKNVITSDTKLNFAKETAGT 180
QY 93 NGDTYVHLNGIGSTLTDTLTNTGATTNVTNDNTDDEKKRAASVKDVLNAGNKGKVP 152
DB 181 NGDTYVHLNGIGSTLTDTLTNTGATTNVTNDNTDDEKKRAASVKDVLNAGNKGKVP 240
QY 153 TPASDNDVFRYDTVEFLSADTKTTTVNYESKDNKGKTEPKIGAKTSVYKEKDGKLYTG 212
DB 241 TPASDNDVFRYDTVEFLSADTKTTTVNYESKDNKGKTEPKIGAKTSVYKEKDGKLYTG 300
QY 213 KDKGENGSSTDEGEGLVTAKEVIDAVNKAQWRMKTATTANGQTQADKFEVTSGTNTFA 272
DB 301 KDKGENGSSTDEGEGLVTAKEVIDAVNKAQWRMKTATTANGQTQADKFEVTSGTNTFA 360
QY 273 SGGTTATYASKDQGNITWYDVNVDALNVLNOLNSGWNLDKAAVAGSSGKATISGNVSP 332
DB 361 SGGTTATYASKDQGNITWYDVNVDALNVLNOLNSGWNLDKAAVAGSSGKATISGNVSP 420
QY 333 SKKMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSTVGDALNVG 392
DB 421 SKKMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSTVGDALNVG 480
QY 393 SKKDNKPVRTTNVAPGVKEGDVTNVAQLKGAONLNRRIDNVGNARAGIAQAIATAGLV 452
DB 481 SKDANKPVRTTNVAPGVKEGDVTNVAQLKGAONLNRRIDNVGNARAGIAQAIATAGLV 540
QY 453 QATLPKSKMAIGGTYRGAGYAIGYSSISDGGNNI IKCTASGNSRGHGASASVGYQW 512
DB 541 QATLPKSKMAIGGTYRGAGYAIGYSSISDGGNNI IKCTASGNSRGHGASASVGYQW 600

RESULT 6
Q9JPS3

ID Q9JPS3 PRELIMINARY; PRT; 590 AA.
AC Q9JPS3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria: Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
NCBI_TaxID=487;
RX SEQUENCE FROM N.A.
RC STRAIN=NE28;
MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappunli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
EMBL: AF226378; AAF42527.1; --
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 95.2%; Score 2474; DB 2; Length 590;
Best Local Similarity 84.7%; Pred. No. 2, 9e-97;
Matches 500; Conservative 4; Mismatches 8; Indels 78; Gaps 2;

QY 1 MNKIRIINNSALNAVAVVSELTRNHTKRASATVKTAVLATLLFAVQASANNE----- 54
DB 1 MNKIRIINNSALNAVAVVSELTRNHTKRASATVKTAVLATLLFAVQANATDEDEEDL 60
QY 55 ----- 54
DB 61 DPQRTVAVLIVNSDKEGTGEKEKEVEENSDMAVYFNEKGLVLTAGTITIKAGDLKIKNG 120
QY 55 ----- 54
DB 121 TNFTYSLKLDLDTLSVGTSEKLSFGANGKNVITSDTKLNFAKETAGTGTTHLNGI 180
QY 104 GSTLTPTLNTGATTNVTNDNTDDEKKRAASVKDVLNAGNKGKVPGTASDNDVFR 163
DB 181 GSTLTPTLNTGATTNVTNDNTDDEKKRAASVKDVLNAGNKGKVPGTASDNDVFR 240
QY 164 TYDVEFLSADTKTTTVNYESKDNKGKTEPKIGAKTSVYKEKDGKLYTGKDKGENGSSTD 223
DB 241 TYDVEFLSADTKTTTVNYESKDNKGKTEPKIGAKTSVYKEKDGKLYTGKDKGENGSSTD 300
QY 224 EGGELVTAKEVIDAVNKAQWRMKTATTANGQTQADKFEVTSGTNTFAFGKTTATVSK 283
DB 301 EGGELVTAKEVIDAVNKAQWRMKTATTANGQTQADKFEVTSGTNTFAFGKTTATVSK 360
QY 284 DDGNTTWYDVNVDALNVLNOLNSGWNLDKAAVAGSSGKATISGNVSPSKGMDETVIN 343
DB 361 DDGNTTWYDVNVDALNVLNOLNSGWNLDKAAVAGSSGKATISGNVSPSKGMDETVIN 420
QY 344 MAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSTVDGD-ALNVGSKDNKPVRT 402
DB 421 MAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSTVDEGALNVGSKDNKPVRT 480
QY 403 TNVAPGVKEGDVTNVAQLKGAONLNRRIDNVGNARAGIAQAIATAGLVQATLPKSKMA 462
DB 481 TNVAPGVKEGDVTNVAQLKGAONLNRRIDNVGNARAGIAQAIATAGLVQATLPKSKMA 540
QY 463 AIGGTYRGAGYAIGYSSISDGGNNI IKCTASGNSRGHGASASVGYQW 512
DB 541 AIGGTYRGAGYAIGYSSISDGGNNI IKCTASGNSRGHGASASVGYQW 590

RESULT 7

ID Q9JPR8 PRELIMINARY; PRT; 599 AA.

AC Q9JPR8; 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DE Outer membrane protein GNA992 (nhba outer membrane protein).

GN GNA992 OR NHBA.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OX NCBI_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NGH38;

RX MEDLINE=20175756; PubMed=10710308;

RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,

RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,

RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

RA Moxon E.R., Grandi G., Rappunli R.;

RT "Identification of Vaccine Candidates Against Serogroup B

RT Meningococcus by Whole-Genome Sequencing.";

RL Science 287:1816-1820(2000).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=H38;

RA Peak I.R., Srihanta Y., Dieckelman M., Moxon R., Jennings M.P.;

RT "Identification and characterization of a gene encoding a novel outer

RT membrane protein of Neisseria meningitidis.";

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF226383; AAF42532.1; -

DR EMBL: AF157608; AAK68869.1; -

DR InterPro: IPR005594; Yada.

DR Pfam: PF03895; Yada; 1.

SQ SEQUENCE 599 AA; 62844 MW; BBA16EBF53C1970C CRC64;

Query Match 94.4%; Score 2453.5; DB 2; Length 599;

Best Local Similarity 83.0%; Pred. No. 2,2e-96;

Matches 497; Conservative 4; Mismatches 11; Indels 87; Gaps 2;

RESULT 8

ID Q9JPS2 PRELIMINARY; PRT; 594 AA.

AC Q9JPS2; 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DE Outer membrane protein GNA992.

GN GNA992.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OX NCBI_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NGE31;

RX MEDLINE=20175756; PubMed=10710308;

RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,

RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,

RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

RA Moxon E.R., Grandi G., Rappunli R.;

RT "Identification of Vaccine Candidates Against Serogroup B

RT Meningococcus by Whole-Genome Sequencing.";

RL Science 287:1816-1820(2000).

DR EMBL: AF226379; AAF42528.1; -

DR InterPro: IPR005594; Yada.

DR Pfam: PF03895; Yada; 1.

SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 94.2%; Score 2450; DB 2; Length 594;

Best Local Similarity 83.5%; Pred. No. 3e-96;

Matches 496; Conservative 3; Mismatches 13; Indels 82; Gaps 2;

RESULT 9

ID Q9JPS2 PRELIMINARY; PRT; 594 AA.

AC Q9JPS2; 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DE Outer membrane protein GNA992.

GN GNA992.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OX NCBI_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NGE31;

RX MEDLINE=20175756; PubMed=10710308;

RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,

RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,

RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

RA Moxon E.R., Grandi G., Rappunli R.;

RT "Identification of Vaccine Candidates Against Serogroup B

RT Meningococcus by Whole-Genome Sequencing.";

RL Science 287:1816-1820(2000).

DR EMBL: AF226379; AAF42528.1; -

DR InterPro: IPR005594; Yada.

DR Pfam: PF03895; Yada; 1.

SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 94.2%; Score 2450; DB 2; Length 594;

Best Local Similarity 83.5%; Pred. No. 3e-96;

Matches 496; Conservative 3; Mismatches 13; Indels 82; Gaps 2;

RESULT 10

ID Q9JPS2 PRELIMINARY; PRT; 594 AA.

AC Q9JPS2; 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DE Outer membrane protein GNA992.

GN GNA992.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OX NCBI_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NGE31;

RX MEDLINE=20175756; PubMed=10710308;

RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,

RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,

RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

RA Moxon E.R., Grandi G., Rappunli R.;

RT "Identification of Vaccine Candidates Against Serogroup B

RT Meningococcus by Whole-Genome Sequencing.";

RL Science 287:1816-1820(2000).

DR EMBL: AF226379; AAF42528.1; -

DR InterPro: IPR005594; Yada.

DR Pfam: PF03895; Yada; 1.

SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 94.2%; Score 2450; DB 2; Length 594;

Best Local Similarity 83.5%; Pred. No. 3e-96;

Matches 496; Conservative 3; Mismatches 13; Indels 82; Gaps 2;

RESULT 11

ID Q9JPS2 PRELIMINARY; PRT; 594 AA.

AC Q9JPS2; 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DE Outer membrane protein GNA992.

GN GNA992.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OX NCBI_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NGE31;

RX MEDLINE=20175756; PubMed=10710308;

RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,

RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,

RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

RA Moxon E.R., Grandi G., Rappunli R.;

RT "Identification of Vaccine Candidates Against Serogroup B

RT Meningococcus by Whole-Genome Sequencing.";

RL Science 287:1816-1820(2000).

DR EMBL: AF226379; AAF42528.1; -

DR InterPro: IPR005594; Yada.

DR Pfam: PF03895; Yada; 1.

SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 94.2%; Score 2450; DB 2; Length 594;

Best Local Similarity 83.5%; Pred. No. 3e-96;

Matches 496; Conservative 3; Mismatches 13; Indels 82; Gaps 2;

RESULT 12

ID Q9JPS2 PRELIMINARY; PRT; 594 AA.

AC Q9JPS2; 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DE Outer membrane protein GNA992.

GN GNA992.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OX NCBI_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NGE31;

RX MEDLINE=20175756; PubMed=10710308;

RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,

RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,

RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

RA Moxon E.R., Grandi G., Rappunli R.;

RT "Identification of Vaccine Candidates Against Serogroup B

RT Meningococcus by Whole-Genome Sequencing.";

RL Science 287:1816-1820(2000).

DR EMBL: AF226379; AAF42528.1; -

DR InterPro: IPR005594; Yada.

DR Pfam: PF03895; Yada; 1.

SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 94.2%; Score 2450; DB 2; Length 594;

Best Local Similarity 83.5%; Pred. No. 3e-96;

Matches 496; Conservative 3; Mismatches 13; Indels 82; Gaps 2;

RESULT 13

ID Q9JPS2 PRELIMINARY; PRT; 594 AA.

AC Q9JPS2; 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DE Outer membrane protein GNA992.

GN GNA992.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OX NCBI_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NGE31;

RX MEDLINE=20175756; PubMed=10710308;

RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,

RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,

RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

RA Moxon E.R., Grandi G., Rappunli R.;

RT "Identification of Vaccine Candidates Against Serogroup B

RT Meningococcus by Whole-Genome Sequencing.";

RL Science 287:1816-1820(2000).

DR EMBL: AF226379; AAF42528.1; -

DR InterPro: IPR005594; Yada.

DR Pfam: PF03895; Yada; 1.

SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 94.2%; Score 2450; DB 2; Length 594;

Best Local Similarity 83.5%; Pred. No. 3e-96;

Matches 496; Conservative 3; Mismatches 13; Indels 82; Gaps 2;

RESULT 14

ID Q9JPS2 PRELIMINARY; PRT; 594 AA.

AC Q9JPS2; 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DE Outer membrane protein GNA992.

GN GNA992.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OX NCBI_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NGE31;

RX MEDLINE=20175756; PubMed=10710308;

RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,

RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,

RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

RA Moxon E.R., Grandi G., Rappunli R.;

RT "Identification of Vaccine Candidates Against Serogroup B

RT Meningococcus by Whole-Genome Sequencing.";

RL Science 287:1816-1820(2000).

DR EMBL: AF226379; AAF42528.1; -

DR InterPro: IPR005594; Yada.

DR Pfam: PF03895; Yada; 1.

SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 94.2%; Score 2450; DB 2; Length 594;

Best Local Similarity 83.5%; Pred. No. 3e-96;

Matches 496; Conservative 3; Mismatches 13; Indels 82; Gaps 2;

RESULT 15

ID Q9JPS2 PRELIMINARY; PRT; 594 AA.

AC Q9JPS2; 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DE Outer membrane protein GNA992.

GN GNA992.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OX NCBI_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NGE31;

RX MEDLINE=20175756; PubMed=10710308;

RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,

RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,

RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

Qy	280	TVSKDOGQINFTWYDVNVWCDALANVQLOLNSGNLDSKRVVASSSGKVISGVNPSKGMDE	33.9
	361	TVSKDOGQINFTKYKVDYVNGDALNVQLOLNSGNLDSKRVVASSSGKVISGVNPSKGMDE	4.20
Qy	340	TVNINAGNNIEITTRNGKNIDIAITSMTPQFSSVSLGADAPTLTSDVD - ALNVGSKKDNK	398
	421	TVNINAGNNIEITTRNGKNIDIAITSMTPQFSSVSLGADAPTLTSDVDGALNVGSKKDNK	480
Qy	399	PVATITVAPGVKEGDTYTNVQLKGYAQNUNRFINVDGNARAGTQAIAATAGLQVAYLPG	458
	481	PVATITVAPGVKEGDTYTNVQLKGYAQNUNRFINVDGNARAGTQAIAATAGLQVAYLPG	540
Qy	459	KSMMAIGGGTYRGEAGVATGYSSISDGGWIIITKGAASNSNGHGAASATGYOM	512
	541	KSMMAIGGGTYRGEAGVATGYSSISDGGWIIITKGAASNSNGHGAASATGYOM	554

ID	Accession	Protein Name	Length
AC	Q930Y4	PRELIMINARY	594 AA
DT	01-DEC-2001	(TREMBLER, 19, Created)	
DT	01-DEC-2001	(TREMBLER, 19, Last sequence update)	
DT	01-OCT-2002	(TREMBLER, 22, Last annotation update)	
DE		Nbha outer membrane protein.	
GN		Nbha.	
OS		Neisseria meningitidis.	
OC		Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;	
OC		Neisseriaceae; Neisseria.	
OX	NCBI_TaxID:487;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-EG327.		
RA	Peak 1.R., Strikhanova Y., Dieckelman M., Moxon R., Jennings M.P.;		
RT	"Identification and characterization of a gene encoding a novel outer		
RT	membrane protein of Neisseria meningitidis."		
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF175605; AAK68866.1;		
DR	InterPro: IPR005594; Yada.		
DR	Pfam: PF03895; Yada.1.		
DR	SEQUENCE 594 AA; 62297 MW; 9DD48B04B3A8EA2 CRC64;		
Query Match	94.2%; Score 2449; DB 2; Length 594;		
Best Local Similarity	83.3%; Pred. No.3-3e-96;		
Matches	495; Conservative 6; Mismatches 11; Indels 82; Gaps 2		
QY	1	MNKYRIIWSALNAWVYSELTRNHRKRASATYKTAVALATLLFATVOASANNE-----	54
DB	1	MNKYRIIWSALNAWVSELTRNHRKRASATYKTAVALATLLFATVOASANNE-----	54
QY	55	-----	54
DB	61	PVQRTAVVLSRSDKEGEGEKEVEDSNGWGYFDKKGVLTAQTTLKAGDNLIKQNTNE	120
QY	55	-----	120
DB	121	NTNASSFTYLSKDLTDLTSTVTEKLEPSANSNKNIISDPRKGLNFAFKTAETNGDTTVH	180
QY	100	LNGIGSTLTDLTLNLTGATTNTNDNVYDDEKKRAASVQVNLNAGNNIGKVGPTTASDNV	159
DB	181	LNGIGSTLTDLTLNLTGATTNTNDNVYDDEKKRAASVQVNLNAGNNIGKVGPTTASDNV	240
QY	160	DFVRYTDPVFEVLADTKTTTNNVNSKONGKRTTEYVIGKTSYIRKDDGLVYGRKGENG	219
DB	241	DFVRYTDPVFEVLADTKTTTNNVNSKONGKRTTEYVIGKTSYIRKDDGLVYGRKGENG	300
QY	220	SSTDEGEGLYAKEVIDAIVNKAQRMKTTPANQGTQADKEETVYSGNTVFASGKTGA	279
DB	301	SSTDEGEGLYAKEVIDAIVNKAQRMKTTPANQGTQADKEETVYSGNTVFASGKTGA	360
QY	280	TVSKDDGQNTTVMTDVNVGDLALNQLONGSMNLDSKAVVAGSSGKAVISGNVSPSKGKME	339

[illegible]

ID	Q9JPI3	PRELIMINARY;	PRF:	594 AA.
AC	Q9JPI3;			
DT	01-OCT-2000 (TREMblrel, 15, Created)			
DT	01-OCT-2000 (TREMblrel, 15, Last sequence update)			
DT	01-OCT-2002 (TREMblrel, 22, Last annotation update)			
DE	Outer membrane protein GNA992.			
GN	GNA992.			
OS	Neisseria meningitidis.			
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;			
OC	Neisseriaceae; Neisseria.			
OX	NCBI_TaxID=487;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NG3/88, and B232;			
RX	MEDLINE=20175756; PubMed=10710308;			
RA	Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,			
RA	Comanducci M., Jennings G.T., Baldi L., Baroloni E., Capecci B.,			
RA	Galetti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,			
RA	Ratti G., Santoli L., Savino S., Scarcelli M., Storti E., Zuo P.,			
RA	Broeker M., Hunt E., Knapp B., Blair E., Mason T., Tettelin H.,			
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,			
RA	Moxon E.R., Grandi G., Rappuoli R.;			
RT	"Identification of Vaccine Candidates Against Serogroup B			
RT	Meningococcus by Whole-Genome Sequencing."			
RL	Science 287:1816-1820(2000).			
DR	EMBL; AF226376; AAF22525.1;			
DR	EMBL; AF226369; AAF22518.1;			
DR	InterPro; IPR005594; Yada.			
DR	Pfam; PF03895; Yada; 1.			
SD	SEQUENCE 594 AA; 62086 MW; 1B25E03B950D04B46 CRC64;			
Query Match	94.1%; Score 2446; DB 2; Length 594;			
Best Local Similarity	83.3%; Pred. No. 4.5e-96;			
Matches 495; Conservative 3; Mismatches 14; Indels 82; Gaps 2				
QY	1 MNKRIIRIWNASALNAAVYVSELTRNHTKRASATYKTAVALTLFATVOASANE-----	54		
DB	1 MNKRIIRIWNASALNAAVAVSELTRNHTKRASATYKTAVALTLFATVOASTDDDDLYLE	60		
QY	55 -----	54		
DB	61 PYQGTAVYLSFHAHDSGEKTEVDEDSNWGYFPDKGVTLGAGTITLLKAGDNLIKQNTDE	120		
QY	55 -----TDLTISVGTREKLSFSAANGKNVNTSDPKGLNFAKETAGTNGDTYVH	99		
DB	121 NTNASSFTYLSLKDKLDTLDTSYETREKLSFGANGKKNVNTSDPKGLNFAKETAGTNGDTYVH	180		
QY	100 LINGGSLTLTDLLMWTGATNTNTNNVMDDEKKRAASVDVNLNAGNINIGVPGTASDV	159		
DB	181 LINGGSLTLTDLLMWTGATNTNTNNVMDDEKKRAASVDVNLNAGNINIGVPGTASDV	240		
QY	160 DEVATYTVFEFLSADTKTTTYNVNESKDKGKTEYVIGKTSYVIREKDKLVYGRKGENG	219		
DB	241 DPAVYTVTVFEFLSADTKTTTYNVNESKDKGKTEYVIGKTSYVIREKDKLVYGRKGENG	300		
QY	220 SSTDEGEGLYVAKFEVIDAVNKAQRMKTTTANGOTGOADKEEYVTSNTVTFASGKGTTA	279		


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Db 301 SSTEDEGLVTAKEDIYAVNKGWRMKTTTANGOTGQADKPEYVTSCTNVTFAASGNGTTA 360
Oy 280 TVSKDDOGNITVMTDVNNGDALNVLNOLNSGMNLDKRAVAGSSGKVISGNVSPSKGKDE 339
Db 361 TVSKDDOGNITVMTDVNNGDALNVLNOLNSGMNLDKRAVAGSSGKVISGNVSPSKGKDE 420
Oy 340 TVTNAGNNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSTVDCD-ALNVGSKKDNK 398
Db 421 TVTNAGNNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSTVDCD-ALNVGSKKDNK 480
Oy 399 PVRTTNVAPGYKEGDVTNVAOLKGYAQNLRNIDVNDGNARAGIAQATATAGLYOAYLP 458
Db 481 PVRTTNVAPGYKEGDVTNVAOLKGYAQNLRNIDVNDGNARAGIAQATATAGLYOAYLP 540
Oy 459 KSMAIGGCTYRGEGYAIYSSISDGNWIIKGTASGNSRHFASASVGYOW 512
Db 541 KSMAIGGCTYRGEGYAIYSSISDGNWIIKGTASGNSRHFASASVGYOW 594
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RESULT 11

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O9JPH7 PRELIMINARY; PRT; 594 AA.
ID O9JPH7 AC O9JPH7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GMA992 (Nhha outer membrane protein).
GN GMA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=B2198; and 297-0;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=B2198;
RA Peak I.R., Srikanta V., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226368; AAF42517.1; -
DR EMBL; AF226368; AAF42517.1; -
DR EMBL; AF157604; AAK6885.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada. 1.
SQ SEQUENCE 594 AA; 62361 MW; 436BDEDE68263C5C CRC64;
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Query Match 93.9%; Score 2442; DB 2; Length 594;
Best Local Similarity 83.3%; Pred. No. 6.6e-96;
Matches 495; Conservative 4; Mismatches 13; Indels 82; Gaps 2;
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Oy 1 MNKIYRIIWSALNAAVVSSELTNRNHTKRASATYKTAVALATLLPATYQAASNNNE----- 54
Db 1 MNKIYRIIWSALNAAVVSSELTNRNHTKRASATYKTAVALATLLPATYQAANATDDDLTXLE 60
Oy 55 ----- 54
Db 61 PVORTAVVLSFRSDKEGTGEKEGTEDSNWAAVYFDEKRVLKAGAITLKAGDNLIKONTNE 120
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Oy 55 -----TDLTSVTEKLSFSANGKNVNTSDPKLNFAKETAGTNGDTVH 99
Db 121 NTNDSFPTSLKDLDTLSTVETEKLSFGANGKNVNTSDPKLNFAKETAGTNGDPTVH 180
Oy 100 LNGIGSTLTDPLLTGATTNTNTNDVTDDEKRAASVADVNLNAGNITKGVAPGTTASDNV 159
Db 181 LNCIGSTLTDPLLTGATTNTNTNDVTDDEKRAASVADVNLNAGNITKGVAPGTTASDNV 240
Oy 160 DVFRTYDVEFLSADTKTTTNVESKDKGKTEYKIGAKTSVIEKDKLVTGKDKENG 219
Db 241 DVFRTYDVEFLSADTKTTTNVESKDKGKTEYKIGAKTSVIEKDKLVTGKDKENG 300
Oy 220 SSTEDEGLVTAKEDIYAVNKGWRMKTTTANGOTGQADKPEYVTSCTNVTFAASGNGTTA 279
Db 301 SSTEDEGLVTAKEDIYAVNKGWRMKTTTANGOTGQADKPEYVTSCTNVTFAASGNGTTA 360
Oy 280 TVSKDDOGNITVMTDVNNGDALNVLNOLNSGMNLDKRAVAGSSGKVISGNVSPSKGKDE 339
Db 361 TVSKDDOGNITVMTDVNNGDALNVLNOLNSGMNLDKRAVAGSSGKVISGNVSPSKGKDE 420
Oy 340 TVTNAGNNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSTVDCD-ALNVGSKKDNK 398
Db 421 TVTNAGNNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSTVDCD-ALNVGSKKDNK 480
Oy 399 PVRTTNVAPGYKEGDVTNVAOLKGYAQNLRNIDVNDGNARAGIAQATATAGLYOAYLP 458
Db 481 PVRTTNVAPGYKEGDVTNVAOLKGYAQNLRNIDVNDGNARAGIAQATATAGLYOAYLP 540
Oy 459 KSMAIGGCTYRGEGYAIYSSISDGNWIIKGTASGNSRHFASASVGYOW 512
Db 541 KSMAIGGCTYRGEGYAIYSSISDGNWIIKGTASGNSRHFASASVGYOW 594
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O9JPS9 PRELIMINARY; PRT; 592 AA.
ID O9JPS9 AC O9JPS9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GMA992.
GN GMA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=860800;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226361; AAF42510.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada. 1.
SQ SEQUENCE 592 AA; 61917 MW; 4A347151AFD3C879 CRC64;
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Query Match 93.9%; Score 2441; DB 2; Length 592;
Best Local Similarity 83.6%; Pred. No. 7.2e-96;
Matches 495; Conservative 3; Mismatches 14; Indels 80; Gaps 2;
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Db 1 MNKIYRIIWSALNAAVVSSELTNRNHTKRASATYKTAVALATLLPATYQAANATDDEEBEL 60
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QY 55 -----54
Db 61 ESVOARSVGSIQASMEGSELETISTSMTNDSEKPEVDPIVYTLKAGDNLIKONTNENT 120
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Db 121 MASSFTYSLKDLTLGTLINTEKLSFGANGKRVNIISDTKGLNFAETAGTNDTTHLN 180
QY 102 GIGSTYLDLTLGATNTVNDVNTDEKRAASVVDVNLNAGNNIKGVKPGTTASDNVD 161
Db 181 GIGSTYLDLTLGATNTVNDVNTDEKRAASVVDVNLNAGNNIKGVKPGTTASDNVD 240
QY 162 VRTDYVEFLSADTKTTTVNVEESKDNKTEVKIGAKTSYIKERDKLYTGKDGKENGSS 221
Db 241 VRTDYVEFLSADTKTTTVNVEESKDNKTEVKIGAKTSYIKERDKLYTGKDGKENGSS 300
QY 222 TDSGEGLYTAKEVIDAVNKGAMRKTTTANGOTGOADKFEVTSGTNVTFASGKTATV 281
Db 301 TDSGEGLYTAKEVIDAVNKGAMRKTTTANGOTGOADKFEVTSGTNVTFASGKTATV 360
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Db 361 SKDDGNITVMDVNVGDALNVNQLNSGNNLDSKAVAGSSGKVIISGNVSPSKMDETV 420
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QY 401 RITNVAPGVESGVTVAOLKGVAQNLNNRIDVNDGNARAGIAQALATAGLYQAYLPKGS 460
Db 481 RITNVAPGVESGVTVAOLKGVAQNLNNRIDVNDGNARAGIAQALATAGLYQAYLPKGS 540
QY 461 MMAIGGTYRGEAGVAGYSSISDGGNMIITKTASGNSRCHFGASASVGYQW 512
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RESULT 13
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AC Q9JPR9;
DT 01-OCT-2000 (TremBurel. 15, Created)
DT 01-OCT-2000 (TremBurel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OX Neisseriaceae; Neisseria.
NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH36;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappunli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226382; AAF42531.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada.
SQ SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;
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Query Match 93.8%; Score 2440; DB 2; Length 598;
Best Local Similarity 82.8%; Pred. No. 8.1e-96;
Matches 495; Conservative 4; Mismatches 13; Indels 86; Gaps 2;

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QY 1 MNKYRIINNSALNAVWVSELTNRHNTKRASATVKTAVIATLLFATVQASANNE-----54
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QY 55 -----54
Db 61 PVQRTAVVLSFRSDEKGTGEGTEGDEDSMNAVPEDEKRVLKAGAITLKAGDNLIKONTNE 120
QY 55 -----TDLTSVGTETKLSFANGKNVITSDTKGLNFAKETAGTNDG 95
Db 121 NTNENNTDSFTYSLKDLTLGTLINTEKLSFGANGKRVNIISDTKGLNFAETAGTNDG 180
QY 96 TTVHLNGISSTLDLTLGATNTVNDVNTDEKRAASVVDVNLNAGNNIKGVKPGTTA 155
Db 181 PTVHLNGISSTLDLTLGATNTVNDVNTDEKRAASVVDVNLNAGNNIKGVKPGTTA 240
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Db 241 SDNVDPVRYDYVEFLSADTKTTTVNVEESKDNKTEVKIGAKTSYIKERDKLYTGKDK 300
QY 216 GENGSTDSGEGLYTAKEVIDAVNKGAMRKTTTANGOTGOADKFEVTSGTNVTFASGK 275
Db 301 DENGSSTDSGEGLYTAKEVIDAVNKGAMRKTTTANGOTGOADKFEVTSGTNVTFASGK 360
QY 276 GTTATVSKDDGNITVMDVNVGDALNVNQLNSGNNLDSKAVAGSSGKVIISGNVSPSKG 335
Db 361 GTTATVSKDDGNITVMDVNVGDALNVNQLNSGNNLDSKAVAGSSGKVIISGNVSPSKG 420
QY 336 KMEETVNNAGNNIETRNKNIDATSMTPQPSVSLGAGADAPTLSDG-DALNVSGK 394
Db 421 KMEETVNNAGNNIETRNKNIDATSMTPQPSVSLGAGADAPTLSDG-DALNVSGK 480
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QY 455 YLPKSMMAIGGTYRGEAGVAGYSSISDGGNMIITKTASGNSRCHFGASASVGYQW 512
Db 541 YLPKSMMAIGGTYRGEAGVAGYSSISDGGNMIITKTASGNSRCHFGASASVGYQW 598
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Q9JPS0 PRELIMINARY; PRT; 598 AA.
AC Q9JPS0;
DT 01-OCT-2000 (TremBurel. 15, Created)
DT 01-OCT-2000 (TremBurel. 22, Last annotation update)
DE Outer membrane protein GNA992 (Nhha outer membrane protein).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OX Neisseriaceae; Neisseria.
NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NH15;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappunli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR [2]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NH15;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
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RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF226381; AAF42530.1; -
DR EMBL: AF157607; AAK68868.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 598 AA; 62763 MW; E6C7AEF0B8A63CB CRC64;

Query Match 93.3%; Score 2427; DB 2; Length 598;
Best Local Similarity 82.3%; Pred. No. 2.9e-95;
Matches 492; Conservative 5; Mismatches 15; Indels 86; Gaps 2;

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QY 1 MNKIYRIIWSALNAAWVVSSELTNRNHTKRASATVATLTLFATVQASANNE----- 54
D 1 MNKIYRIIWSALNAAWVVSSELTNRNHTKRASATVATLTLFATVQANATDDDLXLE 60
QY 55 ----- 54
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QY 55 -----TDLTSVGTSEKLSFSANGKNVNTSDTKGLNFAKETAGTNGD 95
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QY 96 TTVHLNGIGSTLTPTLNTGATVNTNDNTDDEKKRAASVADYLNAGWNITKGVKPGTTA 155
D 181 PTVHLNGIGSTLTPTLNTGATVNTNDNTDDEKKRAASVADYLNAGWNITKGVKPGTTA 240
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D 241 SDNVDVFRITVTEFLSADTKTTTVNVESKDNKGTVEYKIGAKTSVIREKDGKLVGTGDK 300
QY 216 GENGSSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGQADKFEVTSCTNTVTFASGK 275
D 301 DENGSSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGQADKFEVTSCTNTVTFASGK 360
QY 276 GTTATVSKDDGNTTVMYDVNVGDALNVNOLONGSMWLSKAVAGSSGKTVISGNVSPSKG 335
D 361 GTTATVSKDDGNTTVMYDVNVGDALNVNOLONGSMWLSKAVAGSSGKTVISGNVSPSKG 420
QY 336 KMDTVNINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLISVDGD-ALNVGSK 394
D 421 KMDTVNINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLISVDDEGALNVGSK 480
QY 395 KDNKPVRTITNAPGVKEGADVNVNQLKGAONLNRRIDNVGNAAGIAQAIATAGLVQA 454
D 481 DANKPVRTITNAPGVKEGADVNVNQLKGAONLNRRIDNVGNAAGIAQAIATAGLVQA 540
QY 455 YLPGRSMMAIGGTYRGEGAGYAIGYSSISDGNMIKGTASGNSRGHGASASVGYOW 512
D 541 YLPGRSMMAIGGTYRGEGAGYAIGYSSISDGNMIKGTASGNSRGHGASASVGYOW 598
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RESULT 15

Q9JPT0 PRELIMINARY; PRT; 598 AA.

AC Q9JPT0;
DT 01-OCT-2000 (Tremblarel. 15, Created)
DT 01-OCT-2000 (Tremblarel. 15, Last sequence update)
DT 01-OCT-2002 (Tremblarel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=2996;

RX MEDLINE=20175756; PubMed=10710308;

RA Piza M., Scariato V., Malignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechchi B.,
RA Galeotti C.L., Iuzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tetteilin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.,
RT "Identification of Vaccine Candidates Against Serogroup B
RL Meningococcus by Whole-Genome Sequencing."
RL EMBL: AF226359; AAF42508.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 598 AA; 62763 MW; 63A6A3BD7F0F2EE3 CRC64;

Query Match 93.3%; Score 2427; DB 2; Length 598;
Best Local Similarity 82.1%; Pred. No. 2.9e-95;
Matches 491; Conservative 6; Mismatches 15; Indels 86; Gaps 2;

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D 1 MNKIYRIIWSALNAAWVVSSELTNRNHTKRASATVATLTLFATVQANATDDDLXLE 60
QY 55 ----- 54
D 61 PVQRTAVVLSFRSDKEGTGEKEGTEDSNMAVYFDEKRYLKAGAITLAKADNLKIKONTNE 120
QY 55 -----TDLTSVGTSEKLSFSANGKNVNTSDTKGLNFAKETAGTNGD 95
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D 181 PTVHLNGIGSTLTPTLNTGATVNTNDNTDDEKKRAASVADYLNAGWNITKGVKPGTTA 240
QY 156 SDNVDVFRITVTEFLSADTKTTTVNVESKDNKGTVEYKIGAKTSVIREKDGKLVGTGDK 215
D 241 SDNVDVFRITVTEFLSADTKTTTVNVESKDNKGTVEYKIGAKTSVIREKDGKLVGTGDK 300
QY 216 GENGSSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGQADKFEVTSCTNTVTFASGK 275
D 301 GENGSSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGQADKFEVTSCTNTVTFASGK 360
QY 276 GTTATVSKDDGNTTVMYDVNVGDALNVNOLONGSMWLSKAVAGSSGKTVISGNVSPSKG 335
D 361 GTTATVSKDDGNTTVMYDVNVGDALNVNOLONGSMWLSKAVAGSSGKTVISGNVSPSKG 420
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D 421 KMDTVNINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLISVDDEGALNVGSK 480
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D 481 DANKPVRTITNAPGVKEGADVNVNQLKGAONLNRRIDNVGNAAGIAQAIATAGLVQA 540
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D 541 YLPGRSMMAIGGTYRGEGAGYAIGYSSISDGNMIKGTASGNSRGHGASASVGYOW 598
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Job time : 42.6045 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2003, 09:06:20 ; Search time 7.90659 Seconds
(without alignments)
3045.266 Million cell updates/sec

Title: US-09-771-382-23
Perfect score: 2600
Sequence: 1 MNKIRILINSLNANMVVYS.....TASGNSRGHFGASASVGYQW 512

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	245	9.4	1039	1 AG43_ECOLI	P39180 escherichia
2	222	8.5	1286	1 AIDA_ECOLI	Q03155 escherichia
3	214.5	8.2	1325	1 YDEK_ECOLI	P32051 escherichia
4	195.5	7.5	2003	1 YDBA_ECOLI	P33666 escherichia
5	193.5	7.4	2249	1 OMPA_RICRI	P15921 rickettsia
6	178.5	6.9	1577	1 HLVA_PROMI	P16466 proteus mir
7	176.5	6.8	933	1 SLAP_CAME	P35827 campylobact
8	176	6.8	1655	1 OMPB_RICCN	Q9kxk3 r outer mem
9	174.5	6.7	1025	1 SLAP_CAUCR	P35828 caulobacter
10	174.5	6.7	1645	1 OMPB_RICRY	P96989 r outer mem
11	174	6.7	1654	1 OMPB_RICRI	Q53047 r outer mem
12	173.5	6.7	1608	1 HLVA_SPRMA	P15320 serratia ma
13	170.5	6.6	1953	1 BIGA_SALTY	P25927 salmonella
14	169.5	6.5	2660	1 YEEU_ECO57	Q8x8v7 escherichia
15	169	6.5	1567	1 ICEN_XANCT	P18127 xanthomonas
16	166.5	6.4	1569	1 APU_THETU	P38536 t amylopull
17	166	6.4	1569	1 YPJA_ECOLI	P52143 escherichia
18	166	6.4	2021	1 OMPA_RICCN	O52657 rickettsia
19	165	6.3	1300	1 120K_RICRI	P14914 rickettsia
20	164	6.3	3178	1 YS89_CABEL	Q09662 caenorhabd1
21	163.5	6.3	550	1 FLIC_SHIFL	Q08860 shigella fl
22	163.5	6.3	1148	1 ICEN_PSEXS	O30611 pseudomonas
23	163.5	6.3	1656	1 OMPB_RICJA	O06653 r outer mem
24	162.5	6.2	917	1 HXA3_HAEIN	P45355 haemophilus
25	162	6.2	737	1 ALV3_ENTFA	P37710 enterococcu
26	161.5	6.2	1007	1 Y741_CHLMU	Q9pj16 chlamydia m
27	160.5	6.2	1036	1 FLIC_SALON	P13126 delnoccocus
28	159.5	6.1	507	1 FLIC_SALON	O06974 salmonella
29	159.5	6.1	537	1 TEE6_STRPY	P18481 streptococc
30	158.5	6.1	487	1 FLIC_ECOLI	P04949 escherichia
31	157.5	6.1	507	1 FLIC_SALBE	O06968 salmonella
32	157.5	6.1	1643	1 OMPB_RICPR	O53020 r outer mem
33	156.5	6.0	928	1 PM10_CHLPN	Q9rb65 chlamydia p

34	156	6.0	642	1 FLID_CAME	Q9phw6 campylobact
35	156	6.0	918	1 YMB_CABEL	P34487 caenorhabd1
36	155	6.0	504	1 FLIC_SALNA	O52959 salmonella
37	155	6.0	504	1 FLIC_SALRO	O06982 salmonella
38	155	6.0	575	1 FLA2_CAME	P22251 campylobact
39	155	6.0	1153	1 PVDB_PLAKN	P50493 plasmodium
40	154	5.9	1196	1 ICEV_PSEXS	O33479 pseudomonas
41	153.5	5.9	1637	1 MRSP_STRAU	P80544 staphylococ
42	153.5	5.9	2358	1 YEEJ_ECOLI	P76347 escherichia
43	153	5.9	504	1 FLIC_SALBU	O06969 salmonella
44	153	5.9	504	1 FLIC_SALDU	O06971 salmonella
45	153	5.9	1200	1 ICEN_PSEXS	P06620 pseudomonas

ALIGNMENTS

RESULT 1
ID AG43_ECOLI STANDARD: PRT: 1039 AA.
AC P39180; P75614; P76360; P97241; Q46771;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 43 precursor (AG43) (Flufluff protein).
GN FLU OR B2000.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia..
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "the complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Alpha H., Baba T., Fujita K., Hayashi K., Inada T., Isano K.,
RA Ksai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,
RA Sivasubraman S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horinouchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ML 308-225;
RA Henderson I.R., Owen P.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PRELIMINARY SEQUENCE OF 53-78.
RC STRAIN=ML 308-225;
RX MEDLINE=89291704; PubMed=2661530;
RA Caffrey P., Owen P.;
RT "Purification and N-terminal sequence of the alpha subunit of antigen
43, a unique protein complex associated with the outer membrane of
Escherichia coli.";
RL J. Bacteriol. 171:3634-3640(1989).
RN [5]
RP SEQUENCE OF 53-63.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded

RT in the genome of *Escherichia coli* K-12.⁶;
 RA Electrophoresis 18:1259-1313(1997).
 RN [6]
 RP GENE NAME
 RX MEDLINE=97257509; PubMed=9103983;
 RA Henderson I.R., Meehan M., Owen P.;
 RT "Antigen 43, a phase-variable bipartite outer membrane protein,
 RT determines colony morphology and autoaggregation in *Escherichia coli*
 RT K-12."
 RL FEMS Microbiol. Lett. 149:115-120(1997).
 CC -1- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION. MAY
 CC FUNCTION AS AN ADHESIN.
 CC -1- SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA
 CC CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA
 CC CHAIN).
 CC -1- SUBCELLULAR LOCATION: Outer membrane-associated.
 CC -1- SIMILARITY: TO ADHESIN AIDA-1 AND TO BONDRELLA PERTACTIN.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; AE000291; AAC75061.1; ALT_INIT.
 DR EMBL; D90838; BAA15825.1; ALT_INIT.
 DR EMBL; D90839; BAA15832.1; ALT_INIT.
 DR EMBL; U24429; ABA47869.1; -.
 DR HSSP; P07505; ISRD.
 DR Ecogene; EG12686; flu.
 DR InterPro; IPR006315; Autotransport.
 DR InterPro; IPR005546; Autotransporter.
 DR InterPro; IPR004899; Pertactin.
 DR Pfam; PF03797; Autotransporter; 1.
 DR Pfam; PF03213; Pertactin; 1.
 DR TIGRfams; TIGR01414; autotrans_bar1. 1.
 DR Outer membrane; Signal; Complete proteome.
 KW SIGNAL
 FT 1 52
 FT CHAIN 53 551 ANTIGEN 43 ALPHA CHAIN.
 FT CHAIN 552 1039 ANTIGEN 43 BETA CHAIN.
 FT VARIANT 2 2 SL -> N (IN STRAIN ML 308-225).
 FT VARIANT 41 42 K -> FE (IN STRAIN ML 308-225).
 FT VARIANT 46 46 T -> K (IN STRAIN ML 308-225).
 FT VARIANT 157 157 W -> L (IN STRAIN ML 308-225).
 FT VARIANT 188 188 V -> F (IN STRAIN ML 308-225).
 FT VARIANT 303 305 ATN -> STI (IN STRAIN ML 308-225).
 FT VARIANT 320 320 A -> T (IN STRAIN ML 308-225).
 FT VARIANT 372 372 N -> Q (IN STRAIN ML 308-225).
 FT VARIANT 493 493 E -> V (IN STRAIN ML 308-225).
 FT VARIANT 497 497 S -> N (IN STRAIN ML 308-225).
 FT VARIANT 509 509 H -> Y (IN STRAIN ML 308-225).
 FT VARIANT 709 709 E -> K (IN STRAIN ML 308-225).
 FT VARIANT 721 721 M -> T (IN STRAIN ML 308-225).
 FT VARIANT 751 753 GHL -> SHF (IN STRAIN ML 308-225).
 FT VARIANT 803 803 S -> P (IN STRAIN ML 308-225).
 FT VARIANT 815 815 A -> V (IN STRAIN ML 308-225).
 FT VARIANT 824 824 C -> S (IN STRAIN ML 308-225).
 FT VARIANT 829 835 LNLVHTS -> MNLVYNA (IN STRAIN ML 308-
 FT 225).
 FT VARIANT 845 847 QGT -> LGA (IN STRAIN ML 308-225).
 FT VARIANT 855 855 S -> T (IN STRAIN ML 308-225).
 FT VARIANT 888 888 O -> L (IN STRAIN ML 308-225).
 FT VARIANT 1025 1025 S -> I (IN STRAIN ML 308-225).
 FT CONFLICT 61 63 ETV -> TTT (IN REF. 5).
 SO SEQUENCE 1039 AA; 106841 MW; 51/0D647C8DBEB0 CRC64;
 Query Match 9.4%; Score 245; DB 1; Length 1039;
 Best Local Similarity 23.9%; Pred. No. 2e-05;
 Matches 135; Conservative 76; Mismatches 185; Indels 170; Gaps 33;

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Db      5  LNTCYRLVWMMHTGAFFVVASPELARRRGGVAAVALSLAAVTSLPVLAADIVHGEYVN 64
OY      51  ---ANNETDILTSVTEKLSFSAANGKVNTSDTKLNFPAKET-----AGTNGD 95
Db      65  GGTLANHENOIVFGTTNGMTIST-----GLEYPDNEANTGOWVODGGTANK 112
OY      96  TTVHLNGI-----GSTLITDILLNGATNV-----TNDNVTDDEK---KRAASVNDVLN-A 142
Db      113  TTVISGGIQRNPPGGSVDIVISAGGGSILQGRAVNTTILNGGEOMHEGALATGTIVNDK 172
OY      143  GWNIGKVPKPTTASDNVDFVPT-----YDVEPLADTKTIVNVESKDNKKTE 192
Db      173  GMOV--VKPFTVADTV--VNTGAEGGPDALNGDPTGQVVRDPAVTTIN---KNGRQIV 224
OY      193  VKIG-AKTSVLEKEDGKLYTKDKGENSSIDE-----GEGLY---TAKEYIDAVNRKM 243
Db      225  RAEGTANTTV-----YAGDDPTVHGHALDITLNGVQYVHNGFTASDPTV--VNSGWM 275
OY      244  RM-----KTTTANGOTGADKEFEVTSGTNVFASG---KGTATVSKDDG--NTTV 291
Db      276  QIVANGVAGATTYN-QKGR-LQVDAGTATNTVLKQGALVTSAAVTV---GINRLG 329
OY      292  MYDVNVGDALVNVOLNLSGWNLDKRAVAGSSGKVIISGVNPSFKGMDETVINAGNNIEI 351
Db      330  AFVSVEGKADNV-VLENGG-RID-----VLTGTATN-----TVDVGGGTLDV 370
OY      352  TRNGKNIDIASMTPEFSSVSLGAGADAPLTSVGDALNVGSKDKDKPVRTITNVAPGKE 411
Db      371  RNG-----GTAIT-----VSMGNG---VLLADSGAAVSSGTRSDGK-----AFSIGG 409
OY      412  GDVTNVAQKGAONLNRIIDVYDGNARAGIAQAIATAGLVQAVLPKSKMAIGGTYRG 471
Db      410  GQADALMLEKSSFTLN-----ACDPTADTV-----VANGGLETA 443
OY      472  EAGYAIGYSSISDGGNMIIKGTASGN 497
Db      444  RGTLAGITTLNNGAIIITLSEKTYVNN 469

RESULT 2
AIDA_ECOLI
ID      AIDA_ECOLI      STANDARD:      PRT: 1286 AA.
AC      Q03155.
DT      01-JUN-1994 (Rel. 29, Created)
DT      01-JUN-1994 (Rel. 29, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Adhesin aida-1 precursor.
DE      AIDA-1.
OS      Escherichia coli.
OG      Plasmid pIB6.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Escherichia.
OX      NCBI_TaxID=562;
RN      [1]
RP      SEQUENCE FROM N.A., AND SEQUENCE OF 50-56.
RC      STRAIN=O126:H27 / 2787;
RX      MEDLINE=92326638; PubMed=1625582;
RA      Benz I', Schmidt M.A.;
RT      "Aida-1, the adhesin involved in diffuse adherence of the
RT      diarrhoeagenic Escherichia coli strain 2787 (O126:H27), is
RT      synthesized via a precursor molecule.";
RL      Mol. Microbiol. 6:1539-1546(1992).
CC      -!- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE
CC      ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI
CC      TO EPITHELIAL CELLS.
CC      -!- SUBCELLULAR LOCATION: Outer membrane.
CC      -----
CC      THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial

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QY 1MNIYVIMNCTIYNFQACSELTRBRAGKTSYINLKRKSSGLTTKSRLLTGLVLLSSAS 50
1MNIYVIMNCTIYNFQACSELTRBRAGKTSYINLKRKSSGLTTKSRLLTGLVLLSSAS 50
Db 1MNIYVIMNCTIYNFQACSELTRBRAGKTSYINLKRKSSGLTTKSRLLTGLVLLSSAS 60
QY 51-----ANNEIDLTS-----VTEKLSFSAKNEVNTSDTKLNFAKETAGT 92
Db 61GASLEVDNDQITRIDIDVAYDAYLWVGWGTGLNILLACGN--ASLITITTSV-----IGA 113
QY 93NGOTYHLANGISGT--LDT-----LNTG-----ATTWTDNVTDDDEKKRASVKRYLN 141
Db 114NESESECTVNLGLGTWMLYDSCNNAPRLVNVGOSGTGLNIKOKGHVD-----GYLR 164
QY 142AGNINIKVPRGTASNDVFRTYTPVEFLSADTKTTIVNESHDKNCKTE-----YK 194
Db 165LGSSTGCV--GIYVNEGEDSVLTTELFEIGTIGCSLNTI---DKGYTSSYAILIGYO 218
QY 195IGAKTSVIREKDK--LYTGCKDK-----ENGSTDEGELYTAKEVDIVAKAGRM 245
Db 219AGSNGVYVEKGEMLIKNNDSIEFGJONGTGATIRREGILVTAEMTILIGNATG--- 275
QY 246KTTTANGCQTGQADKEFTVTSGTNVTFRASGKTATVSKDDOGNITVIMDVNVDALN--V 303
Db 276-IGTLNVO--DDPSVITVRLYNGFNG--TVNISNNGLINNKEYSLVGVDGSHGV 329
QY 304NQLQNSGWL-----DKKAVAGSGKVIKGNVPSKCKMDET----- 340
Db 330NWTDKHMHNLGTGEAFRIYITIGADGDELNVSSSEKRVDSGIITAG--MKETGTGNITV 386
QY 341-----VINAGNNIETTRNGKNMIDATSMTPQSSVSILGACADAPLTSVDDALNVSKK 395
Db 387KDKNSVITMLGTLGIDGHEMNIINOGILVYVSSGSSLGTC-----ETGCVGVSITTGGM 442
QY 396D-NKPYRITINAVPKEGDVTNVAOLKGVANLNNRIDVNDGNARAGIAQAIATAGLVQA 454
Db 443EVKNKYTYTIGVAGVGNLISDGC--KEVSONITFLDKASGIGITMLNMTATSSFDVTGI 500
QY 455YLP--EKSMMAIGGGYIREAGYAI-----GYSSISDGGNNILIKGTASGNR 499
Db 501NVNCFSGVJNVNNGATLNTSTGTYGITGNASGKGIVNTSLWNLKR--TSSTNQO 554

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RESULT 4
ID ydba.ecoli STANDARD; PRT: 2003 AA.
AC P33666; P76087; P76088; P76836; P76857; P76859;
DT 01-FEB-1994 (Rel. 28, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ydba.
GN ydba OR B1401/B1405.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
RX NCBI_TaxId=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=9742617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.U.,
RA Mau B., Shao Y.
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Sempel G., Seki Y., Sivasubram S., Tagami H., Takada J.,

```

RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horinchi T.;
RT "A 570-kb DNA sequence of the *Escherichia coli* K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RN DNA Res. 3:363-377(1996).
RL [3]
RP SEQUENCE OF 464-2003 FROM N.A.
RC STRAIN-K12;
RX MEDLINE-92190338; PubMed-1665988;
RA Moszer I., Glaser P., Danchin A.;
RT "Multiple *in situ* insertion sequences near the replication terminus in
RT *Escherichia coli* K-12";
RL Biochimie 73:1361-1374(1991).
CC -1- SIMILARITY: TO S. TYPHIMURUM ORF NEAR CYG (AC P25928).
CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR
CC THIS PROTEIN IS INTERRUPTED BY A HYBRID ISZD/IS30C ELEMENT
CC BETWEEN AMINO ACIDS 839 AND 840.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE000237; AAC74483.1; ALT_SEQ.
DR EMBL; AE000237; AAC74487.1; ALT_SEQ.
DR EMBL; D90778; BAA15009.1; ALT_SEQ.
DR EMBL; D90778; BAA18880.1; ALT_SEQ.
DR EMBL; D90779; BAA18881.1; ALT_SEQ.
DR EMBL; X62680; -; NOT_ANNOTATED_CDS.
DR Ecogene; EG11307; ydba.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 489 489 I -> V (IN REF. 2).
FT CONFLICT 495 495 I -> V (IN REF. 2).
SQ SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220EE CRC64;
Query Match 7.5%; Score 195.5; DB 1; Length 2003;
Best Local Similarity 24.1%; Pred. No. 0.014;
Matches 136; Conservative 67; Mismatches 202; Indels 160; Gaps 31;

QY	49	ASANNEDTLTGVSTKELSSANGKNVNTISDQKGLNFKEFTAGNNGDTYHLNG-----	102
		273	ATYDNKGITMTVDDPESMGIQIDGDAIYNN-----GESTITNGGTQIOLINDDATAN
Db			325
QY	103	-IGSTLTDFLTNGATNTVNTDNYVDDDEKKRAASVQVLAAGWNIKGVBGTASDADF	161
		326	NNGKTTVDGKDSFTGEINNGNKVIQD-----GDLVSGGGHGI-DITGDSATVDKGT
Db			378
QY	162	VRIYDIVER-LSADTKTITYVNESD-----NGKTEVKIGAKTSYIKENKGL	209
		379	MTVDEDSIGIQVDDQDAVYNNEGESAITNGTGTOIINGDATANNGKTTV---DGKD
Db			434
QY	210	VTGKD-KGENG-----SSTDEGELVTAKE-----VIDA---237	
		435	STETELAGNNKVIQDGLDVSGGGHGIDITGDSATVNKKTMTVTPESIGIQLDSDQA
Db			494
QY	238	-VAKAGRMKTTTANGQCGADKEFTYVTSNTVTPASCKGTTAATVSKD-----QGNITY	291
		495	IYNNEG---ESTITNGTG-----TOINGNDAT-ANNSGKTTYDGDKDSGTGKLAINIGI
Db			544
QY	292	MYOVNVDGLNV-----NOLONGSMN-LDSK-----AVAGSSGKVISGNTSPSKGKDET	340
		545	---VINDGSLTYTGGAHGVENIGDNGTYANNKGDIVSDTSGIVLINDEGATYSNTGDVN
Db			601
QY	341	VNINAGNNIETIRNGKNIDIAISM-TPOFS-----SVSLGA-----GADAEFLS	383
		602	VS-NEATGFSITTSNGKVSILASMOVGDFSTGVDLNGNNNSVTLLAADKLKVGOKATGIN
Db			660
QY	384	VQSDALNV---GSKDNKRPVRLITNA-----PGV-----KEGVTVAAOLKGAQN-LN	428
		661	VQSDATVITNGVLVDKDKTADNAAEYFEDPSGIVNYGSDNNVTLDGKLTIVYSDSEVT
Db			720

QY	DB	QY	DB	RESULT 5
429 NRINVD-DGNARFAGIAQIAITAGVY-----QAVLPKSSMAIIGCGYRRBAG 474	721 SROSNLEPDGSAE-----KTSGLVIGDGTNTVMNGGLELIGERKMAIADSGVTSIARTG 773	475 YAI-----GYSSISDGNWMIWG 492	774 YSYTSIVIVSGESSVYLNIGDPTTISG 798	
1:	1:	1:	1:	
01-APR-1990 (Rel. 14, Created)	01-APR-1990 (Rel. 14, Last sequence update)	01-APR-1990 (Rel. 14, Last sequence update)	16-OCT-2001 (Rel. 40, Last annotation update)	
Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (OmpA) (comp A).	Rickettsia rickettsii.	Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Rickettsiaceae; Rickettsiaseae; Rickettsia.	NCBI_TaxID=783;	
SEQUENCE FROM N.A.	SPRAIN-R.	MEDLINE=90354033; PubMed=21175568;	Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;	
"A protective protein antigen of Rickettsia rickettsii has tandemly repeated, near-identical sequences."	Infect. Immun. 58:2760-2769(1990).	-1- FUNCTION: ELICITS PROTECTIVE IMMUNITY.	-1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A	
-1- S-LAYER WITH HEXAGONAL SYMMETRY.	-1- PTM: GLYCOSYLATED (PROBABLE).	-1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY		

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EMBL: M31227; AAA26380.1; -	DR DR	PIR: A41477.	DR DR	InterPro: IPR006315; Autotransport.
InterPro: IPR005546; Autotransporter.	DR DR	PIR: PF03797; Autotransporter; 1.	DR DR	TIGRfams: TIGR01414; autotransp_bar1; 3.
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.	FT FT	SIGNAL 1 28	POTENTIAL.	
CHAIN 29 2249	FT FT	DOMAIN 212 1180	OUTER MEMBRANE PROTEIN A.	
REPEAT 212 286	FT FT	REPEAT 287 358	13 x APPROXIMATE TANDEM REPEATS.	
REPEAT 359 430	FT FT	REPEAT 431 505	A (TYPE I).	
REPEAT 506 577	FT FT	REPEAT 578 652	B (TYPE II).	
REPEAT 653 724	FT FT	REPEAT 725 799	C (TYPE II).	
REPEAT 800 874	FT FT	REPEAT 875 949	D (TYPE I).	
REPEAT 950 1021	FT FT	REPEAT 1022 1093	E (TYPE II).	
REPEAT 1094 1165	FT FT	REPEAT 1166 1180	F (TYPE I).	
SEQUENCE 2249 AA: 224333 MW: A9D6646C089DF087 CRC64:			G (TYPE II).	
			H (TYPE I).	
			I (TYPE I).	
			J (TYPE I).	
			K (TYPE II).	
			L (TYPE II).	
			M (TYPE II).	
			TYPE I (COMPLETE).	
Query Match	Best Local Similarity	7.4%; Score 193.5; DB 1; Length 2249;		
		25.2%; Pred. No. 0.02;		

	Matches	152;	Conservative	52;	Mismatches	211;	Indels	187;	Gaps	32;
QY	30	ASATVKT	-AVLATLFA	TVQASANNED	LTLSVGETKLSFSANGK	VITS	SDTKGLN	FAKE	88	
Db	730	ALATVNVGAGAT	ATLGGAVIKAT	TTKTLTNAA	SVLT	----	LTNAAV	-----	LTGAID	776
QY	89	TACINNGDT	-TVHNGIS	TLTDLLMT	-----		GATTNTND	NVTPDEK	130	
Db	777	NT	-TGGDNVGLNLNGAL	SOVTTG	DIGNTSLATISVAGAT	TLGGAVIKAT	TTKLTN	---	832	
QY	131	KRASV	EDVLNAGN	NIKGVR	PGFTAS	NVDFVTRD	VEEFLADTK	TTTYNVESK	DGKK	190
Db	833	--AASV	LELTNAA	NVLGAID	NTTGGDNVGLNLNGAL	SOVTTG	DIGNT	-----	NSLA	882
QY	191	TEVVI	GAKT	-----	SVIKEDGKL	-----			209	
Db	883	T	-ISVGA	FTATLGGAVIKAT	TTKTLTNAA	SVLTLTNAA	NVLGAID	NTTGGDNVGLNLNG		941
QY	210	----	VTGKDK	GENSSR	-DESEGLV	-----	AKEVIDAV	NKAGRM	TTTANGOTG	259
Db	942	ALSO	VTGDNIGN	TNLTATISVAGAT	TLGGAVIKAT	TTKTLTDAA	SAVKEFTNP	VVVTGAIDN		1001
QY	260	FETV	TSGNTVF	AFSGK	TTTATVSKD	OGNITVMVDVNW	GALANVLO	NSGMD	SKAVA	319
Db	1002	TGNANNGI	-VTF	TGNSVT	TGTV	-----	GNLTAL	TVVVGAGL	-LQVGGV	1053
QY	320	GSSG	KVVISGNV	SPSKGMD	ETVNI	NAG	-----	NNIET	RGNK	374
Db	1054	DMA	SAVFTNP	VVVVTGAID	NTGNANNGI	IVFTGNS	VTGAVNG	-----	TNALATV	1106
QY	375	AGAD	APLLSD	GDAL	--NVGSK	DON	-KPV	RTTNA	PCVK	431
Db	1107	AG	----	LLOV	GGVVKANTIN	LTDMA	SAVFTN	--PVV	VGAIDNTG	1153
QY	432	DNDV	GNARA	-----	GIAQAIAT	-----	AGL	-VOAYL	PKSMA	466
Db	1154	VTF	TGNS	TVTG	DIGNTAL	TNALTAV	NVAGAGIT	TLDA	-----	1210
QY	467	GTYR	GEAGV	ALGY	-----	SSISD	GNM	ILIK	-----	507
Db	1211	G	-----	GKA	IPYFK	GA	INANG	NALLNVMTK	LLTASH	1264
QY	508	VG	509							
Db	1265	VG	1266							

RESULT 6

HLTA_PROMI STANDARD; PRT; 1577 AA.

AC P16466;

DT 01-AUG-1990 (Rel. 15, Created)

RT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 01-NOV-1990 (Rel. 16, Last annotation update)

DE Hemolysin precursor.

GN HPMa.

OS Proteus mirabilis.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

CC Enterobacteriaceae; Proteus.

OX NCBI_TaxID=564;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.

RC STRAIN=Isolate 477-12;

RX MEDLINE=90170827; PubMed=2407716;

RA Uphoff T.S., Welch R.A.;

RT "Nucleotide sequencing of the Proteus mirabilis calcium-independent hemolysin genes (hpmA and hpmB) reveals sequence similarity with the Serratia marcescens hemolysin genes (shlA and shlB).";

RL J. Bacteriol. 172:1206-1216(1990).

CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.

CC -1- FUNCTION: CELL-BOUND HEMOLYSIN WHICH RELEASES HEME-IRON FROM

CC ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA
CC REQUIRES HPMB FUNCTION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -1- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA
CC MAY BE RESPONSIBLE FOR PORE FORMATION.
CC -1- SIMILARITY: TO S.MARCSSENS HEMOLYSIN (SHLA).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M30186; AAA25657.1; -
CC PIR: A35140; A35140.
CC KM Hemolysis; Toxin; Outer membrane; Signal.
CC FT SIGNAL 1 29
CC CHAIN 30 1577
CC SEQUENCE 1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;

Query Match 6.9%; Score 178.5; DB 1; Length 1577;
Best Local Similarity 21.4%; Pred. No. 0.076;
Matches 129; Conservative 82; Mismatches 188; Indels 203; Gaps 33;

QY 23 TRNRTRKASATVTAVALATLTFATVOASANNETDLTSVTEKLSFSAANGKVNITSPDK 82
DB 710 TSTETEQANDTSG-----ANVDLQANK--DYFAGSDLTATTG--ASTGTGNAVA 756
QY 83 LNFAGTACT--NGDTTVH-----LNGTGS-----TLTDTLLTGTATNTND 123
DB 757 FVSTENKQJDNMTDTITSGFSYTGVDKVRADPOYKOHQTEVTKNRGSGTEVAGD 816
QY 124 -----NVTDEKRRASVKNVLNAGNI----- 146
DB 817 LTTTANKDLHEGASHHVEGRYSEGENIOHLAVNDEISKTPDSLVNGLDVGVALDYSGV 876
QY 147 -----KGVKPG-----TTASDNVDF--VRYDVEFLS--ADTKTTVNVE----- 183
DB 877 TRPVKKAIEDGVMTTRKGNNTDLKKKYTARDALANLANLSNLETPNVGVEVGIKGGSSQ 936
QY 184 SKNGKTEVKIGAKTSVKEKDKLVTKKGBNGSSVDEGEGLVTAKEVIDA--VNAKG 242
DB 937 SQTDGQAVSTISINAKIKDI--DSNNKL--HDGCTHYOSTOEGISLTANTHTSEATLDKHQ 992
QY 243 WRKKTTPANGFOADKFETVSTGNTVFA--SGKGTA-----TVSKDOGNTVYDY 295
DB 993 TTTHETKGGQIGVSTK-----TGSDDITVAIKGBGOTTDNALMETTKAGSOFTSNGDISI 1047
QY 296 NVGDALNVNQLQNSGNMLDSKAVAGSSGKVIYSGNVSPSKGMDETVAINAGNNIETR-- 353
DB 1048 NVGE-----NAHVEAQFOAQ-----KKG---TV--INAGGDLTLAQAT 1081
QY 354 -----NGK--RTDIATSKTPQFSSVSLGAGADAPL--SYGDALNVGSKKKDKPV 400
DB 1082 DTHSESOSNVNGSANLKVGT--TPE--SKDYGGGFNAGTTHHSKEQTAVAGVITGSGGI 1137
QY 401 RITNVNAPGVEGVTVAQLKGAONLNRRID-----NDGABARAGIAQ--- 444
DB 1138 ELNAGHNLITLG--THLSSEQDIALNNTKVKVDLOSASSETEKGNNSGGVQAGFGKMT 1195
QY 445 --AATAGVLAQVATLPKSMMAIG-----GGTYRGEAGVLAIGSSISDGNWVIKG 492
DB 1196 DDASSVNGL-----GSAQFAIKGDEKSVSREGT-----INNSGNLTING 1236
QY 493 TA 494
DB 1237 NS 1238

ID SLAP_CAMFE STANDARD; PRT; 933 AA.
AC P35827;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE S-layer protein (surface array protein) (SAP).
GN SAPA.
OS Campylobacter fetus.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=196;
RN
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
RC STRAIN=84-32 / 23D;
RX MEDLINE=90354448; PubMed=2387868;
RA Blaser M.J., Gotschlich E.C.;
RT "Surface array protein of Campylobacter fetus. Cloning and gene
RT structure.";
RL J. Biol. Chem. 265:14529-14535(1990).
RN
RN [2]
RX ERRATUM.
RX MEDLINE=91035477; PubMed=2229082;
RA Blaser M.J., Gotschlich E.C.;
RL J. Biol. Chem. 265:19372-19372(1990).
CC -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS
CC CRITICAL FOR VIRULENCE.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: J05577; AAA23032.1; -
CC KM Cell wall; S-layer.
CC SQ SEQUENCE 933 AA; 96757 MW; F88C729B4BA5B1E9 CRC64;

Query Match 6.8%; Score 176.5; DB 1; Length 933;
Best Local Similarity 21.9%; Pred. No. 0.052;
Matches 136; Conservative 74; Mismatches 236; Indels 175; Gaps 30;

QY 1 MNKIYRINMSAL--NAAVYSELTRNHRKRSATVKAVALTLTFATVOASANNETDL 57
DB 246 LNAIFATIRRAALLTDQAEILIT-----TKRRTVENINIIISDL-----ETSGDF 289
QY 58 TSVGETKLSFSANGKNVNITS--TKGLNFAKETAGT----- 92
DB 290 VFNQYEGVGNVLDIVSFATDASKSVN--ETGTGITATTAAGTGKVDVNAKISALTA 347
QY 93 NGDTTVHNLIGSTLDTLNTGATTNVTDNVTD-----DEKRRAA----- 134
DB 348 DSRSTVNLATNTDITILTSANAAVSVALKORAKADATITSAMOOKYNNRRNRITATTSAT 407
QY 135 -----SVKVDLNGMWNKGVKPGCTASDNVDVFRYDVEFLADPRTTVN--VESKNG 188
DB 408 AVENLTVKHATNALNGMDKLATVILDNALTAIDI-----KSASTLNLINSSVNG 460
QY 189 -----KTEVAKIGAKTSVYIKER-----DGLLVYTKDKGNGSSSTDEG 225
DB 461 PKHLYSKRRYCKFRRAAAVKLNTTAATQGYTLKANANRDNLEFDSATKTTSVYASG 520
QY 226 EG--LVTAKEVIDAANKRMRKTTTAN-----GQTGQADKFETVTSCTVNTVPAAGK 275
DB 521 SGKTLVAKGAETVELVN-----IDTFAFNALQSVSGKGTGGGKF--SVKGTGDDKIEFV 574
QY 276 GTTATYSK--DDGNTITVMYDVVGDALANVNOJNSGNMNDSKAVAG--SSGKVIAGNV 330
DB 575 GTTLTREGSVIADAGNDITAAKSAALTSANFTMIKNIEVAISDAVVAADLSSAFKNSVI 634

RESULT 7
SLAP_CAMFE

RESULT 9
SLAP CAUCH STANDARD: PRT: 1025 AA.
AC P35828; 046015; 09RF12;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE S-layer protein (paracrystalline surface layer protein).
GN R5AA OR CCI007.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_Taxid=155892;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21; 646-660 AND 1021-1025.
RC STRAIN-ATCC 19089 / CB15;
RX MEDLINE=93007489; PubMed=1393820;
RA Gilchrist A., Fisher J.A., Smit J.K.;
RT "Nucleotide sequence analysis of the gene encoding the Caulobacter
RL crescentus paracrystalline surface layer protein.";
Can. J. Microbiol. 38:193-202(1992).
RN [2]
RP REVISIONS TO 376; 636 AND 842-843.
RA Awram P.;
RL Submitted (OC7-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-JS3001;
RA Bingle W.H., Awram P.A., Nommellini J.F., Smit J.K.;
RT "The secretion signal of C. crescentus S-layer protein is located in
RL the C-terminal 82 amino acids of the molecule.";
Submitted (OC7-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonyak J.E., Smit J., Craven M.B., Khoult H., Shetty J., Berry K.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
RL [5]
RN SEQUENCE OF 1-313 FROM N.A., AND SEQUENCE OF 1-20.
RP STRAIN-ATCC 19089 / CB15;
RX MEDLINE=89008089; PubMed=3049545;
RA Fisher J.A., Smit J.K., Agabian N.;
RT "Transcriptional analysis of the major surface array gene of
RL Caulobacter crescentus.";
J. Bacteriol. 170:4706-4713(1988).
RN [6]
RP CHARACTERIZATION.
RC STRAIN-ATCC 19089 / CB15;
RX MEDLINE=98292737; PubMed=9620954;
RA Awram P., Smit J.K.;
RT "The Caulobacter crescentus paracrystalline S-layer protein is
RL secreted by an ABC transporter (type 1) secretion apparatus.";
J. Bacteriol. 180:3062-3069(1998).
CC -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. PROBABLY ACTS AS A
CC PHYSICAL BARRIER TO PARASITES AND LYTIC ENZYMES.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY. SECRETED BY AN ABC TRANSPORTER
CC (TYPE 1) SECRETION APPARATUS.
CC -1- MISCELLANEOUS: THE CALCIUM BINDING OF THIS PROTEIN MAY MEDIATE
CC SURFACE ATTACHMENT BY IONIC BRIDGING BETWEEN THE S-LAYER AND A
CC SPECIFIC MEMBRANE-ASSOCIATED OLIGOSACCHARIDE.
CC -----

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CC -----
DR EMBL: AF062345; AAC38665.2; -
DR EMBL: AF193063; AAF19365.1; -
DR EMBL: AE005779; AAK22991.1; ALT_INIT.
DR PIR: A48995; A48995.
DR HSSP: P22629; ISWC.
DR TIGR: CC1007; -
DR InterPro: IPR001343; Hemlysn_Ca_bind.
DR Pfam: PF00353; hemolysincbind; 3.
DR PRINTS: PRO0313; CABDNCRPT.
KW Cell wall; S-layer; Calcium-binding; Complete proteome.
FT INIT_MET 0
FT SEQUENCE 1025 AA; 98001 MW; AD7A326E1363D8AC CRC64;
SQ
Query Match 6.7%; Score 174.5; DB 1; Length 1025;
Best Local Similarity 22.8%; Pred. No. 0.073;
Matches 136; Conservative 65; Mismatches 223; Indels 173; Gaps 28;
QY 34 VKTAVLATLL-----FATVOASANNETDLSVGTETKL-----SFSANGNK 73
DB 191 VKAALIGTILNATVYSGIGYATATPAMINDSLDGLSTDMAGVNLFTAYSSGVSST 250
QY 74 VNITSPTKGLN-----FAKETAG-----TNGDTHVHLNGISTLTD-----TLNMT 114
DB 251 LSLTGTDTPLTGTTANNDFVAGEVAGAAATLVGDTLV--SGGAGTDLVNMVQAAVYALPT 308
QY 115 GAT-TNVTNDNTYDDEKRAASVQDLNMGWNLKGVKPGTTASDNVDFRTYDFVFLSA 173
DB 309 GVTISGIEITMNVTS-----GAAL--TLNSSGVYTGTLALNTNLSGAQVYTAGACONLTA 361
QY 174 DRTTTVNESKDNKRTVEKIGAKTSVIREKDKLVTKDKENG-----SSTDE 224
DB 362 TTAQAQANNAVADGAGANTV---ASTGV---TSGTTVGANSAASTVSIVANSSTTTT 415
QY 225 GEGVYAKVEIVAVNKAQRMTT-----TANG-----QFGQADKEFTVYSGTN 268
DB 416 GAIYAVGTAVYAOAGANVNTLLQADVTVYVGNSSSTAIVTVYOTPAATAGATVAGRVN 475
QY 269 --VTF-----ASGKGTATVSKDQGNITV---MYOVNVD----- 299
DB 476 GAVTTTDSAAASHTTAGKIAITVTLGSGFAATTDSALTYVNLSTGTSIGIGRGALTATP 535
QY 300 -----ALNVNOLNDSGWNLSKRAVAGS-----SGKVISGNVSPSKRMDETVINAGN 347
DB 536 TANTTLNVNGLTTTGATIDSEAAADGFTTINAGSTASTIASLVAADATLNTISGDA 595
QY 348 NIETIRN-----GKNI--DIATSKTPPFSSVIGACADAPPLSYVDGALNV 391
DB 596 RVYITTSHTAALGTVTNSVGAATLGAELATGLV--FTG---GAGADSIILATTKAIY 650
QY 392 GSKKDNKPVRTINVARP--VKEGDYVNVQALGVANLNNRIDNV-----GN 437
DB 651 GAQDDTVTVYSATLGGSYNGGDTDV-----LVANVGSSESPADPAEGEPTLVAGA 705
QY 438 ARAG-----IAQAIATAGLVQ---AYLPKSKMAIAGGTYRGEAGYAIQYSI 482
DB 706 AAGGSHNANGFTALQIGATAGATVFTFNVVNVGLVLAAPTGTVTTLANAGTSDV 762
RESULT 10
OMBP_RICTY STANDARD: PRT: 1645 AA.
AC P96989;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT -----

DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scas) (rOMP B)
DE (Comp B) [Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB OR SLP.
OS Rickettsia typhi.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=785;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Williamington;
RX MEDLINE=94040787; PubMed=8224886;
RA Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;
RT "Cloning and sequence analysis of the gene encoding the crystalline
RT surface layer protein of Rickettsia typhi.";
RL Gene 133:129-133(1993).
RN [2]
RP PARTIAL SEQUENCE.
RC STRAIN=Williamington;
RX MEDLINE=92114896; PubMed=1370573;
RA Ching W.M., Carl M., Dasch G.A.;
RT "Mapping of monoclonal antibody binding sites on CNBr fragments of
RT the S-layer protein antigens of Rickettsia typhi and Rickettsia
RT prowazekii.";
RL Mol. Immunol. 29:95-105(1992).
RN [3]
RP IDENTIFICATION OF CLEAVAGE SITE.
RC MEDLINE=92104668; PubMed=1729180;
RX Hackstadt T., Messer R., Cieplik W., Peacock M.G.;
RT "Evidence for proteolytic cleavage of the 120-kilodalton outer
RT membrane protein of rickettsiae: identification of an avirulent
RT mutant deficient in processing.";
RL Infect. Immun. 60:159-165(1992).
CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP B FAMILY.
CC -----
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CC -----
DR EMBL: L04661; AAB48987.1; -;
DR PIR: JN0896; JN0896;
DR InterPro: IPR005315; Autotransport.
DR InterPro: IPR005346; Autotransporter.
DR Pfam: PF03797; Autotransporter. 1.
DR TIGRFAMs: TIGR01414; autotrans_bar1; 1.
KW Antigen; S-layer; Transmembrane; Cell wall.
FT CHAIN 1 1353 120 KDA SURFACE-EXPOSED PROTEIN.
FT TRANSMEM 1354 1645 32 KDA BETA PEPTIDE.
FT CONFLICT 1415 1429 MEMBRANE ANCHOR (POTENTIAL).
FT CONFLICT 657 657 H->N (IN REF. 2).
FT CONFLICT 842 842 V->I (IN REF. 2).
FT CONFLICT 1071 1071 G->A (IN REF. 2).
FT CONFLICT 1306 1306 G->S (IN REF. 2).
SQ SEQUENCE 1645 AA; 169698 MW; 0CB5641C7B155EE CRC64;
Query Match 6.7%; Score 174.5; DB 1; Length 1645;
Best Local Similarity 21.2%; Pred. No. 0.13;
Matches 120; Conservative 81; Mismatches 208; Indels 157; Gaps 26;

OY 87 KETAGTNGDTVHLNGIGSTLTDLTLNTGATTNTNDVNTDEKKRAASVKNLWAGNI 146
DB 194 QEAPLTLTLDNAKIYNGANGIL-----NITNGV-----KVSDFKTFAG--I 231
OY 147 KGVPCTTASDNVDVFRTYDVEFLSADTKTTTYNVESKD-----NGKRTYKTI- 195
DB 232 KTIINGD--NGLMFNTPPDAAANLNLGGCGNTINFNRODGTGLVLSKNGNMTEFVVT 289
OY 196 ---GAKTSVIREKD-----GKL-----VTGKDKGENS-----STDEG-----EGL 228
DB 290 GSLGKLVKGYIEFTTAAGKLIANGAANAVIGTDNAGRAAGFIYSVDGNMATTISGQ 349
OY 229 VTAKVIDAVAKACMPKTTTANOT-----GGADKFEYTSGTNTVPASGKGT 278
DB 350 VYAKDIY-----IOSANAGQVTFEHLVDVGLGKTFFKTAADSVIITENISFGST 400
OY 279 ATVSKDDGNTIYVDVN-----VGDAIYNVOLNSGMNLSKAVAGSSGKVISGN 329
DB 401 -----DEGNLAQIYVPPNNKILGNFIGDA-----KNNG--NTAGVTFNANGTLVSGN 447
OY 330 VSPS-----GKMDIYNT-----NAGNNIETTRNGKIIDATSMTPQFS 369
DB 448 TDPNIVVTNKAIEVEGAGIVQLSGIHGAELELRLNAGSIFKLA--DGFVINGPVQNPLVN 506
OY 370 SVSLGAGADAPTLSDGDAL---NVGSKKDKPVRITVAVAGVEGDTVNTAOLKGVAN 426
DB 507 NNALAG-----SIQDSALITTDIGNCAVVAALODITLA-----NDASKLITLSGA--- 554
OY 427 LNNRIDVYGNARAGIAQAIATAGLYAQLPGRKSMALIGGTYRGEAGYAIGSISDGG 486
DB 555 -----NIGANAGAGAIHFQANGGTIQLTSTQNNILVDFDVTDTDQGVVDASSLTNQ 608
OY 487 NWITKT-----ASGNSRKHFGASAS 507
DB 609 TLTINGSIGTIGANTKTLGRNVGSS 634
RESULT 11
OMP B, RICRI
ID OMP B, RICRI STANDARD; PRT; 1654 AA.
AC Q53047;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scas) (rOMP B)
DE (Comp B) [Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=92167802; PubMed=1724278;
RA Gilmore R.D., Jr., Cieplik W. Jr., Policastro P.F., Hackstadt T.;
RT "The 120 kilodalton outer membrane protein (rOMP B) of Rickettsia
RT rickettsii is encoded by an unusually long open reading frame:
RT evidence for protein processing from a large precursor.";
RL Mol. Microbiol. 5:2361-2370(1991).
RN [2]
RP SEQUENCE OF 279-1654 FROM N.A.
RC STRAIN=R;
RX MEDLINE=90136087; PubMed=2515418;
RA Gilmore R.D., Jr., Joste N., McDonald G.A.;
RT "Cloning, expression and sequence analysis of the gene encoding the
RT 120 kD surface-exposed protein of Rickettsia rickettsii.";
RL Mol. Microbiol. 3:1579-1586(1989).
CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL

CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.
 CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.
 CC -----
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 CC -----
 DR EMBL; X16353; CAA34403.1; -
 DR PIR; S18227; S18227.
 DR InterPro; IPR006315; Autotransport.
 DR InterPro; IPR005546; Autotransporter.
 DR Pfam; PF03797; Autotransporter; 1.
 DR TIGRPFAMS; TIGR01414; autotrans_bar1; 2.
 KW Antigen; S-layer; Cell wall.
 FT CHAIN 1 1333 120 kDa SURFACE-EXPOSED PROTEIN.
 FT CHAIN 1334 1654 32 kDa BETA PEPTIDE.
 FT DOMAIN 1181 1188 POLY-THR.
 SQ SEQUENCE 1654 AA; 168184 MW; D7AB70FB7087F618 CRC64;
 Query Match 6.7%; Score 174; DB 1; Length 1654;
 Best Local Similarity 21.9%; Pred. No. 0.13;
 Matches 149; Conservative 76; Mismatches 236; Indels 220; Gaps 32;
 QY 9 WNSALNAAVYVSELTNRHTRKASATYKTVAVLATLRLATVOASANNEDTLTSG----- 61
 DB 123 FNLTLNAGKTLTTGGGVNNAQAATKMAQNVVYVFNNGAIDNN-DLKGVRIDEGAP 180
 QY 62 -----TEKL-----SEFANG--NKVNIT-----SDTK 81
 DB 181 ASLTVENLANPTOKAPLILGDNAVJANGVNGTLNLTNGTIOYSNKSFAVKAINTADGQ 240
 QY 82 GLNFAKETAGT-----GDTVLHNGISSTLTDLTNTGATNTVNDVTTDEKKRAAS 135
 DB 241 GLIFNDANNANFLNLQAGCTTINFCTDGTGRVLISKHA--ATNFNTITG----- 290
 QY 136 VKVVLNAGNIRKVKRGTTSADVRYRTDYEFLSADTKITTVN-----VESKDN 187
 DB 291 -----SLGGLNKGVIFENFVA-----VDGGLTANAGANAVIGTNGAGRAAGFVSVDN 340
 QY 188 GKTEV--KIGATSVYKEKDGKLYTK-----DKGEGS----- 220
 DB 341 GKATIDGVOYAADMTIOQAN---ATGQVNFRIIDVGADGTTAFTASKVITTDQSNF 397
 QY 221 -STDEGEGLVTAKEVIDAV-----NKGWRMKTTTANG--QTGOADKFEYV 263
 DB 398 GNTDFG-NLAAQIKVFNALITLGNFTGDASNPGNTAG--VITPDANGTTLESASADNAVAV 454
 QY 264 TSGTNTVTFASGKT-----TATVSKDQDGNITTVMDVANGALN--VOQLONGNLD 314
 DB 455 TNNITAEASGAVVOLSGTHAEELRLGNAGSIFKILAD---GTVINGKVAQTLVYGALA 511
 QY 315 SKVASSSGKVISGNSPSKGM-----DEYNINA-GN 347
 DB 512 AGTITLDGSAITTDIGNAGGAALQRIITLANDAKTTLTGANIIAGAGCTIDLOANGG 571
 QY 348 NIEITRNGKNI-----DIATSMTPQFSSVSLGAGADAPTLTSDG-----PALNY 391
 DB 572 TIKLTSTQNNIIVDFDLAIA-TDQGTGVASSLTNMQTLTINKIGITGANNKTLQGFNI 630
 QY 392 GSKK---DNKPVITVAVPGVKEGV-----TNVAQLKVAQNLNRRINDVDGNAR 439
 DB 631 GSKSTYLSNGNVAINELVIG-NDGAVOFAHDTYLIPTTNAAGCGKIIFNPVYNNGTTLA 689
 QY 440 AGTAAQAIATAGLVOAVLPK-----SMMAIGGCTYREAGYA-----IGYSSISDG 485
 DB 690 AGNIGLSATNPFLAEINFGSKGVAVDTVLNVEGVNL---YATNITTTDANVGSFVFNAG 745

QY 486 GNNIINGTAGSGNRGHRGASA 506
 DB 746 GTNIVSGTVGQGGQGNKFNFVA 766
 RESULT 12
 ID HLYA_SERMA STANDARD; PRT; 1608 AA.
 AC P15320;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-NOV-1990 (Rel. 16, Last annotation update)
 DE Hemolysin precursor.
 GN SHLA.
 OS Serratia marcescens.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Serratia.
 OX NCBI_TaxID=615;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
 RP STRAIN=SN8;
 RC MEDLINE=88257037; PubMed=3290200;
 RA Poole K., Schiebel E., Braun V.;
 RT "Molecular characterization of the hemolysin determinant of Serratia marcescens";
 RL J. Bacteriol. 170:3177-3188(1988).
 CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.
 CC -1- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA REQUIRES SHLB FUNCTION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -1- SIMILARITY: TO P. MIRABILIS HEMOLYSIN (HPMA).
 CC -----
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 CC -----
 DR EMBL; M22618; AAA50323.1; -
 DR PIR; A28182; A28182.
 KW Hemolysins; Toxin; Outer membrane; Signal.
 FT STGNAL 1 30
 FT CHAIN 31 1608 HEMOLYSIN.
 SQ SEQUENCE 1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;
 Query Match 6.7%; Score 173.5; DB 1; Length 1608;
 Best Local Similarity 21.9%; Pred. No. 0.14;
 Matches 113; Conservative 72; Mismatches 207; Indels 125; Gaps 22;
 QY 28 KRASATVATVATLLPAIVQASANNEDTLTSGTEKLSFSGANKVNITS----- 78
 DB 933 KRSSSS--QAVVSSVOAGSIDINAKGE--VRDQGTQ--YQASKGAVNLTDASHRESEAA 985
 QY 79 -----DRKGLNFAKETAGTNGDPTVHLNIGSLTDLTLMTGATTNT----- 121
 DB 986 NRDEGSRDTRGSAGVAVYTTTGSDLTVDAKKGEGTQRS--NSSASQAVTSGSIDANGI 1042
 QY 122 NDNVTTDEKKRASV-----KDVINA-----GNNIRKGVKPGTTASDN 158
 DB 1043 NVNVKKDAITVQGLALNGRKRTAVNMGDRLDQASDKQSESGSFRVAKSAGGFTADS 1102
 QY 159 VDFKRTDYVEFLSADTKTTTVNVEKSKDKKTEVIGAK-----TSVIREKDGKLVG- 212
 DB 1103 KNFGAGCGGCTH-NGSSSSSTAQVGNISGQGVELAKGRDLTLOGTDVKKSGQGVSLSAGN 1161
 QY 213 -----KDKGEGSSTDEGEGVYAKAVIDAVNKAAGWRMKTTTANGTGQADKF 260
 DB 1162 KVALQAAESTQTRKESKLSCNIDLGAAGSSDSKE-----KTGGLN-----SGAGAFDIKVN 1212

OY 261 ETVTSGTNTVFEAS-GKGTATATVSKD-----OCNTTMYVDVNGDALN--VNOLO 307
 DB 1213 ESATEROGATIASOGKVTLSANGKDDALHOGAKVSGSAALEKNGGILLESKKNQCH 1272
 OY 308 NSGNLDSKAVAGSS--GKVISGNVSPSKGMDETVINAGNNIETRNCKNIDATSM 364
 DB 1273 KDNMSLIGIKANAKGGQFENKDGAGVDPNTGK--DTHRLGAGLKVGVQODKTHANNGI 1330
 OY 365 TPQSSSVSLGAGAPLTL--VDDGA-----LNVSKDKNRPVRTTNVAPGKEDV 414
 DB 1331 TA--GDVTLNSGKPTRLAGARVDADSVQKVGDLVHSRSD-----VENGVKVDVD 1380
 OY 415 TNVAOLKGAONLNNRIDVGNARAGIAQIATAGL 451
 DB 1381 AGLSHNDPSSITSKSLSKVGTPTXAGKVKREKLEAGV 1417
 RESULT 13
 BIGA_SALTY STANDARD: PRT: 1953 AA.
 AC B25927: P25928: Q9XCQ3:
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Putative surface-exposed virulence protein biga precursor.
 GN BIGA OR STM3478.
 OS Salmoneella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmoneella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stojiljkovic I., Valentine P., Heffron F.;
 RT "Salmoneella typhimurium rhs homolog."
 RT Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RC MEDLINE=21534948; Pubmed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmoneella enterica serovar Typhimurium
 LT2."
 RL Nature 413:852-856(2001).
 RN [3]
 RP SEQUENCE OF 1-765 FROM N.A.
 RC STRAIN=LT2;
 RX MEDLINE=91100301; Pubmed=1987123;
 RA Wu J.Y., Siegel L.M., Kredich N.M.;
 RT "High-level expression of Escherichia coli NADPH-sulfite reductase:
 RT requirement for a cloned cysG plasmid to overcome limiting streheme
 cofactor";
 RT J. Bacteriol. 173:325-333(1991).
 RL -1- CAUTION: Ref.3 sequence differs from that shown due to frameshifts
 in positions 414 and 732.
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 CC -----
 CC EMBL: AF133696; AAD39458.1; -
 DR EMBL: AE008859; AAL22340.1; -
 DR EMBL: M64606; AAA27042.1; ALT_FRAME.
 DR EMBL: M64606; AAA27043.1; ALT_FRAME.

DR StyGene; SG10437; biga.
 KM Virulence: Repeat; Signal; Complete proteome.
 FT SIGNAL 1 27
 FT CHAIN 28 1953
 FT
 FT DOMAIN 101 252
 FT REPEAT 101 103
 FT REPEAT 104 113
 FT REPEAT 114 122
 FT REPEAT 123 133
 FT REPEAT 134 144
 FT REPEAT 145 155
 FT REPEAT 156 166
 FT REPEAT 167 177
 FT REPEAT 178 188
 FT REPEAT 189 199
 FT REPEAT 200 210
 FT REPEAT 211 221
 FT REPEAT 222 232
 FT REPEAT 233 243
 FT REPEAT 244 252
 FT CONFLICT 207 207
 FT CONFLICT 514 514
 FT CONFLICT 1698 1698
 FT CONFLICT 1795 1798
 FT CONFLICT 1836 1837
 SQ SEQUENCE 1953 AA; 200150 MW; 611B3F1C954D91AE CRC64;
 Query Match 6.6%; Score 170.5; DB 1; Length 1953;
 Best Local Similarity 23.1%; Pred. No. 0.25;
 Matches 124; Conservative 60; Mismatches 199; Indels 154; Gaps 28;
 OY 68 SANGKRVITSDTKLNRAKETAGT-----NGDT-----YVHLNGISITLT----- 108
 DB 422 SGNGTTTFPAD-----IAVSGGTAIIIDGNATIKNTGTSIDASGSGTVIDGNAR 476
 OY 109 -----DTLWLTGATTNTVNDVNT--DDEKRRASVYK-----VLNAG--WNIGK 148
 DB 477 VNNDGDMTITDOGTGHTGDVNVVDNAGSTTVSGADATALYIEGDNALVINEGNOTISG 536
 OY 149 VKPGTASDVNDFVETVTEFLSADRTTTVNVESKDKNGKTEVKGAKTSVIREKDGK 208
 DB 537 GAVGTRIDG-----DAHTTNGDIAVDGASAAVYI----- 568
 OY 209 LVYTGKDKENGSSPTDEGEIVT--AKEYI--DAVKKAGRMKTTTANQOTGADKFEVYT 264
 DB 569 -----NGDNGLVTOAGDLVTDGAMGITTYGTGNEA-----KNTGNATVTRDADSVGFVY 617
 OY 265 SGTNTVF-----ASGKGTATATVSKDOGNITVYVDVNGDALVNOLONSGWNIDSKA 317
 DB 618 AGEKRTFKNKGDIDVSLNGTGALVS--GMSQVTLTLDGDLNV---VSQDSSEGVFSATGVS 673
 OY 318 VAGSSGKV-IGSNVSPS-----KKMDETVINAGNNIETRNCK-NI--DIATS 363
 DB 674 VSGDSNAVDINGNVNISADYGGODDLAAGAPLTVGVVGGNGTNTVLNGLALNIDDDLSAT 733
 OY 364 MTPQSSSVSLGAGAPLTLSDGDALNYSKDKNRPVITTNVAPVKGKEDVNVNQLKGV 423
 DB 734 GGQYLDVVGSLVTDGDNDEVIDG--GINTHSD--PLDGT-----ADITGISVSGNS 783
 OY 424 AONLNNRIDVGNARAG-----IAQIATAGLV-----QAYLP-----GKSMA 463.
 DB 784 TVTLNGH-STIDTNTVVGGHVILARVNNNGSLILDDSDVVDVNVSYITPTGYTVALLMA 842
 OY 464 IGGTYRGEAG-----YAI-----GYSIDSGWMITKGTASGSKRCHFGASASVG 509
 DB 843 DGEGTISRNKGDITSHGYSVIATRDNGSEVNSGDLIVATYATSSNSEDRAATRASG 899
 RESULT 14
 YEEJ_ECO57 STANDARD: PRT: 2660 AA.
 AC Q8X8V7; Q8X2B9; Q8X2C0;

DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, last sequence update)
 DT 28-FEB-2003 (Rel. 41, last annotation update)
 DE Hypothetical protein yeeJ.
 GN 23135 OR ECS2775/ECS2776.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=0157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potomous K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohemorrhagic Escherichia coli O157:H7";
 RL Nature 409:529-533(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=0157:H7 / RMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayaishi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Toke T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kohara S., Shiba T., Hatori M., Shlnagawa H.;
 RT "Complete genome sequence of enterohemorrhagic Escherichia coli
 O157:H7 and genomic comparison with a laboratory strain K-12";
 RL DNA Res. 8:11-22(2001).
 CC -1- SIMILARITY: CONTAINS 16 Big-1 domains.
 CC -1- SIMILARITY: BELONGS TO THE INTIMIN/INVASIN FAMILY.
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to a
 frameshift in position 1315.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC -----
 CC EMBL: AEO05423; AAG57041.1; -
 CC EMBL: AP002559; BAB36198.1; ALT_FRAME.
 CC EMBL: AP002559; BAB36199.1; ALT_FRAME.
 DR InterPro: IPR003344; Big_1.
 DR InterPro: IPR003353; IntImIn.
 DR InterPro: IPR000601; PKD_domain.
 DR Pfam: PF02369; Big_1; 16.
 DR PRINTS: PRO1369; INTIMIN.
 DR SMART: SM00634; BID_1; 16.
 DR SMART: SM00089; PKD; 8.
 KW Hypothetical protein; Repeat; Complete proteome.
 FT DOMAIN 738 834
 FT DOMAIN 840 929
 FT DOMAIN 931 1033
 FT DOMAIN 1042 1132
 FT DOMAIN 1134 1236
 FT DOMAIN 1245 1335
 FT DOMAIN 1337 1439
 FT DOMAIN 1448 1539
 FT DOMAIN 1548 1652
 FT DOMAIN 1653 1750
 FT DOMAIN 1751 1855
 FT DOMAIN 1856 1957
 FT DOMAIN 1963 2056
 FT DOMAIN 2065 2156
 FT DOMAIN 2157 2252
 FT DOMAIN 2254 2355
 SQ SEQUENCE 2660 AA; 280062 MW; 01EB92A08F5C09D2 CRC64;

Query Match 6.5%; Score 169.5; DB 1; Length 2660;
 Best Local Similarity 23.8%; Pred. No. 0.4;
 Matches 135; Conservative 56; Mismatches 258; Indels 119; Gaps 26;
 QY 18 VSELETRNRHTRKRSATV-----KTAVALTLFAVAQASANNETDLSVGTCKLSFSAANGK 73
 DB 1424 VTATLSNNNTSDSPQTPFVADKTSALVLQISKEITGNVDASATLATVAKDQFDEEVN 1483
 QY 74 VNITSDP--KGLNFAKETAGTN--GDPVTALNGIG--STLTPTLLNMGATVNTDNT 126
 DB 1484 LPVFTSTASGLTLTGESNTNSGIAQATLAVAAGEQVTVTASLANNAGSDNKKTYHFIG 1543
 QY 127 DDEKR--AAVKDYLAN--WNKGVKPTASDNVDFVRYDYVEFLSADTKTTVN 181
 DB 1544 DTAAKRIELTPPDSDIAGTPOSSGVITATVVDNNGPVGATVNFSTNATAMFN 1603
 QY 182 ---VESKDNCKTEVKIGATSVYKEKDGKLVTKCKGENGST-----DEGEGLV 229
 DB 1604 GGAATVNEQKATVYTYNTRRSI--ESGAPDVEASLENGSSSTLSINVNADASTAHL 1661
 QY 230 TAKEVIDAVNKGAG-----WRMKT TANQGTGQ-----ADKFTVTSGTN----- 268
 DB 1662 TLQALPDTYSADDTNLTLEVNDNGVPOQDEVLTSVSPSGVTPSNNAITTHDGN 1721
 QY 269 --VTFASGKG---TATVSKDDQGNITVYDVNVDALNVLQNSGMNLSKAVAGSS 322
 DB 1722 FYASFATKAGVYQVATLENGDSMQQTVYVNVANA-----EISLAASK 1767
 QY 323 GKVISGN-----VSPSKGKMDENVNNAENNIETFGNKIDATSMTPQFSSVL 373
 DB 1768 DPVIANNNDITLTATVADTEG-----NATANSEVFTLPE-DVRAFT-----L 1811
 QY 374 GAGADAPTLSDGDA-LNWSKKDKNRPVRTYNAFPGVEGDVTN-VAQLKGVAQNINRI 421
 DB 1812 GDGGKVT-DTEBKAVITLTKGATHTVYASAGKSEDLVYVNFADITLQAVNLNVPTE 1870
 QY 432 DN-VDCNARAGIAQAIATAG-----LYQAVLPKGSMAIGCGYRGEAGYAIQYSS 482
 DB 1871 DNFIANVGMTRTQAVTYTDGNGNPLANEAVFTFLPAD---VASFTLGGGSAI--TDI 1924
 QY 483 SDGCGNMTIKGTASGN-----SRGHFGAS 505
 DB 1925 NGRAEVTLSGTSKSTYPTVSVNNYVS 1952
 RESULT 15
 ICEN_XANCT STANDARD; PRT; 1567 AA.
 AC P18127;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Ice nucleation protein.
 GN INAX.
 OS Xanthomonas campestris (pv. translucens).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=343;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=X56S;
 RX MEDLINE=91080859; PubMed=2259339;
 RA Zhao J., Orser C.S.;
 RT "Conserved repetition in the ice nucleation gene inax from
 RT Xanthomonas campestris pv. translucens.";
 RL Mol. Gen. Genet. 223:163-166(1990).
 CC -1- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
 CC CRYSTALLIZATION IN SUPERCOOLED WATER.
 CC -1- SUBCELLULAR LOCATION: Outer membrane (by similarity).
 CC -1- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
 OCTAPEPTIDE A-G-Y-G-S-T-L-T. FURTHER ON A 16-RESIDUE AND A
 CC REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.


```
CC -|- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE
CC NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
CC -|- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
CC FAMILY.
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CC -----
DR EMBL; X52970; CAA37140.1; -.
DR HSSP; P06620; INA.
DR InterPro; IPR000258; Ice_nucleatn.
DR Pfam; PF00818; Ice_nucleation; 81.
DR PRINTS; PR00327; ICENUCLEATN.
DR PROSITE; PS00314; ICE_NUCLEATION; 57.
KM Ice nucleation; Repeat; Outer membrane.
SQ SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;

Query Match 6.58; Score 169; DB 1; Length 1567;
Best Local Similarity 20.3%; Pred. No. 0.23;
Matches 112; Conservative 81; Mismatches 243; Indels 116; Gaps 22;

QY 20 SELTRNHTKRASATVKTAVLA-----TLLEFATVQASANNETDLT---SVG 61
Db 760 SDVTAGSTGTGTAGADSTLTAGYGSTGTSGSDSLTAGYGSTQ-TARKGSDITAGYGSTG 818
QY 62 TEKL-----SFSANKNKVNITSDTKGLNFAKE-----TAGTNGDPTVHLNGI 103
Db 819 TAGADSTLTAGYGSTGTSGSDSLTAGYGSTGTAREGSDVTAGYGSTGTAGADSTLTISG 878
QY 104 GSTLT--DPLNTGATTNTNDNVTDDEKKRAASVADVNLNAGNINIKVKGPTTASDNVD 160
Db 879 GSTGTAGSDSLTAGYGSTGTARKGSD-----VTAGYGSTG---TAGADST 921
QY 161 FVRTYDVEFLSADTFTTVNVESKDNCKTEVKIGAKTSVIEKDGKLTGKDKGENS 220
Db 922 LINGYGSTGTSGSDSLTAGYGSTGTARKGSDMTAGYGSTGTAGADSTLTAG-----YGS 976
QY 221 STDEGEGLYTAKEVIDAVNKAQMRKTTTANGQTGQADKPEVTYSGTNTVFASGKTTAT 280
Db 977 TQTSQS-----DSSLTAGYGSTGTAREGSDVTAGYGSTGTAGADSTLTAGYGSTGT 1027
QY 281 VSKDDGNTVTMDVNVGDLNVLNQLNSGMNLSKRAVAGSSGKVISGNVSPSKKMDET 340
Db 1028 AGSD--SSLTGY----GSTGTARQGSVDYTAGYGSTGTAGADSTLTLAGYGSTGTAGSDSS 1081
QY 341 VNINAGNIEITRNKNKIDATMTPOFSSVSLGAGADAPTLISVDGDLNVSCKDKNPV 400
Db 1082 LITAGYGST-QTARQGSIT-----TAGYGSTGT-AGADSSLTLAGYGSTGTAGYD----- 1127
QY 401 RITNVAPGV-----KEGDTVNVQOLKGYAQNLMNRIDVNDGNARAGIAQAIATA-GLV 452
Db 1128 --SNLTAGYGSTGTAREDSLTLAGYGSTGTAGHDSLTLAGYGSTGTAGYNSILITGYGST 1185
QY 453 QATLPKSKMAATGGGTYRERAGY---AIGYSSISDGG--NWITIKTAGSNSRCH----- 501
Db 1186 QTAQESSSLTAGYGST--STAGYDSTLTLAGYGSTGTAGYKSTLTLAGYGSNSTAGHESLI 1243
QY 502 --FGASASVGYO 511
Db 1244 AGIGSTQIAGYE 1255
```

Search completed: October 6, 2003, 09:23:55
Job time: 11.9066 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:35 : Search time 14.6561 Seconds
(without alignments)
3359.577 Million cell updates/sec

Title: US-09-771-382-23

Perfect score: 2600

Sequence: 1 MNKIYRIINMSALNMAVYVS.....TASGNSRGHFGASASVGYQM 512

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :
1: PIR_76:*
2: pir1:*
3: pir2:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2550.5	98.1	591	2 G81133	adhesin NMB0992 [i
2	2289	88.0	592	2 A81888	adhesin surface f
3	536.5	20.6	298	2 I64138	adhesin homolog HI
4	378	14.5	2059	2 D82671	surface protein XF
5	372.5	14.3	1190	2 A82615	surface protein XF
6	371.5	14.3	1107	2 AC0976	probable autotrans
7	370.5	14.2	1588	2 A86036	probable adhesin Z
8	370.5	14.2	1588	2 H91188	probable adhesin E
9	338	13.0	658	2 AH0110	probable surface p
10	245	9.4	1091	2 G64964	hypothetical prote
11	234	8.5	1004	2 C82672	surface-exposed ou
12	222	8.5	1286	2 S28634	adhesin AIDA-I pre
13	214.5	8.2	1325	2 A64905	Adhesin AIDA-I pre
14	214	8.2	949	2 D90803	Adhesin AIDA-I pre
15	214	8.2	1005	2 H85611	probable adhesin Z
16	208	8.0	4919	2 T31105	hypothetical prote
17	207	8.0	1536	2 A43855	high-molecular-we
18	204	7.8	1018	2 H83135	probable adhesin P
19	201.5	7.8	1910	2 AF0394	probable adhesin h
20	198	7.6	936	2 I40711	sapB protein - Cam
21	197.5	7.6	585	2 F90961	flagellin [impor
22	197.5	7.6	585	2 F85809	hypothetical prote
23	197	7.6	3705	2 AD0123	hypothetical prote
24	196.5	7.6	1343	2 E90893	hypothetical prote
25	196.5	7.6	1477	2 B43855	high-molecular-we
26	195.5	7.5	2020	2 C48399	ABC-type transport
27	194	7.5	2468	2 A83412	hypothetical prote
28	194	7.5	3029	2 S76109	hypothetical prote
29	193.5	7.4	2249	2 A41477	190K surface anti

30	193.5	7.4	5188	2 B85547	probable RTX fam1
31	191.5	7.4	1343	2 D85724	hypothetical prote
32	191.5	7.4	5291	2 F90696	hypothetical prote
33	190.5	7.3	2232	2 T34434	hypothetical prote
34	190	7.3	1109	2 A56143	surface-array prot
35	188	7.2	3013	2 AB0480	probable invasin y
36	185	7.1	365	2 AB3486	cell surface prote
37	184	7.1	1428	2 AC2224	hypothetical prote
38	184	7.1	1461	2 E90696	hypothetical prote
39	183	7.0	584	2 C48558	flagellin - Escer
40	183	7.0	1335	2 T17508	glycoprotein VP260
41	183	7.0	1651	2 JC1340	outer membrane pro
42	182	7.0	2551	2 B98047	hypothetical prote
43	181.5	7.0	980	2 H90681	probable flagellin
44	181.5	7.0	980	2 D85332	probable structura
45	181	7.0	364	2 A81019	adhesin/invasin, p

ALIGNMENTS

RESULT 1

G81133

adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)

C:Species: Neisseria meningitidis

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001

C:Accession: G81133

R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.

ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizsa, M.

Science 287, 1809-1815, 2000

A:Authors: Grandt, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;

A>Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; M01D:2017575; PMID:10710307

A:Accession: G81133

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-591 <TEXT>

A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:ANF41395.1; PID:g722

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB0992

Query Match	Score	2550.5	DB 2	Length	591
Best Local Similarity	86.6%				
Matches	512	Conservative	0	Mismatches	0
Indels	79	Gaps	1		
QY	1	MNKIYRIINMSALNMAVYVSELTNRNHTKRASATVKTAVLTLLFATVQASANNE-----	54		
DB	1	MNKIYRIINMSALNMAVYVSELTNRNHTKRASATVKTAVLTLLFATVQASANNEDEQEDL	60		
QY	55	-----	54		
DB	61	YLDPVORTAVVLVNSDEKGTGKEKVEENSDMAVYFNEKGVLTAREITLKAGDNLIKQ	120		
QY	55	-----	101		
DB	121	NGNFTYSLKKDLTDLTLSVTEKLSRANKNKNITSDTGLNFAKTAAGTNGDTYHLN	180		
QY	102	GIGSTLTDLTLNTGATTTNTNDVNTDEKRRASVSKDVLNAGNNIKGVKGTASDVNF	161		
DB	181	GIGSTLTDLTLNTGATTTNTNDVNTDEKRRASVSKDVLNAGNNIKGVKGTASDVNF	240		
QY	162	VRTYDVVEELASDPTKTTTVVESKDKNKTVEVIGATSVIKERDKGLVYKDKGEGSS	221		
DB	241	VRTYDVVEELASDPTKTTTVVESKDKNKTVEVIGATSVIKERDKGLVYKDKGEGSS	300		
QY	222	TIDGEGGLVTAKEVIDAVNKRAGMKTTTAGCGTGAADKFEFTVSGTWTFRASGKTATV	281		
DB	301	TIDGEGGLVTAKEVIDAVNKRAGMKTTTAGCGTGAADKFEFTVSGTWTFRASGKTATV	360		
QY	282	SKDQGNITVYDVNVGDALNVQNLQNSGNNLDSKAVAGSSGKVGISGNSPSKGMDET	341		

Db 361 SKDDGNTITVWYDVNVGDALNVNOLQNSGMNDSKAVAGSSGKVISGKVMDETV 420
 QY 342 NINAGNNEITRNKGNIDATSMTPQFSSVSLGAGADAPTLVDDGALVWSSKKNKPPR 401
 Db 421 NINAGNNEITRNKGNIDATSMTPQFSSVSLGAGADAPTLVDDGALVWSSKKNKPPR 480
 QY 402 ITNVAPEGVEGDVTNVAOLKGYAQNLMNRIDNVNAGARAGIAQAATATAGLVOAYLPGKSM 461
 Db 481 ITNVAPEGVEGDVTNVAOLKGYAQNLMNRIDNVNAGARAGIAQAATATAGLVOAYLPGKSM 540
 QY 462 MAIGGCTTREGAGYAIIGSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 512
 Db 541 MAIGGCTTREGAGYAIIGSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 591

RESULT 2

probable surface fibril protein NMA1200 [Imported] - Neisseria meningitidis (strain 2249
 C:Species: Neisseria meningitidis
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C:Accession: A81888
 R:Parthill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
 ; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, M.A.; Rajamoram,
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.
 A:Reference number: A81775; MUID:20222556; PMID:10761919
 A:Accession: A81888
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-592 <PAR>
 A:Cross-References: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737989
 A:Experimental source: serogroup A, strain 22491
 C:Genetics:
 A:Gene: NMA1200

Query Match 88.0%; Score 2289; DB 2; Length 592;
 Best Local Similarity 79.1%; Pred. No. 1,6e-111;
 Matches 470; Conservative 12; Mismatches 28; Indels 84; Gaps 4;

QY 1 MKKIIRIINSAALNMAVYSELTRNHTKRASATVATLTLFATVOASNN----- 54
 Db 1 MKKIIRIINSAALNMAVYSELTRNHTKRASATVATLTLFATVOANATDEDEEEL 60
 QY 55 ----- 54
 Db 61 ESORSVSGIQASMEGSELEFISLMTNDSKEFDPYIVYTLKAGNMLKIKONTNEMT 120
 QY 55 -----TDLTSTGTEKLSFSAANGKVNITSDPKGLNFAKETGCTGDTTVHLN 101
 Db 121 NASSFTYSLKDLTGTLINTEKLSFGANGKRVNIISDTKGLNFAKETAGTNGDTTVHLN 180
 QY 102 GIGSTLTDLTLNMTGATNTNNDVDEKRAASVYKRVNAGNKGVRGPTTA--SDNV 159
 Db 181 GIGSTLTDLTLNMTGATNTNNDVDEKRAASVYKRVNAGNKGVRGPTTA--SDNV 238
 QY 160 DEVRATYDVEPLSADTKTTTVNESKDNCKTEVKIGATSVYKEKDKGLVYKDGKENG 219
 Db 239 DEVRATYDVEPLSADTKTTTVNESKDNCKTEVKIGATSVYKEKDKGLVYKDGKENG 298
 QY 220 SSTDEGEGLVTAKEVDAVNKAGMRKTTTANGQIGQADKFEYVSGIVNTRASGKTGA 279
 Db 299 SSTDEGEGLVTAKEVDAVNKAGMRKTTTANGQIGQADKFEYVSGIVNTRASGKTGA 358
 QY 280 TVSKDDGNTITVWYDVNVGDALNVNOLQNSGMNDSKAVAGSSGKVISGKVMDETV 339
 Db 359 TVSKDDGNTITVWYDVNVGDALNVNOLQNSGMNDSKAVAGSSGKVISGKVMDETV 418
 QY 340 TVNINAGNNEITRNKGNIDATSMTPQFSSVSLGAGADAPTLVDDGALVWSSKKNKPPR 398
 Db 419 TVNINAGNNEITRNKGNIDATSMTPQFSSVSLGAGADAPTLVDDGALVWSSKKNKPPR 478
 QY 399 PVRTITNVAPEGVEGDVTNVAOLKGYAQNLMNRIDNVNAGARAGIAQAATATAGLVOAYLPG 458

Db 479 PVRTITNVAPEGVEGDVTNVAOLKGYAQNLMNRIDNVNAGARAGIAQAATATAGLVOAYLPG 538
 QY 459 KSMMAIGGCTTREGAGYAIIGSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 512
 Db 539 KSMMAIGGCTTREGAGYAIIGSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 592

RESULT 3

adhesin homolog H11732 - Haemophilus influenzae (strain Rd KW20)
 C:Species: Haemophilus influenzae
 C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997
 C:Accession: I64138
 R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
 ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.T.; Glodek, A.; Kelley, J.M.; Weidman
 , D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghagen, N.S.M.
 Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A:Reference number: A64000; MUID:95350630; PMID:7542800
 A:Accession: I64138
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-298 <TIGR>
 A:Cross-References: GB:U32846; GB:U42023; NID:g1574588; PID:g1574589; TIGR:H11732

Query Match 20.6%; Score 536.5; DB 2; Length 298;
 Best Local Similarity 44.7%; Pred. No. 4,6e-21;
 Matches 132; Conservative 28; Mismatches 62; Indels 73; Gaps 8;

QY 1 MKKIIRIINSAALNMAVYSELTRNHTKRASATVATLTLFATVOA----- 49
 Db 1 MKKIFKIVNVTQGVWVYSELTRNHTKRASATVATLTLFATVOAINDAGTFVKVO 60
 QY 50 -----SANNETD-----LT-----SVGTREK 64
 Db 61 STEDIEDSAAATKDKNKNQALKAGDTLTLKAGKNLAKIDGCKSVTFALAKDLDVTKAK 120
 QY 65 LS--FSANGN-----KVNITSPTKGLNFAKETAGTNGDTTVHLNIGSTLNDTLN 113
 Db 121 VSDTLIGNTPTAAGATPKVSIITSTADSLKAK--GINSQPTVAHLNLSLATLDDVYTN 177
 QY 114 TGAATVNTDNTVDEKRAASVYKRVNAGNKGVRGPTTA--SDNVDPYRTYDEFLSA 173
 Db 178 TGAATVNTVDEKRAASVYKRVNAGNKGVRGPTTA--SDNVDPYRTYDEFLSA 236
 QY 174 DFKTTTVNESKDNCKTEVKIGATSVYKEKDKGLVYKDGK--KQENGSPTEGE 226
 Db 237 DFKTTTVNESKDNCKTEVKIGATSVYKEKDKGLVYKDGK--KQENGSPTEGE 291

RESULT 4

surface protein Xp1529 [Imported] - Xylella fastidiosa (strain 9a5c)
 C:Species: Xylella fastidiosa
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: D82671
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: A82515; MUID:20365717; PMID:10910347
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: D82671
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-2059 <SIK>
 A:Cross-References: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1; GSPDB:GN
 A:Experimental source: strain 9a5c
 R:Simmons, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
 Britones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier
 as-Neto, E.; Docena, C.; El-Deiry, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tshahko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
C;Contents: annotation
A;Gene: Xf1529

Query Match 14.58; Score 378; DB 2; Length 2059;
Best Local Similarity 25.44; Pred. No. 8.2e-12;

Matches 158; Conservative 77; Mismatches 184; Indels 202; Gaps 27;

QY 47 VQASAN-----NETDLTS-VGTEKLSFSAANG-----NKVNITSPTKGLNFAKTAGTNGDT 96
DB 1486 VKVSSNVLLDSNELVYTHSSSTSVKTLANGSESVNRTVVGND-----GVNIDID 1534
QY 97 TVHLNGI-----GSTLDFLNTGA--TTNVT-----NDNVTDDKKRAASVKVYLNA 143
DB 1535 VVVVNDIGLSTVGGASLTLSGINAGSHKITTNTAGTEDDVAVNSQLK--SVSEADK 1591
QY 144 WNI-----KGVKPGTASDNVD-----FVRTYDVEFLSADTK-----TTVN 181
DB 1592 WTLTASGANGSKVVSQYVDLKNITDGLAISKSGSDNDVFNLSKPEKVDVETAGTNNV 1651
QY 182 VESKDNGKTEVYIGAKTSYIKEDGKLYTGKDKGEN-----GSSTDEGELVTAKEV 234
DB 1652 TDDVKVYG--SDVSLGAMGLEIANGPSVTASGFNAGDKVISHVAVMADTDVAVNSQLKQA 1709
QY 235 IDAVNKGAMVMTKTTT-----ANGOTGQ--ADKFEYVSGTNV-----TTSAG 275
DB 1710 VQSYTKATRYTSTNCGGTGGNGYDGDGATGSKAIAAGVGTQASGEGAAVSGAASGK 1769
QY 276 GTTA-----TVS-----KDDOGN 288
DB 1770 GSTAIGRNATASADGSVALDGAKGAGAESYTGKSYGVNNTVGTVSVDAAKGETRS 1829
QY 289 ITVMYVYVNG--DALNNOL-----QNSGMNDS----- 315
DB 1830 ISNVAAKEMADVNLRQIDAIVAOKSMLQTDKRHEINNIEDYFKITKGDSASSYKMGV 1889
QY 316 KAVAGSSGKVIYSGNVSPEKMDFTYNINAGNIEITRNKNIDIASMTPOPSVSLGA 375
DB 1890 NMAAIGTNAVSGTESVAALCK---NTNVSADNAVAI--GNG-----SVADRANSYSVGS 1938
QY 376 GADAPTLSDVDALNVGSKKDNKPVRLTNVAPGVKEGDTNVAQLKGVAQNLRNRIIDNV 435
DB 1939 G-----GSEK-----QVTNVAAGTADPDVAVNSQLNGCLITAKOYTDGMV 1978
QY 436 GNR-----AGIAQATATAGLVQAVLPKSMMAIGGTYRGEAGYALCYSISDGMNIT 491
DB 1979 GNRRETSGGVAALITANLPQAYVVGRTSVGVSYSOGOSAIANGVSASHGHWFK 2038
QY 492 GTASGNSRGHFSGASASVGYOW 512
DB 2039 FSGSANTRSHVGVAGVGYOW 2059

RESULT 5

A82615
surface protein Xf1981 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: A82615
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: A82615

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 11190 <SIM>

A;Cross-references: GB:AE004017; GB:AE003849; MID:99107083; PIDN:AAF84783.1; GSPDB:GN
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Brienes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre
as-Neto, E.; Docena, C.; El-Dorfy, H.; Facincan, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; France, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sava
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tshahko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A;Reference number: A59328
C;Contents: annotation
A;Gene: Xf1981

Query Match 14.38; Score 372.5; DB 2; Length 1190;
Best Local Similarity 24.88; Pred. No. 8.1e-12;

Matches 143; Conservative 77; Mismatches 209; Indels 147; Gaps 21;

QY 17 VVSELRNTRKASATVKTAVLATLTFARVQASANNETDLTSVTEKLSFSAN----- 70
DB 682 VTSSGISAGNQKTTNAAAGTADPDVAVNSQLQAVNST--AAKGNLNLASGNSSVAP 737
QY 71 GNRVNITSPTKGLNFAKTAGT-----TNGDTTVHLNGISTLDFLNT 114
DB 738 GESVDLKNITDGNIVISKESSNDVFNLSLKLKLTVEGDYWTNGV--TVGS 790
QY 115 GATTNTYNDVTDDEKKRAASVKVYLNA--WNKGVKPGTTASD----- 157
DB 791 GVTLSGKGLVITDGPSTVSGI--NAGSQKTTNAAAGTADPDVAVNSQLNTAMAGSGA 846
QY 158 -NVDFVRYTVEFLSADTKTTTVNVNVESSKNGKTEVYIGAKTSYIKEDGKLYTGKDKG 216
DB 847 KSVHYSTYD-----GGTGGNNGDAGTGTISIAVGTTLSA--EGATAVSGAA 896
QY 217 ENG--STDEGELVTAKEVDAVNAKAGRMKTTTANQGTQADKFEYVSGTNVTFASG 275
DB 897 ASGKGSTAIRNNAVASDGSVALGD--GAKGAGAESYTGKSYGLQNNVTGYVSVDASK 955
QY 276 GTTATVSKDQGNITVYDVNVGDALNVOL-----QNSGMNLSKAVAGSSGKVIYSGNVS 331
DB 956 GETRTVS--NVADAKEAT--DAVNLRLDRAVADANRYVNNKIESLESGOTF----- 1003
QY 332 PSKGMDEFYNINAGNIEITRNKNIDIASMTPOPSVSLGADAPTLV-----DG 386
DB 1004 -----VKVNSLNN-----SAP-----IAGVDATIGCATRSGA 1034
QY 387 DALNVGSK-----KDNKEV-----RTNVAAGVEGDTNVAQL 420
DB 1035 DSIAMGKASASADNNAVAIINHVSADRAVNSVSGASGEQYVNVAACTADTDAVNSQL 1094
QY 421 KGVANLNNRIIDNVGNAR--AGIAQATATAGLVQAVLPKSMMAIGGTYRGEAGYA 476
DB 1095 NOGLITAKOYTDGVGSLRBDTDCGVAAALITANLPQAYIPGRGMSVGVSSYRGOAIA 1154
QY 477 IGYSTSDDGNMTIIGTASGNSRGHFSGASASVGYOW 512
DB 1155 VGVSVSESGRWFKFSGSANTRSQVIGAGVGYOW 1190

RESULT 6

AC0976
probable autotransporter sabp [imported] - Salmonella enterica subsp. enterica serova
C;Species: Salmonella enterica subsp. enterica serovar Typh
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001
C:Accession: H91188
C:Species: *Yersinia pestis*
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AH0110
C:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell, Nature 413, 523-527, 2001
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360

Query Match 14.2%; Score 370.5; DB 2; Length 1588;
Best Local Similarity 27.5%; Pred. No. 1.5e-11;
Matches 150; Conservative 59; Mismatches 189; Indels 147; Gaps 23;

5 YRIIWSALNMMVVSLEFNRHTRASATYKTAIVLALLLPATVQASANN-ETDLTSYTE 63
1154 YRQIIN-----VADGSEAHDAVYRQLOMAIGAVATPTKYFHNSTEEDSLAVGTD 1205

QY 64 KLSFSA-----NGNK-----VNITSDTKGLNFAKETAGTNGDPTVHLNGI-----GSTLTD 110
DB 1206 SLAMGAKTIYNGDKIGIGYAYVDANALNGI--AIGSMAQ-VIHVSIAGNSTTT-- 1260

QY 111 LMTGATNTVNTDNVDEDEKRAASVKDVLNAGNNIKVKGTTASDNVDFRTYVEF 170
DB 1261 ---RGAQNTYAYN-----MDAPQN---SVGEFVSADGQROITVAA 1298

QY 171 LSADTKTTYNVESKDKGKTEYKIGAKTSYKREKDKIYTKGKKG-----ENG-----SST 222
DB 1299 GSADTDVAVNG-----OLKATDAQVSONTOSITNLDNR-VYNLDSRYNTIENGIGDIYTT 1352

QY 223 DEGEGLYAKEDIVAVKAKGRMKTNTANGQTGADFEFVTSCTNYTFASGKGTATVS 282
DB 1353 GSTFYKFTNIDGVDA--SAQKSDVAIGSGSIANA--NSVALGTG-SVAITEENTISVGS 1407

QY 283 KDDOGNTT-VMYDVNVGDALNVNOLNS---GNLDSKAVAAGSSGKVIISGNVSPSKGMD 338
DB 1408 STNORRITNVAAGKATDAVAVVQLOKSEAGVRYDPA-----DGSID 1451

QY 339 ETVNINNGNIETIRNKNIDIAISMTPPOSSVSLGACAPLTISVGDALNVGSKDNK 398
DB 1452 -----YSNITLGGGNGGTT----- 1465

QY 399 PVRTTNVAPGVKEGDYTNVAOLKGVAO-----NLNRRIDNVGNARAGIAOAIA 447
DB 1466 --RISNVSAGVNNNDVYNYAOLKOSVQETQYTDQRMVEMDNKLSKESKLSGASAMA 1523

QY 448 TAGLVQAYLPKGSMAAIGGTYRGEAGYAGYSSISDGMMIIRKGTASGNSRHFPGASAS 507
DB 1524 MTGILPOAYTPGASMASIGGYNGESAVALGVSMVANGRWYKLGSTNSGGEYSALG 1583

QY 508 VGQYOW 512
DB 1584 AGIOW 1588

RESULT 9
AH0110
probable surface protein (partial) YPO0902 [imported] - *Yersinia pestis* (strain CO92)
C:Species: *Yersinia pestis*
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AH0110
C:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell, Nature 413, 523-527, 2001
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AH0110
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-658 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:915978974; GSPDB:GN00175
C:Genetics:
A:Gene: YPO0902

Query Match 13.0%; Score 338; DB 2; Length 658;
Best Local Similarity 23.8%; Pred. No. 2.4e-10;
Matches 146; Conservative 76; Mismatches 205; Indels 186; Gaps 24;

27 TKRASATYKTVK---AVLALLLPATVQ-----ASANNEDTLTSVTEKLSFSANGKVN 75
DB 105 TNLAPATISSSTPAVVSQSLYNLYOQCTRFHANSVNPFDLSLAGELETIAV-----GPAT 160

QY 76 ITSPTKGL---NEAKETAGTNGDPTVHLNGISGTLT-----DFTLNTG 115
DB 161 VVSGDNGVIGIGNTALVGAATGTAI---GCGTQVTAAGATAIGSAAOAGOSLALGAG 217

QY 116 ATTAVTNDNTVDEDEKRAASVKDVLNAGNNIKVKGTTASDNVDFRTYVEF 170
DB 218 AVTSQANSIALG-----AASINTVGAQSSYSAYVALTPAQASVGLIGTALGNKRTGVA 272

QY 151 PGTTASDNVDFVR-----TYDVEFLSADTKTTV--NVESKDNK-----K 189
DB 273 AGSASSDAVNVAVQLTAVGDVQONTANTISLGRVTTIEGSMASIANCGVKYFHNSTQ 332

QY 190 KTEYKIGAKTSVI-----KEKDKLVTKDKGENGSTD 223
DB 333 PDSVASGTSNSVAIGPASILASGNAALASGAGAVAIIGDAAASADBSVAIGQSGDNGRVE 392

QY 224 EGSELVYAKEDIVAVKAKGRMKTNTANGQTGADFEFVTSCTNYTFASGKGTATYK 283
DB 393 NYIS-----KYSNASSTSSG-----TVSVGTAT-----GETRTVSN 424

QY 284 DDQGNITVMYDVNVGDALNVNOLNSGNLDSKAVAGSSGKVIISGNVSPSKGMDYVNI 343
DB 425 VADG-----LQATDAVNLRLQDQ-----IAASTVVENNVSGIONGNDGMQV 467

QY 344 NAGNNT-EITRNGKNIDI--ATSMTPPOSSVSLGACADAP-----TLVSDGALN 390
DB 468 NNSGLAKPSATGANSATGAGSVAAGNSSTAFSGAKATPAANSAALGANSVADRANSVS 527

QY 391 VGSKDKKPVARTVAVAGYKEDYTNVAOLKGVAN---LNNRIDNVGNARAGIAOAIA 447
DB 528 VGSVGNR--QITVVAAPATQCTDAVNFQDKLSISQNTNAYTORYSELKODLRQNSVLS 585

QY 440 AGIQAATATAGLVQAYLPKGSMAAIGGTYRGEAGYAGYSSISDGMMIIRKGTASGNSR 499
DB 586 AGIASAMSMSLTPYISGSSMTTIGAASTYRGOSALSIGVSSISDSGRWYKLGASSTVQ 645

QY 500 GHFGASASVGYOW 512
DB 646 GDFEIGVGYOW 658

RESULT 10
G64964
hypothetical protein b2000 - *Escherichia coli* (strain K-12)
C:Species: *Escherichia coli*
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: G64964
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: G64964
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1091 <BLAT>
A:Cross-references: GB:AE000291; GB:U00096; NID:g1788298; PIDN:AAC75061.1; PID:g17883

A: Experimental source: strain K-12, substrain MG1655
C: Keywords: nucleotide binding; P-loop
F: 683-690/Region: nucleotide-binding motif A (P-loop)

Query Match	9.4%;	Score 245;	DB 2;	Length 1091;
Best Local Similarity	23.9%;	Pred. NO. 2.9e-05;		
Matches 135;	Conservative	76;	Mismatches 185;	Indels 170;
				Gaps 33

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OY      1 MNKYRIITMNSALNAAVVELTJRNHTRKASAFYKTAVALATLPAFVAOS-----50
Db      57 LNTCYRLVNMHMGAFYVASELARARCKRGVAVALSAAVTSILPYLAADIVHPGETVN 116
OY      51 ----ANNEPDTJVSYTEKLSFSAANGKNVITSPTKGLNFAKET-----AGTNGD 95
Db      117 GGTLANHDNQIVFEGTNGMTIST-----GLEYPDNEMANTGGQVWDGGRANK 164
OY      96 TTYVALNG-----GSTLTDTLLNTGATTNV-----TNDNVYDDEK---KRAASVADYLN-A 142
Db      165 TTVTSGGIQRVPNGSGSVSDTVISAGGQSLQGRAVNTTLNGEEDQMEHGALATGTVINDK 224
OY      143 GWNKIGKVPQGTASDNDVEVRT-----YPTVELSADPTKTTTVNYESKNKNGKTE 192
Db      225 GWOY--YKPFVAIDTV--VNTGAEGGPDAENSDTGGVRCDAVPTIIN---KNGQIV 276
OY      193 VKIG-AKTSVYKEKDKLVTKDKGENGSSPTDE---GEGLY---TAKEVYDAVNRAGW 243
Db      277 RAETANTYTV-----YAGGDQTVHGHADTTLNGYQYVHNGGASADIV--VNSDGW 327
OY      244 RM-----KTTANGOTGQADKEFYVTSCTNVTPFASG---KGTATVSKDDGQ-NITV 291
Db      328 QIVANGGVAGNTTVN-QKGR-LQVDAGGTATNTLKGALVSTATAVT---GINRLG 381
OY      292 MYDVNVDGALVNLOLNGSMWLDKRAVASSGKVIYSGNVSPSKKMDETVAINANGNIEI 351
Db      382 AFSVEVEGADNV-VLENGG-RLD-----VLTGHTATN-----TRVDDGGTLDV 422
OY      352 TRNGKNIDIAFMSMTPQESSVSLGAGADAPTLTSYGDALNVSKKDKNPKVRTITNAPGVKE 411
Db      423 -RNG-----GTAFT-----VSMGNGG--VLLASGAAVSGTSRBDGK-----AFS1GG 461
OY      412 GDVTNVAQLKGVAQNLNRRIDNVDGNAKAGIAQAIAFAGLVQAYVLPKSSMAIGGTYRG 471
Db      462 GQADALMLEKSSFTLN-----ACDATTDTT-----VNGGLFTA 495
OY      472 EAGYALGYSLSIDGGMNLIKGTASGN 497
Db      496 RGGTLAGTTLNNGAILTLISGTVNN 521

```

RESULT 11

C82672

surface-exposed outer membrane protein Xrp1516 [imported] - Xylella fastidiosa (strain 9a

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: C82672

R:Anonymous: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A62515; MUID:2036571/; PMID:10910347

A:Note: For a complete list of authors see reference number A59328 below

A:Accession: C82672

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1004 <STM>

A:Cross-references: GB:AE003981; GB:AE003849; NID:99106543; PIDN:AAF84325.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; P

R:Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, b

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitzajima, J.P.; Klieger, J.E.; Kuramae, E.E.; Laigis, M

chnado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B

A:Authors: Martins, E.M.F.; Matsushima, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.J. de M.; de Rosa, J.; V.E.; de Sa, R.G.; Santelli, R.V.; Sawaia, R.G.;
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., M.A.; da Silva,
M.; Tsuchako, M.H.; Valada, H.; Van Sluys, R.A.; Verjovski-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1516

Query Match	9.08;	Score 234;	DB 2;	Length 1004;
Best Local Similarity	21.68;	Pred. No. 9.8e-05;		
Matches 151;	Conservative 86;	Mismatches 249;	Indels 212;	Gaps 31.

OY	2	NKIRYIINMSALAAVVVSELT-----FNH-----TRKASATVK	35
Db	4	NOIKRFEMNLSLGSWSHMHMTINDGCSOVYLRHSYGNRRBSLYLALIGLALTSYTHASVK	63
OY	36	TAVLAT---LLEFATYQASANNETDL--TSVGTETKLS-----FSANGKNVITSDTK-	81
Db	64	SPAMVATASKMVAHVADSOVNRTADRIPIRGDGSSELTTHALDMKFEFFEGNNSIAGYPSKA	123
OY	82	-----GLNFKEKTAGTNGDPTVYHLNIGSTLDTLLNATGNTNTN-----DNVT	126
Db	124	PAPNAIALGN--SVYTOSANGVALGSNTYSGVNSVALGSGMASSELYISVGGGDVY	182
OY	127	DDEKKAASAYKDLV--NAGMNIKGVKPGTASDNDVFRYDVEFLSADTKTTVWES	184
Db	183	GPAVRIRLVNGDGIIGNDAVN--KSOLDGVTASVN--DVAASYKTIALTFNOMVTGSSVASAG	240
OY	185	KDN-----GKTKFKIAGAT-----SVTKEDG-	207
Db	241	KESTAIIGSGAQAAYADNTVAFGGRAIAMAAGALGFDSSHAKINSTVTGOTSLSLGGGV	300
OY	208	-----KLVTGDKCKENGSS-----STDEEGGL--VTAK	232
Db	301	SLGYSNPFVGBGFNGIALGSLNSLYLLOGVDSVALGSGMASSEPNVSYSGSDGLRGPAVR	366
OY	233	EVL-----DAVKKACWRMKTTTANGQTSQADKFETV--TSGTNVTFPASKGCTTAT-	280
Db	361	RIYVNGDGIIGNDAVNRKSOLDGVTASVNDVYASVKNIGALIQIGSGVASVSGDSTAAAG	420
OY	281	VSXDDOGCNTVMTDVNVGDLNVNOLONGMNL-----SKAVAGSSGKVIIGANVSPS	333
Db	421	ASQAQAGDSSIA--LGAISRANALIGSALGDVDHALGANSIALGOGSTASISGCTSLG	476
OY	334	GKMKDETVMINAGNIEITRNGKNIDTASMTPOFSSVSLGACADAPTLVS---DGDAL	389
Db	477	---YNSEFVGOSAFNGIALGSLN-----AIVSGVNSVALGASVASELNIYVGGGDGV	525
OY	390	NVGSKKDNKRVRTTNYAPGVKEGDVTVNAOLKGVANONLN---RIDVNDGNAR---AGIA	443
Db	526	TGPAVR-----RIYVNGDGIIGNDAVNRKSOLDGVTASVNDVYASVKKIYGTIQTIGSGVA	580
OY	444	QAI--ATAGLVOAYLPGKSMMAIG-----GGTYRGEAGYAIG	478
Db	581	SAIGKSTATGASQAQAVGDDSSVALGTRATANAIGSSVLTGVDSPRAGINSTALGROSNAIG	640
OY	479	YSSISDGGNNIIR-----GTASGNRNGHGA--SASYV	510
Db	641	DGVSUSLGFENSEVROSGEHGVALGTDAGVSGKSTIALGY	678

RESULT 12
S28634
adhesin AIDA-I precursor - Escherichia coli plasmid PIB6
C:Species: Escherichia coli
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 08-Oct-1999
C:Accession: S28634, S22680, S28881, S72657
R:Benz, I.
submitted to the EMBL Data Library, March 1992
A:Reference number: S28634
A:Accession: S28634

A:Molecule type: DNA
A:Residues: 1-1286 <BEN>
A:Cross-references: EMBL:X65022; NID:q42254; PIDN:CAA6156.1; PID:q42255
R:Benz, I.; Schmidt, M.A.
Mol. Microbiol. 6, 1539-1546, 1992
A:Title: AIDA-, the adhesin involved in diffuse adherence of the diarrhoeagenic *Escherichia coli* serotype O157:H7
A:Reference number: S22680; MUID:92326638; PMID:1625582
A:Accession: S22680
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 839-1286 <BE2>
A:Cross-references: EMBL:X65022
A:Experimental source: strain 2787
A:Accession: S28881
A:Molecule type: protein
A:Residues: 50-56 <BE3>
A:Experimental source: strain 2787
R:Suhr, M.; Benz, I.; Schmidt, M.A.
Mol. Microbiol. 22, 31-42, 1996
A:Title: Processing of the AIDA-I precursor: removal of AIDA and evidence for the outer
A:Reference number: S72657; MUID:97055419; PMID:8899706
A:Accession: S72657
A:Molecule type: protein
A:Residues: 847-856 <SNH>
A:Experimental source: DABC strain 2787
C:Genetics:
A:Genome: plasmid p1b6
F:1-49/Domain: membrane protein
F:50-1206/Product: adhesin AIDA-I #status predicted <STG>
F:50-1206/Product: adhesin AIDA-I #status predicted <MTV>

Query Match	8.5%	Score 222;	DB 2;	Length 1286;
Best Local Similarity	21.6%	Pred. NO. 0.00056;		
Matches 142; Conservative	88;	Mismatches 229;	Indels 198;	Gaps 31;

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OY      MNKYIRYINNSLMAWVYVSELTTRH--TKRASATVTAVALTL--LEATVQASANNETD 56
Db      1 MNKAYISLHSHQAMIVASELARHGHYLAKNILLVAVSTIGMAFVNIISCTVSSGG 60
OY      57 LTVSGTEKLSFSANGKNVITSDTKGL-----NFAKETAGT--NGDTPVHLNGISLETDLT 111
Db      61 TVSSGTEQIYVSGRGS--NATVNSGGTQIVNNCGKRTATVTVNSSGSGQVGTSGATIS--TI 118
OY      112 LNTGATNTYNTDNYVDDDEKKRAASVKDVLNMGWNIKGVKPGTISADNVDPYRTIYDFEL 171
Db      119 VNSGGIQVRSVSGV-----ASATNLNSGAQNIYNL--GHA$NVTYIFSGNQTI--FS 166
OY      172 SAPTKTTTYN-----VESKDNKGKTEYKIGAKTIVKEKDKGLVYTGKDKEN-----GS 220
Db      167 GGTIDSTNISSGQGVSSGQVAV$NTTINSSAQNIILSE--EGALSTHSSSGNMYISAGA 225
OY      221 STDEGGLVTAKEVIDAVNKAQWRMKT-----TTANGOT-----QADKEFTYVSGT 267
Db      226 NATE-----TVNSGGFQVNSGAVATGVTLSGGTQVNSSGGSALSTVSYNSGV 274
OY      268 NVTFASGKGTATVSKD-----DOENITVMDVNV-----GDALNVN-----OLONS 309
Db      275 QYTFACATYDTLTYNVSGNIGNISSGQIYSEITTVNSGTQNIYSSG$SAL$NINIKSOQVNS 334
OY      310 -GNWLD$KAVAG-----SSGKVI--SGNVS$PKGMD$ETVININAGNIEITRNG-- 355
Db      335 EGT$AITLWSDGQYQHIRNGCIASCTIYVNSG$YVNISSG$AE$TIINS$GTLVLS$DGY 394
OY      356 -----KNID-----IAT$MTQF$SV$SLGAGADA 379
Db      395 ARCTIILNNSGREVNSNGVSYNAMITNGENQIYSDG$AT$AIVNT$GFORIN--SGGTA 452
OY      380 P-----TUS-----VDGDALVNG$K-----D$KPYRITV$APGV$EGDVTN 416
Db      453 PVQNSVYVYTRTIS$SA$KPFDAEVY$SGGQTYV$LM$GVI$YNS$FLAIVN$M$PFGTAS$ANVN 512
OY      417 VA-QLGKGV$QNLN$R$IDV$DGN-----ARAGIA 443

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Db 513 LSRLLAFAGNVTGTLINQGRQRYVSGATATSTYGNNEGEFEVLSGGITDGTPLNSGGL 572

QY 444 QATATAGLVQAYL---PKSMAIG-----GCTRGEGAGTGYSSISDGN 487

Db 573 QAVSSGKASATFYINCGAQFYVDDGQVYGFNIKNGCTIRVDSASALNIALSSGN 629

RESULT 13
A64905
ydxK protein - Escherichia coli (strain K-12)

C:Species: Escherichia coli
N:Alternate names: protein 1
C:Date: 12-Sep-1997 #sequence-revision 17-Sep-1997 #text_change 01-Mar-2002

C;Accession: A64905; I52440; S34315
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.

Science 277, 1453-1462, 1997

A:Reference number: A64720; MID:97426617; PMID:9278503
A:Accession: A64905

A:Residues: 1-1335 <BLAT>
A:Molecule type: DNA
A:status: nucleic acid sequence not shown; translation not shown

A; Cross-references: GB:AE000248; GB:U00096; NID:91787783; PIDN:AAC74583.1; PID:q1787783
A; Experimental source: strain K-12, substrain MG1655

R:Cartwright, P.; Timms, M.; Litgow, T., Hoj, P.; Hoogenraad, N.
 Biochim. Biophys. Acta 1153, 345-347, 1993

A:Reference number: 152440; MUID:94100243; PMID:8274505
A:Accession: 152440

A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 680-883 /K/ 885-1316 /S/ 1318-1325 /PCS/

A:Cross-references: EMBL:X73395; NID:g312392; PIDN:CA5A1730.1; PID:g312393
 !:Note: the difference in length is due to a frameshift error at pos 653

C;Genetics:
A;Gene: ydek
C;Function:

C:Function:
A:Description: probably involved in protein translocation apparatus
;Keywords: nucleotide binding; P-loop

F,712-719/Region: nucleotide-binding motif A (P-loop)

Query Match	8.2%;	Score 214.5;	DB 2;	Length 1325;
Best Local Similarity	24.5%;	Pred. No. 0.0014;		
Matches 146; Conservative	62;	Mismatches 250;	Indels 137;	Gaps 28;

09 1 MNKIYRIIWSNALMWWVSELR-----NHTKRASATYKTA--VLATLLFATVQAS 50

Dp
1 MNRIRYIWNCTLOYEQACSELTFRAGCTSTVNLKSSGLTTFKSRLLTGLVLLAIGSAS 60

```
QY 51 -----ANNEEDLPS-----VGTREKLSISANCKNVITSDPTKGINFAKETACT 92
      |::|      | | | | | |::| | |
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Db 61 GASLEVDNDQITINIDTDAVDATLVGVGVTGLNLNLAGSN-ASLTFTTTTSV-----IGA 113

114 NEBSEGVIVNLTGSTRKRLYDSGNNAARPLNVCOSGTITLTKÖKHVDS-----GYLR 164

142 AGNNIKVKKPGTASDNVDFVRTYDVEEFLSADFTTTVNVESKDNGKTE-----VK 194

Db 165 LGSSTGCV - GTVNEVEGEDSVLTFTELFIEISSYGTSLNIT - - - DKQYVSSIVALLGQ 218

[illegible]

246 KTTTANGOTGQADKEFETVSGTNTVFASGKTTATVSKDQGNITVWYDVNVGDA LN - V 303
 219 AGSNGQVVERXGGEMLINNDSSIEFQIGNGIGTGAFTINREGGLVLAENITIIIGNMG --- 215

Db 276 -IGTLNQ--DQDSVITVRLRYNGYFCNG--TVNINSGNLINNKESLVGVQDSHGTV 329

```

QY      304 NQJLQNSGMNL-----DSKAVAGSSGKVIISGNVSPKKGKMDET----- 340

```

Db 330 NVTDKGHWNJCTGTAFFRIYITGDAGDGLNVSSEKVDGIIAG--MKETGIGNITV 386

Db	495	GHRESTLTLAAGSLSGRTQLSKGASWVLNGDVSTGDIYNAGEI-----RPDN-QT	544
QY	437	NARAGIAQATATAG-----LYQAYLPK-----SMAIGGTYRGEA	473
Db	545	TPNALSRVAKSNSPVTFHKLTFTTNLTGGGTINMRVRLDGSNASDQLVINGGOATGKT	604
QY	474	GVA---IGYSSI	482
Db	605	WLFTNVGNSNL	616

Search completed: October 6, 2003, 09:33:13
 Job time : 19.6561 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:05:45 ; Search time 46.4588 Seconds
(without alignments)
1848.329 Million cell updates/sec

Title: US-09-771-382-34
Perfect score: 2735
Sequence: 1 TDEDEEELESYQSRVYGSII.....TASGNSRGHFGASASVGYQW 541

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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25: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2735	100.0	592	20	AAV23744
2	2735	100.0	592	22	AAU06172
3	2527	92.4	592	22	AAU06180
4	2504	91.6	592	20	AAU27203
5	2447.5	89.5	599	20	AAV23743
6	2447.5	89.5	599	20	AAU06176
7	2426.5	88.7	598	20	AAU23738
8	2426.5	88.7	598	20	AAU23742
9	2426.5	88.7	598	22	AAU06177

10	2426.5	88.7	598	22	AAU06178	N. meningitidis BZ
11	2423.5	88.6	594	20	AAV23739	A. surface protein
12	2423.5	88.6	594	20	AAU06179	N. meningitidis BZ
13	2404.5	87.9	594	20	AAV23740	A. surface protein
14	2404.5	87.9	594	21	AAV57044	BASB029 amino acid
15	2404.5	87.9	594	22	AAU06174	N. meningitidis EG
16	2337	85.4	513	22	AAU06183	N. meningitidis H4
17	2334.5	85.4	513	21	AAV57045	BASB029 amino acid
18	2330.5	85.2	591	20	AAV23702	Amino acid sequenc
19	2330.5	85.2	591	20	AAV23746	A. surface protein
20	2330.5	85.2	591	22	AAU06171	N. meningitidis PM
21	2323.5	85.0	591	20	AAV23741	A. surface protein
22	2323.5	85.0	591	22	AAU06175	N. meningitidis EG
23	2315.5	84.7	592	20	AAV23737	A. surface protein
24	2256.5	82.5	589	20	AAV23745	A. surface protein
25	2256.5	82.5	589	22	AAU06173	N. meningitidis P2
26	2207.5	80.7	512	22	AAU06182	N. meningitidis PM
27	2119	77.5	502	22	AAU06181	N. meningitidis PM
28	2033	74.3	604	22	AAU06181	N. meningitidis su
29	1861.5	68.1	433	22	AAU06185	N. meningitidis PM
30	1740.5	63.6	407	22	AAU06184	N. meningitidis PM
31	946	34.6	2353	17	AAV9393	Haemophilus adhesi
32	930.5	34.0	2411	21	AAV23860	Haemophilus influe
33	889.5	32.5	1094	21	AAV23858	Haemophilus influe
34	869.5	31.8	1098	17	AAV9392	Haemophilus adhesi
35	841.5	30.8	245	20	AAV27201	Amino acid sequenc
36	766.5	28.0	679	17	AAV9394	Haemophilus adhesi
37	766.5	28.0	679	21	AAV23855	Haemophilus influe
38	585	21.4	1002	21	AAV23854	Haemophilus influe
39	580	21.2	116	21	AAV37832	Neisseria conserv
40	570.5	20.9	1004	21	AAV23857	Haemophilus influe
41	563	20.6	1104	21	AAV23856	Haemophilus influe
42	563	20.6	1104	21	AAV23859	Haemophilus influe
43	435.5	15.9	298	24	AAV30477	Haemophilus influe
44	391	14.3	2122	24	ABU08784	Moraxella catarrha
45	391	14.3	2123	22	AAV0701	Moraxella catarrha

ALIGNMENTS

RESULT 1
ID AAV23744
AAV23744 standard; Protein: 592 AA.
AC AAV23744:
XX
XX 08-SEP-1999 (first entry)
XX
XX
XX A surface protein of Neisseria meningitidis.
XX
XX Surface protein; surface glycoprotein; infection; vaccine;
XX Immunoreactive peptide.
XX
XX Neisseria meningitidis.
XX
XX
XX W09931132-AL.
XX
XX 24-JUN-1999.
XX
XX
XX 14-DEC-1998; 98WO-AU01031.
XX
XX 12-DEC-1997; 97GB-0026398.
XX
XX
XX (ISIS-) ISIS INNOVATION LTD.
XX (UYOU) UNIV QUEENSLAND.
XX
XX Jennings MP, Moxon ER, Peak IRA;
XX WPI, 1999-418754/35.
XX N-PSDB; AAX85796.
XX
XX Neisseria meningitidis surface proteins useful for treating N.

PT meningitidis infections
 XX
 PS Claim 1: Page 118-120; 132pp; English.
 CC
 CC The present sequence represents a surface protein of *Neisseria*
 CC meningitidis which is approximately 62 kDa. The N. meningitidis
 CC surface glycoproteins, nucleic acids, the primers and optionally
 CC a thermostable polymerase, or antibodies are useful in a kit for
 CC the detection or diagnosis of N. meningitidis infection in humans.
 CC The N. meningitidis surface glycoproteins can also be used to
 CC prevent or treat N. meningitidis infection in humans, especially
 CC in the form of vaccines. The proteins and antibodies can also
 CC be used to identify immunoreactive peptides.
 CC
 XX Sequence 592 AA:
 Query Match 100.0%; Score 2735; DB 20; Length 592;
 Best Local Similarity 100.0%; Pred. No. 1.2e-150;
 Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TDEDEEEELSVORSVSGSIQASMEGSELEETISLMTNDSKEFVDPYIVTLKAGDMLK 60
 DB 52 TDEDEEEELSVORSVSGSIQASMEGSELEETISLMTNDSKEFVDPYIVTLKAGDMLK 111
 QY 61 IKONTNENTNASSFTYSLKADLTGLINTEKLSFGANGKKVNIISDTKGLNFAKETAGT 120
 DB 112 IKONTNENTNASSFTYSLKADLTGLINTEKLSFGANGKKVNIISDTKGLNFAKETAGT 171
 QY 121 NGDTVHLNGTSLTDLMLNTGATNTYNDVTDDEKKRAASVDVLNAGNIGVAPG 180
 DB 172 NGDTVHLNGTSLTDLMLNTGATNTYNDVTDDEKKRAASVDVLNAGNIGVAPG 231
 QY 181 TTASDNVDFVRTYDVEELASADTKTTTVNVESSKDKGKTEVKIGAKTSVIREKDKLVTG 240
 DB 232 TTASDNVDFVRTYDVEELASADTKTTTVNVESSKDKGKTEVKIGAKTSVIREKDKLVTG 291
 QY 241 KKGKNGSSTDEGELVTAKEVIDAVNKAGRMKTTTANGOTGADKEFTVTSGTKVTPA 300
 DB 292 KKGKNGSSTDEGELVTAKEVIDAVNKAGRMKTTTANGOTGADKEFTVTSGTKVTPA 351
 QY 301 SGNGTATVSKDQGNITVKKYDVNVGDALNVQNLNSGMNLDKRAVAGSSGKVIISGNVSP 360
 DB 352 SGNGTATVSKDQGNITVKKYDVNVGDALNVQNLNSGMNLDKRAVAGSSGKVIISGNVSP 411
 QY 361 SKGKMETVNIAGNNIETTRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDEGALNV 420
 DB 412 SKGKMETVNIAGNNIETTRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDEGALNV 471
 QY 421 GSKDANKRVRTTNVAPGVKEGDVTVVAQLKGYAQLNNRIDNVNNGNARAGIAQAIATAGL 480
 DB 472 GSKDANKRVRTTNVAPGVKEGDVTVVAQLKGYAQLNNRIDNVNNGNARAGIAQAIATAGL 531
 QY 481 VQAYLPGRSMAIIGGGTYLGEAGVAYIGYSISAGNWIITKGTASNSRGHFGASASVGYQ 540
 DB 532 VQAYLPGRSMAIIGGGTYLGEAGVAYIGYSISAGNWIITKGTASNSRGHFGASASVGYQ 591
 QY 541 W 541
 DB 592 W 592

OS *Neisseria meningitidis* strain H41.
 XX
 XX Key
 FT Peptide
 FT 1..51
 FT /label= Signal_peptide
 FT 1..50
 FT /label= C1
 FT /note= "Conserved region 1"
 FT 51..102
 FT /label= V1
 FT /note= "Variable region 1"
 FT 52..592
 FT /label= Mature_Nhha
 FT /note= "Predicted mature protein, specifically
 FT claimed in claim 12"
 FT 103..114
 FT /label= C2
 FT /note= "Conserved region 2"
 FT 115..124
 FT /label= V2
 FT /note= "Variable region 2"
 FT 125..188
 FT /label= C3
 FT /note= "Conserved region 3"
 FT 189..210
 FT /label= V3
 FT /note= "Variable region 3"
 FT 211..229
 FT /label= C4
 FT /note= "Conserved region 4"
 FT 230..236
 FT /label= V4
 FT /note= "Variable region 4"
 FT 237..592
 FT /label= C5
 FT /note= "Conserved region 5"
 FT
 FT W020015182-A1.
 FT
 FT 02-AUG-2001.
 FT
 FT 25-JAN-2001; 2001WO-AU00069.
 FT
 FT 25-JAN-2000; 2000US-0177917.
 FT
 FT (UYOU) UNIV QUEENSLAND.
 FT
 FT Peak IRA, Jennings MP;
 FT
 FT WPI; 2001-488774/53.
 FT
 FT N-PSDB; AAS09162.
 FT
 FT New Nhha surface antigen polypeptides and polynucleotides from
 FT *Neisseria meningitidis*, useful in producing vaccines for treating or
 FT preventing broad spectrum of *Neisseria meningitidis* -
 FT
 FT Claim 9; Fig 1; 91pp; English.
 PS
 XX
 CC The present invention relates to the isolation of novel *Neisseria*
 CC meningitidis mutant polypeptides of the surface antigen Nhha
 CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
 CC characterised by deletions of non-conserved amino acids, particularly
 CC the deletion of variable regions. The deletion mutants are useful in
 CC diagnostics, therapeutic and prophylactic vaccines against a broader
 CC spectrum of N. meningitidis, and in designing and/or screening of
 CC medicaments. The mutant proteins when used as a vaccine can effectively
 CC immunise against a broader spectrum of N. meningitidis strains than
 CC would be expected from a corresponding wild-type surface antigen.
 CC The present sequence representing the wild type surface antigen Nhha
 CC from N. meningitidis strain H41 is 1 of 10 Nhha polypeptide sequences
 CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
 CC the present invention.
 CC
 XX

```

SQ Sequence 592 AA;
Query Match 100.0%; Score 2735; DB 22; Length 592;
Best Local Similarity 100.0%; Pred. No. 1.2e-150;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDEDEEEELSVQSRVVGSIQASMEGSELETTISLMTNDSKEFVDPYIVVTLKAGDNLK 60
D 2 TDEDEEEELSVQSRVVGSIQASMEGSELETTISLMTNDSKEFVDPYIVVTLKAGDNLK 111
QY 61 IKONTNENTNASSFTYSLSKKDLTGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAGT 120
D 112 IKONTNENTNASSFTYSLSKKDLTGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAGT 171
QY 121 NGDITVHLNGIGSTLTMLNTGATVNTDNDVDDKKRAASVKDVLNAGMNIRKGYKPG 180
D 172 NGDITVHLNGIGSTLTMLNTGATVNTDNDVDDKKRAASVKDVLNAGMNIRKGYKPG 231
QY 181 TTASDNVDFRTYDVEFLSADTKTTTVNESKDNKGKTEYKIGAKTSVIEKDKLVTG 240
D 232 TTASDNVDFRTYDVEFLSADTKTTTVNESKDNKGKTEYKIGAKTSVIEKDKLVTG 291
QY 241 KKGENGSSSTDEGEGLVTAKEVIDAVNKKAGRMKTTTANGOTGQADKFEVTSCTKYTFA 300
D 292 KKGENGSSSTDEGEGLVTAKEVIDAVNKKAGRMKTTTANGOTGQADKFEVTSCTKYTFA 351
QY 301 SGNGTATVSKDDOGNTTVKVDVNVGDALNVNOLONGMNIDSKAVAGSSGKVTISGVNSP 360
D 352 SGNGTATVSKDDOGNTTVKVDVNVGDALNVNOLONGMNIDSKAVAGSSGKVTISGVNSP 411
QY 361 SKGKMDETVINAGNNIEITRNKNIDIASMTPOFSSVSIAGADAPTLTSVDEGALNV 420
D 412 SKGKMDETVINAGNNIEITRNKNIDIASMTPOFSSVSIAGADAPTLTSVDEGALNV 471
QY 421 GSKDANKPVRITNVAPVKGEDVTNVAQLKGVAONLNRRIDNVGNARAGIAQAIAATAGL 480
D 472 GSKDANKPVRITNVAPVKGEDVTNVAQLKGVAONLNRRIDNVGNARAGIAQAIAATAGL 531
QY 481 VQAVLPKSMMAIGGGYIGEGAGYATIGSSISAGCNMTITAGSNGRHFHASASVGYO 540
D 532 VQAVLPKSMMAIGGGYIGEGAGYATIGSSISAGCNMTITAGSNGRHFHASASVGYO 591
QY 541 W 541
D 592 W 592

RESULT 3
AAU06180
ID AAU06180 standard; Protein; 592 AA.
AC
XX AAU06180;
XX
DT 24-OCT-2001 (first entry)
DE N. meningitidis 22491 surface antigen Nhma polypeptide sequence.
XX
XX Surface antigen Nhma; meningococcal disease; meningitis vaccine.
XX
OS Neisseria meningitidis strain 22491.
XX
XX Key location/Qualifiers
FH 1..50 /label= C1
FT 51..102 /note= "Conserved region 1"
FT /label= V1
FT /note= "Variable region 1"
FT 103..114 /label= C2
FT /note= "Conserved region 2"
FT 115..124 /label= V2
FT

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FT /note= "Variable region 2"
FT 125..188 /label= C3
FT /note= "Conserved region 3"
FT 189..208 /label= V3
FT /note= "Variable region 3"
FT 209..227 /label= C4
FT /note= "Conserved region 4"
FT 228..236 /label= V4
FT /note= "Variable region 4"
FT 237..592 /label= C5
FT /note= "Conserved region 5"

W020015182-A1.
02-AUG-2001.
25-JAN-2001; 2001W0-AU00069.
25-JAN-2000; 2000US-0177917.
(UYQU ) UNIV QUEENSLAND.
Peak IRA, Jennings MP;
WPI: 2001-488774/53.
N-PSDB; AAS09170.

New Nhma surface antigen polypeptides and polynucleotides from
Neisseria meningitidis, useful in producing vaccines for treating or
preventing broad spectrum of Neisseria meningitidis -
Claim 9; Fig 1; 91pp; English.

XX
XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhma
CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhma
CC from N. meningitidis strain 22491 is 1 of 10 Nhma polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
SQ Sequence 592 AA;
Query Match 92.4%; Score 2527; DB 22; Length 592;
Best Local Similarity 93.4%; Pred. No. 1.3e-138;
Matches 507; Conservative 9; Mismatches 23; Indels 4; Gaps 2;

QY 1 TDEDEEEELSVQSRVVGSIQASMEGSELETTISLMTNDSKEFVDPYIVVTLKAGDNLK 60
D 52 TDEDEEEELSVQSRVVGSIQASMEGSELETTISLMTNDSKEFVDPYIVVTLKAGDNLK 111
QY 61 IKONTNENTNASSFTYSLSKKDLTGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAGT 120
D 112 IKONTNENTNASSFTYSLSKKDLTGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAGT 171
QY 121 NGDITVHLNGIGSTLTMLNTGATVNTDNDVDDKKRAASVKDVLNAGMNIRKGYKPG 180
D 172 NGDITVHLNGIGSTLTMLNTGATVNTDNDVDDKKRAASVKDVLNAGMNIRKGYKPG 229
QY 181 TTA--SDNVDFRTYDVEFLSADTKTTTVNESKDNKGKTEYKIGAKTSVIEKDKLV 238
D 181 TTA--SDNVDFRTYDVEFLSADTKTTTVNESKDNKGKTEYKIGAKTSVIEKDKLV 238

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Db      230 STTGQSENVDFVRYTDVFEFLSADTKTTTVNVEKDNKRTEVKIGAKTSVKEKDKLY 289
OY      239 TKGKGENGSTDEGEGLVTAKEVIDAVKAKGRMKTATTANGOTGQADRFETVTSGETYT 298
        |||||
Db      290 TKGKGENGSTDEGEGLVTAKEVIDAVKAKGRMKTATTANGOTGQADRFETVTSGETYT 349
OY      299 FASGNGTTATVSKDDOGNITTVKYDVNVGDALNVNOLNSGWNLDKRAVAGSSGKVI SGNV 358
        |||||
Db      350 FASGNGTTATVSKDDOGNITTVKYDVNVGDALNVNOLNSGWNLDKRAVAGSSGKVI SGNV 409
OY      359 SPSKGMDETVINMAGNNIEITRNGKNIDIASMPFOFSSVSLGAGADAPTLSDVEDEGL 418
        |||||
Db      410 SPSKGMDETVINMAGNNIEITRNGKNIDIASMPFOFSSVSLGAGADAPTLSDVEDEGL 469
OY      419 NVGSKDANKPVRITTVNAPGVKEGDVTVNVALKGVANLNNRIDNVNGNARAGIAQAIATA 478
        |||||
Db      470 NVGSKDANKPVRITTVNAPGVKEGDVTVNVALKGVANLNNRIDNVNGNARAGIAQAIATA 529
OY      479 GLVOAYLPKGSMAIIGGTYLGEAGYAIGYSSISAGGNMIIKGTASGNSRGHFGASASVG 538
        |||||
Db      530 GLVOAYLPKGSMAIIGGTYLGEAGYAIGYSSISAGGNMIIKGTASGNSRGHFGASASVG 589
OY      539 YQM 541
        |||
Db      590 YQM 592

RESULT 4
AA27203
ID      AA27203 standard; Protein; 592 AA.
AC      AA27203;
DT      24-SEP-1999 (first entry)
XX      Amino acid sequence of N. meningitidis protein ORF40a.
XX      Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;
XX      bacterial infection; treatment.
XX      Neisseria meningitidis.
XX      WO936544-A2.
XX      22-JUL-1999.
XX      14-JAN-1999; 99WO-IB00103.
XX      09-OCT-1998; 98GB-0022143.
XX      14-JAN-1998; 98GB-0000760.
XX      01-SEP-1998; 98GB-0019015.
XX      (CHIR-) CHIRON SPA.
XX      Grandi G, Masignani V, Pizze M, Rappuoli R, Scarlato V;
XX      WPI; 1999-444400/37.
XX      N-PSDB; AA299125.
XX      New protein and its nucleotide sequence, useful in vaccines or
XX      diagnostic compositions for treating and/or preventing Neisseria
XX      meningitidis infections
XX      Claim 1; Page 63; 123pp; English.
XX      The invention provides proteins (AA27201-245) from Neisseria
XX      meningitidis (strains A and B) and nucleic acid sequences (AA299123-167)
XX      encoding the proteins. Compositions comprising the protein, nucleic acid
XX      or antibody specific to the protein are useful as pharmaceuticals, e.g. a
XX      vaccine composition or a diagnostic composition. The composition is also
XX      useful for treating or preventing an infection due to Neisseria
XX      bacteria, especially Neisseria meningitidis.

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SQ      Sequence      592 AA:
Query Match      91.6%; Score 2504; DB 20; Length 592;
Best Local Similarity 92.4%; Pred. No. 2,9e-137;
Matches 502; Conservative 10; Mismatches 27; Indels 4; Gaps 2;

OY      1 TDEDEEEELSVQSVYSGISQASMEGSVELETTISLSPNDSEKFPDPYIVVTLKAGDNK 60
        |||||
Db      52 TDEDEEEELSVQSVYSGISQASMEGSVELETTISLSPNDSEKFPDPYIVVTLKAGDNK 111
OY      61 IKONNENNTNASSFTYSLKDLJGLINVTETKLSFGANKKYNII SDPTGLNPAKETAGT 120
        |||||
Db      112 IKONNENNTNASSFTYSLKDLJGLINVTETKLSFGANKKYNII SDPTGLNPAKETAGT 171
OY      121 NGDTTVHLNGISSTLDMILNTGATNTVNDVVTDEDEKRAASVXVDVLNAGNIRGVKPG 180
        |||||
Db      172 NGDTTVHLNGISSTLDMILNTGATNTVNDVVTDEDEKRAASVXVDVLNAGNIRGVKPG 229
OY      181 TTA--SDNVDVRYRTDVFELSLADTKTTTVNVEKDNKRTEVKIGAKTSVKEKDKLY 238
        |||||
Db      230 STTGQSENVDFVRYTDVFEFLSADTKTTTVNVEKDNKRTEVKIGAKTSVKEKDKLY 289
OY      239 TKGKGENGSTDEGEGLVTAKEVIDAVKAKGRMKTATTANGOTGQADRFETVTSGETYT 298
        |||||
Db      290 TKGKGENGSTDEGEGLVTAKEVIDAVKAKGRMKTATTANGOTGQADRFETVTSGETYT 349
OY      299 FASGNGTTATVSKDDOGNITTVKYDVNVGDALNVNOLNSGWNLDKRAVAGSSGKVI SGNV 358
        |||||
Db      350 FASGNGTTATVSKDDOGNITTVKYDVNVGDALNVNOLNSGWNLDKRAVAGSSGKVI SGNV 409
OY      359 SPSKGMDETVINMAGNNIEITRNGKNIDIASMPFOFSSVSLGAGADAPTLSDVEDEGL 418
        |||||
Db      410 SPSKGMDETVINMAGNNIEITRNGKNIDIASMPFOFSSVSLGAGADAPTLSDVEDEGL 469
OY      419 NVGSKDANKPVRITTVNAPGVKEGDVTVNVALKGVANLNNRIDNVNGNARAGIAQAIATA 478
        |||||
Db      470 NVGSKDANKPVRITTVNAPGVKEGDVTVNVALKGVANLNNRIDNVNGNARAGIAQAIATA 529
OY      479 GLVOAYLPKGSMAIIGGTYLGEAGYAIGYSSISAGGNMIIKGTASGNSRGHFGASASVG 538
        |||||
Db      530 GLVOAYLPKGSMAIIGGTYLGEAGYAIGYSSISAGGNMIIKGTASGNSRGHFGASASVG 589
OY      539 YQM 541
        |||
Db      590 YQM 592

RESULT 5
AA23743
ID      AA23743 standard; Protein; 599 AA.
AC      AA23743;
DT      08-SEP-1999 (first entry)
XX      A surface protein of Neisseria meningitidis.
XX      Surface protein; surface glycoprotein; infection; vaccine;
XX      immunoreactive peptide.
XX      Neisseria meningitidis.
XX      WO9311132-A1.
XX      24-JUN-1999.
XX      14-DEC-1998; 98WO-AU01031.
XX      12-DEC-1997; 97GB-0026398.
XX      (ISTS-) ISTIS INNOVATION LTD.
XX      (UYOU ) UNIV QUEENSLAND.

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PI	Jennings NP, Moxon ER, Peak IRA;
XX	DR WPI: 1999-418754/35.
XX	DR N-PSDB: AAX85795.
XX	Neisseria meningitidis surface proteins useful for treating N.
PT	meningitidis infections
PS	Claim 1; Page 114-115; 132pp; English.
CC	The present sequence represents a surface protein of Neisseria
CC	meningitidis which is approximately 62 kDa. The N. meningitidis
CC	surface glycoproteins, nucleic acids, the primers and optionally
CC	a thermostable polymerase, or antibodies are useful in a kit for
CC	the detection or diagnosis of N. meningitidis infection in humans.
CC	The N. meningitidis surface glycoproteins can also be used to
CC	prevent or treat N. meningitidis infection in humans, especially
CC	in the form of vaccines. The proteins and antibodies can also
CC	be used to identify immunoreactive peptides.
XX	
SO	Sequence 599 AA;
Query Match	89.5%; Score 2447.5; DB: 20; Length 599;
Best Local Similarity	90.3%; Pred. No. 5.5e-134;
Matches 496; Conservative 11; Mismatches 33; Indels 9; Gaps 4	
QY	1 TDEDEEEELSEYORS-VVGSIOASMEGSVELET---TISMTNDSEKFEVDPIYVTLKAG 56
DB	52 TDEDEEEELFVRRALVLQFMIDKEGNGENSTNIGMSIYDHNHLHG-ATVTLKAG 110
QY	57 DNLKIKQ---NTNENTNASSFTYSLKDLTGLINVEETKLSFGANGKRVNIISDTKGIN 112
DB	111 DNLKIKQKNTNNTNENTNDSFTYSLKDLTGLTVEETKLSFGANGKRVNIISDTKGIN 170
QY	113 FAKETAGNNGDTVHLNGISLTLDMLNTGATVNTDNTDDEKKRAAYKDVLANGW 172
DB	171 FAKETAGNNGDTVHLNGISLTLDTLNTGATVNTDNTDDEKKRAAYKDVLANGW 230
QY	173 NIKGKPGSTTASDNDVFRYDVEFLSADTKTTTVNVEESKNGKTEYKIGAKTSYIKE 232
DB	231 NIKGKPGSTTASDNDVFRYDVEFLSADTKTTTVNVEESKNGKTEYKIGAKTSYIKE 290
QY	233 KDKGLVTGKKGGENSSSTDEEGELVTAKEVIDAVNKAQRMKTTTANGOTGADKFEHYT 292
DB	291 KDKGLVTGKKGGENSSSTDEEGELVTAKEVIDAVNKAQRMKTTTANGOTGADKFEHYT 350
QY	293 SGTAKTFPSAGNGTATYVSKDDOGNTTVYDVAVGALVNVNOLONGSMINDSAVAGSSGK 352
DB	351 SGTAKTFPSAGNGTATYVSKDDOGNTTVYDVAVGALVNVNOLONGSMINDSAVAGSSGK 410
QY	353 VISGWNVSQSKGMDETVININAGNNNEIRNGCNIDTATSMTPQSFSSVSGACADAPTLTSLV 412
DB	411 VISGWNVSQSKGMDETVININAGNNNEIRNGCNIDTATSMTPQSFSSVSGACADAPTLTSLV 470
QY	413 DDEGALNVSQSKDANKPVRITNVAPEVSKGADVTYVNAQLGVAQNLNLRNIDVNGNARAGIA 472
DB	471 DDKGALNVSQSKDANKPVRITNVAPEVSKGADVTYVNAQLGVAQNLNLRNIDVNGNARAGIA 530
QY	473 QAIATAGLVOAYLPEKSSMAIGGGTYLCEAGYAGISSISACGNMIIKGTASGNSRGHFG 532
DB	531 QAIATAGLVOAYLPEKSSMAIGGGTYRCEAGYAGISSISDGNMIIKGTASGNSRGHFG 590
QY	533 ASASVGYOM 541
DB	591 ASASVGYOM 599
RESULT 6	
AAU06176	
ID	AAU06176 standard: Protein; 599 AA.
AC	AAU06176;
XX	

Seq	Sequence	599 AA:	89.5%:	Score 2447.5:	DB 22:	Length 599:
	Query Match		89.5%:	Score 2447.5:	DB 22:	Length 599:
	Best Local Similarity		90.3%:	Pred. No. 5.3e-134:		
	Matches 496:	Conservative 11:	Mismatches 33:	Indels 9:	Gaps 4:	
QY	1	TDEDEEEELSEVOSS-VYGSIQASMEGSEVELET---ISLSMTNDSEKEFVDPIYVTLKAG	56			
Db	52	TDEDEEEELSEVVRNALVLOFMIDKEGSENESTNICMSIYYDHNHLHG-AIYTLKAG	110			
QY	57	DNLKIKO---NTNENTNASSFTYSLKDLTGLINVEFEKLSFGANGKKNVITSDTKGIN	112			
Db	111	DNLKIKOTNKNNTNENTNDSSEFTYSLKDLTGLISVEFEKLSFGANGKKNVITSDTKGIN	170			
QY	113	FAKETAGNAGPTVYHLNIGISTLMDMLNTGATTVNDNVTNDDEKRAASVKDVLNAGW	172			
Db	171	FAKETAGNAGPTVYHLNIGISTLMDMLNTGATTVNDNVTNDDEKRAASVKDVLNAGW	230			
QY	173	NIKGVKPGTTASDNVDVFRVYDYVEFLSADTKTTTVNESKDKNGKTEVKIGAKTSVIAKE	232			
Db	231	NIKGVKPGTTASDNVDVFRVYDYVEFLSADTKTTTVNESKDKNGKTEVKIGAKTSVIAKE	290			
QY	233	KDGLKLVNKGKGENSSSTDEEGELVTAKEVIDAVKAKGRMKTITANQOTGADKFEIYT	292			
Db	291	KDGLKLVNKGKGENSSSTDEEGELVTAKEVIDAVKAKGRMKTITANQOTGADKFEIYT	350			
QY	293	SGTWTVEFASNGGTTATVASKDOGNITVYDYVNVGALNVNOLONGSMNLSKAIVAGSSGK	352			
Db	351	SGTWTVEFASNGGTTATVASKDOGNITVYDYVNVGALNVNOLONGSMNLSKAIVAGSSGK	410			
QY	353	VISGNVSPSKKMDETVINAGNNIETTRNGKNIDIASMTPOFSSVSGAGADAPTLISV	412			
Db	411	VISGNVSPSKKMDETVINAGNNIETTRNGKNIDIASMTPOFSSVSGAGADAPTLISV	470			
QY	413	DDEGALNAGSKDANKPVRITTVAPGVKEGDYTNVAQLKGVAQNLNRRIDNVGNARAGIA	472			
Db	471	DDEGALNAGSKDANKPVRITTVAPGVKEGDYTNVAQLKGVAQNLNRRIDNVGNARAGIA	530			
QY	473	QAIAITAGLVQAYLPEKSMMAIGGGTYLCEBAGTAIGTSSISAGANNIITGTAAGSRGHG	532			
Db	531	QAIAITAGLVQAYLPEKSMMAIGGGTYLCEBAGTAIGTSSISAGANNIITGTAAGSRGHG	590			
QY	533	ASASVGYQW 541				
Db	591	ASASVGYQW 599				
RESULT 7						
ID	AAAY23738	standard; Protein; 598 AA.				
AC	AAAY23738;					
XX	08-SEP-1999	(first entry)				
DE	A	surface protein of Neisseria meningitidis.				
KW	Surface protein; surface glycoprotein; infection; vaccine;					
XX	Immunoreactive peptide.					
OS	Neisseria meningitidis.					
PN	W09931132-A1.					
PD	24-JUN-1999.					
PE	14-DEC-1998;	98WO-AU01031.				
PR	12-DEC-1997;	97GB-0026398.				
RA	(ISIS-) ISIS INNOVATION LTD.					
XX	(UNIV) UNIV QUEENSLAND.					

[illegible]

DT	08-SEP-1999	(first entry)
XX		
DE	A surface protein of <i>Neisseria meningitidis</i> .	
XX		
KW	Surface protein; surface glycoprotein; infection; vaccine;	
KW	immunoreactive peptide.	
XX		
OS	<i>Neisseria meningitidis</i> .	
XX		
PN	WO9931132-A1.	
PD		
XX		
XX	24-JUN-1999.	
PF		
XX	14-DEC-1998;	98WO-AU01031.
XX		
PR	12-DEC-1997;	97GB-0026398.
XX		
PA	(ISIS-) ISIS INNOVATION LTD.	
XX	(UYOU) UNIV QUEENSLAND.	
PI	Jennings MP, Moxon ER, Peak IRA;	
XX		
DR	WPI; 1999-418754/35.	
DR	N-PSDB; AAX85794.	
XX		
PT	<i>Neisseria meningitidis</i> surface proteins useful for treating <i>N.</i>	
PT	<i>meningitidis</i> infections	
XX		
PS	Claim 1; Page 108-110; 132pp; English.	
XX		
CC	The present sequence represents a surface protein of <i>Neisseria</i>	
CC	<i>meningitidis</i> which is approximately 62 kDa. The <i>N. meningitidis</i>	
CC	surface glycoproteins, nucleic acids, the primers and optionally	
CC	a thermostable polymerase, or antibodies are useful in a kit for	
CC	the detection or diagnosis of <i>N. meningitidis</i> infection in humans.	
CC	The <i>N. meningitidis</i> surface glycoproteins can also be used to	
CC	prevent or treat <i>N. meningitidis</i> infection in humans, especially	
CC	in the form of vaccines. The proteins and antibodies can also	
XX	be used to identify immunoreactive peptides.	
XX		
Sequence	598 AA;	

[illegible][illegible]

Query Match	88.7%	Score 2426.5	DB 22	Length 598
Best Local Similarity	89.0%	Pred. No. 9.1e-133		
Matches 492	Conservative 12	Mismatches 28	Indels 21	Gaps 5
QY	3	EDEEEELSVQR-SVYSGISQAMSESVLEITISLMTDSKEFVPII-----VYT	52	
DB	53	DDDDLYLPPVORTAVVLSFRSDKEGTGEKEG-----TEDSNMAV--YFDEKRVLKAGAIT	105	
QY	53	LKAGDNLKIKONTNENTNA-----SSEFTSLKDDLGLINVEPEKISFGANKKVVIIISDT	108	
DB	106	LKAGDNLKIKONTNENTNENTNDSEFTSLKDDLTLDSVETEKLSFGANGKKNVITSDT	165	
QY	109	KGILFAKETAGTNGDPTVHLNGISSTLMDLMLNTGATTNVTNDNTDDEKKRAASVKKVL	168	
DB	166	KGILNPAKTAETAGNGDPTVHLNGISSTLMDLMLNTGATTNVTNDNTDDEKKRAASVKKVL	225	
QY	169	NAGNNIKGVKPGTTASDNVDFVRYDIVEEFLSADTKTTTVNVESSKDKGKTEVKIGARTS	228	
DB	226	NAGNNIKGVKPGTTASDNVDFVRYDIVEEFLSADTKTTTVNVESSKDKGKTEVKIGARTS	285	
QY	229	VIKKEDGKLVYGGKGGENGSSSTDEEGLVTAKEVIDAANKAGMRKKTITTAGNGTQQAOKF	288	
DB	286	VIKKEDGKLVYGGKGGENGSSSTDEEGLVTAKEVIDAANKAGMRKKTITTAGNGTQQAOKF	345	
QY	289	ETVTSIGTVPFAAGNGTATATVSKDDQGNITVYKDYVNVGDALNVNOLONGMNLDSKAVAG	348	
DB	346	ETVTSIGTVPFAAGNGTATATVSKDDQGNITVYKDYVNVGDALNVNOLONGMNLDSKAVAG	405	
QY	349	SSGKIVSGVNSPSPKGMDETVINAGNNEIETTRNGKNIDIATSMTPQESSVSLGAGADAP	408	
DB	406	SSGKIVSGVNSPSPKGMDETVINAGNNEIETTRNGKNIDIATSMTPQESSVSLGAGADAP	465	
QY	409	TLSDVDEBALVWGSNDANKPVRITNVAPGVCEGDVTNNAQLKGVAQNLNRRIDNVNGAR	468	
DB	466	TLSDVDEBALVWGSNDANKPVRITNVAPGVCEGDVTNNAQLKGVAQNLNRRIDNVNGAR	525	
QY	469	AGIQALITAGLVQAYILPGKSMMAIGGGTYLGEAGYAIGSYSSISAGNMIIKGTASGNSR	528	
DB	526	AGIQALITAGLVQAYILPGKSMMAIGGGTYLGEAGYAIGSYSSISDTGMWVILKGTASGNSR	585	
QY	529	GHFGASASVGYQW 541		
DB	586	GHFGTSASVGYQW 598		
RESULT 11				
AAV23739				
ID	AAV23739	standard; Protein: 594 AA.		
AC	AAV23739;			
XX	08-SEP-1999	(first entry)		
XX	A surface protein of Neisseria meningitidis.			
DE	Surface protein: surface glycoprotein; infection; vaccine.			
KW	immunoreactive peptide.			
XX	Neisseria meningitidis.			
OS	MO9931132-A1.			
PN	24-JUN-1999.			
XX	14-DEC-1998;			
PF	98WO-AU01031.			
XX	12-DEC-1997;			
PR	97GB-0026398.			
XX	(ISIS-) ISIS INNOVATION LTD.			
PA	(UYOU) UNIT QUEENSLAND.			
XX				

Query Match	Best Local Similarity	88.6%	Score 2423.5	DB 20	Length 594
Matches 491	Conservative 10	Mismatches 31	Indels 17	Gaps 4	
Sequence 594 AA:					
Query Match	Best Local Similarity	88.6%	Score 2423.5	DB 20	Length 594
Matches 491	Conservative 10	Mismatches 31	Indels 17	Gaps 4	
Sequence 594 AA:					
Query Match	Best Local Similarity	88.6%	Score 2423.5	DB 20	Length 594
Matches 491	Conservative 10	Mismatches 31	Indels 17	Gaps 4	
Sequence 594 AA:					

DT	24-OCT-2001	(first entry)
XX		
DE	N. meningitidis BZ198 surface antigen Nhha polypeptide sequence.	
XX		
KW	Surface antigen Nhha; meningococcal disease; meningitis vaccine.	
XX		
OS	Neisseria meningitidis strain BZ198.	
XX		
FH	Key	Location/Qualifiers
FT	Region	1..50
FT		/label= C1
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FT	Region	51..104
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FT		/note= "Variable region 1"
FT	Region	105..116
FT		/label= C2
FT		/note= "Conserved region 2"
FT	Region	117..126
FT		/label= V2
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FT	Region	127..190
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FT		/label= V3
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FT		/label= C4
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FT	Region	239..594
FT		/label= C5
FT		/note= "Conserved region 5"
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XX		
PD	02-AUG-2001.	
XX		
PE	25-JAN-2001; 2001WO-AU00069.	
XX		
PR	25-JAN-2000; 2000US-0177917.	
XX		
PA	(UYQU) UNIV QUEENSLAND.	
XX		
PI	Peak IRA, Jennings MP;	
XX		
DR	WPI; 2001-488774/53.	
DR	N-PSDB; AAS09169.	
XX		
PT	New Nhha surface antigen polypeptides and polynucleotides from	
PT	Neisseria meningitidis, useful in producing vaccines for treating or	
XX	preventing broad spectrum of Neisseria meningitidis .	
XX		
PS	Claim 9; Fig 1; 91pp; English.	
XX		
CC	The present invention relates to the isolation of novel Neisseria	
CC	meningitidis mutant polypeptides of the surface antigen Nhha	
CC	(AAU06182-AAU06186). The modified or mutant Nhha polypeptides are	
CC	characterised by deletions of non-conserved amino acids, particularly	
CC	the deletion of variable regions. The deletion mutants are useful in	
CC	diagnosis, therapeutic and prophylactic vaccines against a broader	
CC	spectrum of, Neisseria meningitidis, and in designing and/or screening of	
CC	medicaments. The mutant proteins when used as a vaccine can effectively	
CC	immunise against a broader spectrum of N. meningitidis strains than	
CC	would be expected from a corresponding wild-type surface antigen.	
CC	The present sequence representing the wild type surface antigen Nhha	
CC	from N. meningitidis strain BZ198 is 1 of 10 Nhha polypeptide sequences	
CC	(AAU06171-AAU06180) from 10 different N. meningitidis strains given in	
XX	the present invention.	

Seq	Sequence	594 AA:	88.6%:	Score 2423.5;	DB 22;	Length 594;
QY	Query Match		88.6%;	Score 2423.5;	DB 22;	Length 594;
Db	Best Local Similarity	89.4%;	Pred. No. 1.3e-132;			
	Matches 491;	Conservative 10;	Mismatches 31;	Indels 17;	Gaps 4	
QY	3 EDEERLESEVOR-SVVGSIQASMEGSVELEFITSLSMINDSKKEFDPI-----VVT	52				
Db	53 DDDDLYLEPVQRTAVVLSFRSDKESTGEKG-----TEDSMAV--YDEKRLKKAALT	105				
QY	53 LKAGDLKIKQNTNENTNAASFEYTSLKADLTGLINVEETKLSFGANGKKNIIISDTRGLN	112				
Db	106 LKAGDLKIKQNTNENTNDSSTYSLKADLDLTLVSFETKLSFGANGKKNIIISDTRGLN	165				
QY	113 FAKETAGINDPTVHLNLGISTLDDMLNTGATTNVTNDVTDDEKKAASVKVDLNAGW	172				
Db	166 FAKETAGINDPTVHLNLGISTLDDTLNTGATTNVTNDVTDDEKKAASVKVDLNAGW	225				
QY	173 NIKGVPRGTASDNDVFRYTDYVEFLSADTKTTTVVESKDNCKTEVIGAKTSVIRE	232				
Db	226 NIKGVPRGTASDNDVFRYTDYVEFLSADTKTTTVVESKDNCKTEVIGAKTSVIRE	285				
QY	233 KDCGLVTGKGEKNGSSSTDEGEGLYTAKEVIDAVNKKAGMRKTTTANGOTGQADKFEYV	292				
Db	286 KDCGLVTGKGEKNGSSSTDEGEGLYTAKEVIDAVNKKAGMRKTTTANGOTGQADKFEYV	345				
QY	293 SGTGYTFASGNGTTATVSKDDGNTTVYVDVNVGDALNVOLONGMNLDSKAVAGSSGR	352				
Db	346 SGTGYTFASGNGTTATVSKDDGNTTVYVDVNVGDALNVOLONGMNLDSKAVAGSSGR	405				
QY	353 VTSNGVSPKGMDETVINAGNNIEITRNKNIDITSMTPQFSSVSLGADAPTLV	412				
Db	406 VTSNGVSPKGMDETVINAGNNIEITRNKNIDITSMTPQFSSVSLGADAPTLV	465				
QY	413 DDEGALNVSSKRNKPVRLITNVAPVEKGDYTNVAOLKGYAQNLNRIIDNVGNARAGIA	472				
Db	466 DDEGALNVSSKRNKPVRLITNVAPVEKGDYTNVAOLKGYAQNLNRIIDNVGNARAGIA	525				
QY	473 QAIATAGLVOALPLPKSMMAIGCGTYLGEAGYAGYSSISAGNMIIKGTASGNSRGHFG	532				
Db	526 QAIATAGLVOALPLPKSMMAIGCGDYRGEAGYAGYSSISDGGNMIIKGTASGNSRGHFG	585				
QY	533 ASASVGYQW 541					
Db	586 ASASVGYQW 594					
RESULT 13						
AAV23740						
ID	AAV23740 standard; Protein; 594 AA.					
AC	AAV23740;					
XX						
DT	08-SEP-1999 (first entry)					
XX						
DE	A surface protein of Neisseria meningitidis.					
XX						
KW	Surface protein; surface glycoprotein; infection; vaccine;					
XX	Immunoreactive peptide.					
XX	Neisseria meningitidis.					
OS						
PN	MO9311132-AI.					
XX						
PD	24-JUN-1999.					
XX						
PF	14-DEC-1998; 98WO-AU01031.					
XX						
PR	12-DEC-1997; 97GB-0026398.					
XX						
PA	(ISIS-) ISIS INNOVATION LTD.					
XX	(UYOU) UNIV OUEENSLAND.					


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Db      |||||
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Db      266 KDGLVTGKKGKGENSSSTDEGEGLYTAKEVIDAVNKAQRMTTANQOTGQADFEFYT 345
OY      293 SGTWTFASGNGTATVASKDDQGNITVYKDVNVGDALNVNOLQNSGMWLDKRAVAGSSGK 352
Db      346 SGTWTFASGNGTATVASKDDQGNITVYKDVNVGDALNVNOLQNSGMWLDKRAVAGSSGK 405
OY      353 VTSQNVSPSKGMDTIVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSV 412
Db      406 VTSQNVSPSKGMDTIVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSV 465
OY      413 DDEGALNNGSKDANKPVRITVNAPEVKEGDTVNAOLKGVAONLNHNDVGNARAGIA 472
Db      466 DDEGALNNGSKDANKPVRITVNAPEVKEGDTVNAOLKGVAONLNHNDVGNARAGIA 525
OY      473 QAIATAGLVQAVLPEKSMMAIGGTYTGEGAGYAGYSSISAGNMIIKGTASGNSRGHFG 532
Db      526 QAIATAGLVQAVLPEKSMMAIGGTYTGEGAGYAGYSSISAGNMIIKGTASGNSRGHFG 585
OY      533 ASASVGYOM 541
Db      586 ASASVGYOM 594

RESULT 15
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ID      AAU06174 standard; Protein: 594 AA.
AC      AAU06174;
XX      XX
DT      24-OCT-2001 (first entry)
XX      XX
DE      N. meningitidis EG327 surface antigen Noha polypeptide sequence.
XX      XX
KM      Surface antigen Noha; meningococcal disease; meningitis vaccine.
XX      XX
OS      Neisseria meningitidis strain EG327.
XX      XX
PH      Key
FT      Location/Qualifiers
FT      1..50
FT      /label= C1
FT      /note= "Conserved region 1"
FT      51..104
FT      /label= V1
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FT      127..190
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FT      /note= "Conserved region 3"
FT      191..212
FT      /label= V3
FT      /note= "Variable region 3"
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FT      239..594
FT      /label= C5
FT      /note= "Conserved region 5"
XX      XX
XX      WO20015182-A1.
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PD      02-AUG-2001.
XX      XX
PF      25-JAN-2001; 2001WO-AU00069.
XX      XX
PR      25-JAN-2000; 2000US-0177917.
XX      XX
PA      (UYOU ) UNIV QUEENSLAND.
XX      XX
PI      Peak IRA, Jennings MP;
XX      XX
DR      MPI: 2001-488774/53.
XX      N-PSDB: AAS09164.
XX      XX
PT      New Noha surface antigen polypeptides and polynucleotides from
XX      preventing broad spectrum of Neisseria meningitidis -
PS      Claim 9; Fig 1; 91pp: English.
XX      XX
CC      The present invention relates to the isolation of novel Neisseria
CC      meningitidis mutant polypeptides of the surface antigen Noha
CC      (AAU06182-AAU06186). The modified or mutant Noha polypeptides are
CC      characterised by deletions of non-conserved amino acids, particularly
CC      the deletion of variable regions. The deletion mutants are useful in
CC      diagnostics, therapeutic and prophylactic vaccines against a broader
CC      spectrum of N. meningitidis, and in designing and/or screening of
CC      medicaments. The mutant proteins when used as a vaccine can effectively
CC      immunise against a broader spectrum of N. meningitidis strains than
CC      would be expected from a corresponding wild-type surface antigen.
CC      The present sequence representing the wild type surface antigen Noha
CC      from N. meningitidis strain EG327 is 1 of 10 Noha polypeptide sequences
CC      (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC      the present invention.
XX      XX
SQ      Sequence 594 AA:
XX      XX
Query Match 87.9%; Score 2404.5; DB 22; Length 594;
Best Local Similarity 88.7%; Pred. No. 1.7e-131;
Matches 487; Conservative 15; Mismatches 34; Indels 13; Gaps 3;
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Db      51 TTDDDDLYLEPVQRTAVLSPRSDEKGEGERK-----VTEDSNMGVYDKKGVLTAQTIT 105
OY      53 LKAGDNLKIKONTNENTNASSFTYSLKKDLTGLINVEYEKLSFGANGKKVNIISPTKGLN 112
Db      106 LKAGDNLKIKONTNENTNASSFTYSLKKDLTGLINVEYEKLSFGANGKKVNIISPTKGLN 165
OY      113 FAKETAGNGDTVHLNGISGTLTDLMLNTGATTNVTNDVNTDDEKKRAASVKDYLNAGW 172
Db      166 FAKTAETNGDVTYHLNGISGTLTDLMLNTGATTNVTNDVNTDDEKKRAASVKDYLNAGW 225
OY      173 NIKGVKPGTTASDNDVFRITDYVEFLSADTKTTTVNESKNGKRTVEKIGAKTSVKE 232
Db      226 NIKGVKPGTTASDNDVFRITDYVEFLSADTKTTTVNESKNGKRTVEKIGAKTSVKE 285
OY      233 KDGLVTGKKGKGENSSSTDEGEGLYTAKEVIDAVNKAQRMTTANQOTGQADFEFYT 292
Db      286 KDGLVTGKKGKGENSSSTDEGEGLYTAKEVIDAVNKAQRMTTANQOTGQADFEFYT 345
OY      293 SGTWTFASGNGTATVASKDDQGNITVYKDVNVGDALNVNOLQNSGMWLDKRAVAGSSGK 352
Db      346 SGTWTFASGNGTATVASKDDQGNITVYKDVNVGDALNVNOLQNSGMWLDKRAVAGSSGK 405
OY      353 VTSQNVSPSKGMDTIVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSV 412
Db      406 VTSQNVSPSKGMDTIVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSV 465
OY      413 DDEGALNNGSKDANKPVRITVNAPEVKEGDTVNAOLKGVAONLNHNDVGNARAGIA 472
Db      466 DDEGALNNGSKDANKPVRITVNAPEVKEGDTVNAOLKGVAONLNHNDVGNARAGIA 525
OY      473 QAIATAGLVQAVLPEKSMMAIGGTYTGEGAGYAGYSSISAGNMIIKGTASGNSRGHFG 532
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Db	526	QAIATAGLVQAYLPGKSMMAIGGTGRGEAGYAIGYSSIDGNNWIKGTASGNSRGHFG	585
QY	533	ASASVGYQW	541
Db	586	ASASVGYQW	594

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2735	100.0	592	3	US-09-377-155-17 Sequence 17, Appl
2	2735	100.0	592	4	US-09-669-974-17 Sequence 17, Appl
3	2447.5	89.5	599	3	US-09-377-155-15 Sequence 15, Appl
4	2447.5	89.5	599	4	US-09-669-974-15 Sequence 15, Appl
5	2426.5	88.7	598	3	US-09-377-155-5 Sequence 5, Appl
6	2426.5	88.7	598	3	US-09-377-155-13 Sequence 13, Appl
7	2426.5	88.7	598	4	US-09-669-974-5 Sequence 5, Appl
8	2426.5	88.7	598	4	US-09-669-974-13 Sequence 13, Appl
9	2423.5	88.6	594	4	US-09-377-155-7 Sequence 7, Appl
10	2423.5	88.6	594	4	US-09-669-974-7 Sequence 7, Appl
11	2404.5	87.9	594	4	US-09-377-155-9 Sequence 9, Appl
12	2404.5	87.9	594	4	US-09-669-974-9 Sequence 9, Appl
13	2330.5	85.2	591	3	US-09-377-155-21 Sequence 21, Appl
14	2330.5	85.2	591	4	US-09-669-974-21 Sequence 21, Appl
15	2333.5	85.0	591	3	US-09-377-155-11 Sequence 11, Appl
16	2333.5	85.0	591	4	US-09-669-974-11 Sequence 11, Appl
17	2315.5	84.7	592	3	US-09-377-155-2 Sequence 2, Appl
18	2315.5	84.7	592	4	US-09-669-974-2 Sequence 2, Appl
19	2256.5	82.5	589	3	US-09-377-155-19 Sequence 19, Appl
20	2256.5	82.5	589	4	US-09-669-974-19 Sequence 19, Appl
21	946	34.6	2353	3	US-09-377-155-33 Sequence 33, Appl
22	946	34.6	2353	3	US-08-913-942-4 Sequence 4, Appl
23	946	34.6	2353	4	US-09-669-974-33 Sequence 33, Appl
24	945	34.6	2354	4	US-09-268-347-47 Sequence 47, Appl
25	930.5	34.0	2411	4	US-09-268-347-36 Sequence 36, Appl
26	925	33.8	607	1	US-08-409-995-6 Sequence 6, Appl
27	925	33.8	607	3	US-08-685-467-6 Sequence 6, Appl

28	925	33.8	607	3	US-08-913-942-6 Sequence 6, Appl
29	925	33.8	1912	1	US-08-409-995-4 Sequence 4, Appl
30	925	33.8	1912	3	US-08-685-467-4 Sequence 4, Appl
31	889.5	32.5	1094	4	US-09-268-347-32 Sequence 32, Appl
32	869.5	31.8	1098	1	US-08-409-995-2 Sequence 2, Appl
33	869.5	31.8	1098	3	US-08-685-467-2 Sequence 2, Appl
34	869.5	31.8	1098	3	US-09-377-155-32 Sequence 32, Appl
35	869.5	31.8	1098	3	US-08-913-942-2 Sequence 2, Appl
36	869.5	31.8	1098	4	US-09-669-974-32 Sequence 32, Appl
37	869.5	31.8	1098	4	US-09-268-347-44 Sequence 44, Appl
38	866.5	31.7	658	1	US-08-409-995-5 Sequence 5, Appl
39	866.5	31.7	658	3	US-08-685-467-5 Sequence 5, Appl
40	866.5	31.7	658	3	US-08-913-942-5 Sequence 5, Appl
41	766.5	28.0	679	4	US-08-913-942-15 Sequence 15, Appl
42	766.5	28.0	679	3	US-09-268-347-26 Sequence 26, Appl
43	585	21.4	1002	4	US-09-268-347-24 Sequence 24, Appl
44	570.5	20.9	1004	4	US-09-268-347-30 Sequence 30, Appl
45	563	20.6	1104	4	US-09-268-347-28 Sequence 28, Appl

ALIGNMENTS

RESULT 1									
US-09-377-155-17									
Sequence 17, Application US/09377155									
Patient No. 6197312									
GENERAL INFORMATION:									
APPLICANT: PEAK, Ian Richard Anselm									
APPLICANT: JENNINGS, Michael Paul									
APPLICANT: MOXON, E. Richard									
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN									
FILE REFERENCE: 065064/0128									
CURRENT APPLICATION NUMBER: US/09/377,155									
CURRENT FILING DATE: 1999-08-19									
PRIOR APPLICATION NUMBER: PCT/AU98/01031									
PRIOR FILING DATE: 1998-12-14									
PRIOR APPLICATION NUMBER: GB 9726398.2									
PRIOR FILING DATE: 1997-12-12									
NUMBER OF SEQ ID NOS: 33									
SOFTWARE: Patentin Ver. 2.0									
SEQ ID NO 17									
LENGTH: 592									
TYPE: PRT									
ORGANISM: Neisseria meningitidis									
US-09-377-155-17									
Query Match									
Best Local Similarity 100.0%; Score 2735; DB 3; Length 592;									
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	TDEDEEEELSVQSRVSGSIQASMEGSELETTISLSMTNDSKEFVDPYIVYTLKAGCNLK	60						
DB	52	TDEDEEEELSVQSRVSGSIQASMEGSELETTISLSMTNDSKEFVDPYIVYTLKAGCNLK	111						
QY	61	IKONTNNTAASPTVSLKDLGLINVEETKISFGANGKRVNISPDKGLNFAKTAGT	120						
DB	112	IKONTNNTAASPTVSLKDLGLINVEETKISFGANGKRVNISPDKGLNFAKTAGT	171						
QY	121	NGDTYVHLNIGSTLTDMNLNTGATNTVNDNTDDEKRAASVKDVLNAGWNKGYKPG	180						
DB	172	NGDTYVHLNIGSTLTDMNLNTGATNTVNDNTDDEKRAASVKDVLNAGWNKGYKPG	231						
QY	181	TTASDNVDYRYTDYVEFSLADRTKTTVNVESKDNKTEVKIGAKTSVIREKDKLYTG	240						
DB	232	TTASDNVDYRYTDYVEFSLADRTKTTVNVESKDNKTEVKIGAKTSVIREKDKLYTG	291						
QY	241	KKGGENSSNDEGEGVTAKEVIDAVNKAARMKTTTANGOTGADFEETVTSCTKYTFA	300						
DB	292	KKGGENSSNDEGEGVTAKEVIDAVNKAARMKTTTANGOTGADFEETVTSCTKYTFA	351						
QY	301	SGNGTTATVSKDDGNTTVKVDVNVGDALNVNOLNSGWNLDKRAVSGSSGKVTSGNVSP	360						

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Db 352 SGNNGTATVSKDDGNTITVKYVNVGDALNVNQLNSGNNLDSKAVAGSSGKVIAGNSVP 411
Oy 361 SKGKDEFTVINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLVSVDDEGALNV 420
Db 412 SKGKDEFTVINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLVSVDDEGALNV 471
Oy 421 GSKDANKPVRITNVAPGVKESDVTVAOLKGYAQNINRINIDVNGNARAGIAQAIATAGL 480
Db 472 GSKDANKPVRITNVAPGVKESDVTVAOLKGYAQNINRINIDVNGNARAGIAQAIATAGL 531
Oy 481 VQAYLPKSKMAIGGGTYLGEAGYAIQYSSISAGGNMIIKGTASGNSRCHFGASASVGYQ 540
Db 532 VQAYLPKSKMAIGGGTYLGEAGYAIQYSSISAGGNMIIKGTASGNSRCHFGASASVGYQ 591
Oy 541 W 541
Db 592 W 592
```

```
RESULT 2
US-09-669-974-17
; Sequence 17, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 592
; TYPE: PRN
; ORGANISM: Neisseria meningitidis
US-09-669-974-17
```

```
Query Match 100.0%; Score 2735; DB 4; Length 592;
Best Local Similarity 100.0%; Pred. No. 5.9e-208;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 TDEDEEELESVQORSVGSIOASMEGSVELETTISLMTNDSKEFYDPIYIVTLKAGDNLK 60
Db 52 TDEDEEELESVQORSVGSIOASMEGSVELETTISLMTNDSKEFYDPIYIVTLKAGDNLK 111
Oy 61 IKONTNENTNASSFTYSLSKKDLGLINVTETKLSFGANGKKNIIISDTKGLNFAKETACT 120
Db 112 IKONTNENTNASSFTYSLSKKDLGLINVTETKLSFGANGKKNIIISDTKGLNFAKETACT 171
Oy 121 NCDTIVHLNGISLTLDMLNTGATTNVNDVTDDEKRRASVADVNLAGNNINGVYKFG 180
Db 172 NCDTIVHLNGISLTLDMLNTGATTNVNDVTDDEKRRASVADVNLAGNNINGVYKFG 231
Oy 181 TTASDNVDFVRTYDVEFLSADTKTTTVNVESEKNGKTEVKIGAKTSYIKEDKLVYG 240
Db 232 TTASDNVDFVRTYDVEFLSADTKTTTVNVESEKNGKTEVKIGAKTSYIKEDKLVYG 291
Oy 241 KKGKNGSSTDEGEBLVYAKVEYIDAVNKAQRMTKTTTANGOTGQADKEFTVTSGTKVYFA 300
Db 292 KKGKNGSSTDEGEBLVYAKVEYIDAVNKAQRMTKTTTANGOTGQADKEFTVTSGTKVYFA 351
Oy 301 SGNNGTATVSKDDGNTITVKYVNVGDALNVNQLNSGNNLDSKAVAGSSGKVIAGNSVP 360
Db 352 SGNNGTATVSKDDGNTITVKYVNVGDALNVNQLNSGNNLDSKAVAGSSGKVIAGNSVP 411
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Oy 361 SKGKDEFTVINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLVSVDDEGALNV 420
Db 412 SKGKDEFTVINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLVSVDDEGALNV 471
Oy 421 GSKDANKPVRITNVAPGVKESDVTVAOLKGYAQNINRINIDVNGNARAGIAQAIATAGL 480
Db 472 GSKDANKPVRITNVAPGVKESDVTVAOLKGYAQNINRINIDVNGNARAGIAQAIATAGL 531
Oy 481 VQAYLPKSKMAIGGGTYLGEAGYAIQYSSISAGGNMIIKGTASGNSRCHFGASASVGYQ 540
Db 532 VQAYLPKSKMAIGGGTYLGEAGYAIQYSSISAGGNMIIKGTASGNSRCHFGASASVGYQ 591
Oy 541 W 541
Db 592 W 592
```

```
RESULT 3
US-09-377-155-15
; Sequence 15, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRN
; ORGANISM: Neisseria meningitidis
US-09-377-155-15
```

```
Query Match 89.5%; Score 2447.5; DB 3; Length 599;
Best Local Similarity 90.3%; Pred. No. 3.1e-185;
Matches 496; Conservative 11; Mismatches 33; Indels 9; Gaps 4;
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Oy 1 TDEDEEELESVQORS-VVGSIOASMEGSVELETTISLMTNDSKEFYDPIYIVTLKAG 56
Db 52 TDEDEEELEPVRSALVLOFMIDKEGNGENSTGNIGSIYDNNHTLHG-ATVTLKAG 110
Oy 57 DNLIKIKO---NTNENTNASSFTYSLSKKDLGLINVTETKLSFGANGKKNIIISDTKGLN 112
Db 111 DNLIKIKONTNNTNENTNDSFTYSLSKKDLGLTSEVEKLSFGANGKKNVNTISDTKGLN 170
Oy 113 FAKETAGTNGDTIVHLNGISLTLDMLNTGATTNVNDVTDDEKRRASVADVNLAGW 172
Db 171 FAKETAGTNGDTIVHLNGISLTLDMLNTGATTNVNDVTDDEKRRASVADVNLAGW 230
Oy 173 NIKGVKPGTTASDNVDFVRTYDVEFLSADTKTTTVNVESEKNGKTEVKIGAKTSYIKE 232
Db 231 NIKGVKPGTTASDNVDFVRTYDVEFLSADTKTTTVNVESEKNGKTEVKIGAKTSYIKE 290
Oy 233 KDKLVYTGKKGKNGSSTDEGEBLVYAKVEYIDAVNKAQRMTKTTTANGOTGQADKEFTVT 292
Db 291 KDKLVYTGKKGKNGSSTDEGEBLVYAKVEYIDAVNKAQRMTKTTTANGOTGQADKEFTVT 350
Oy 293 SGTKVYFASGNGTATVSKDDGNTITVKYVNVGDALNVNQLNSGNNLDSKAVAGSSGK 352
Db 351 SGTNVTFFASGKGTATVSKDDGNTITVKYVNVGDALNVNQLNSGNNLDSKAVAGSSGK 410
Oy 353 VTSGNVSPSKGMDFTVINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLVS 412
Db 411 VTSGNVSPSKGMDFTVINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLVS 470
```

[illegible][illegible]

Db 526 AGAQAQIAATAGAAQAALPEKSMMAALGGGYRREAGAYALGYSSIDTGNWYIKGTASQNSR 565

QY 529 GHEGASASVGYQW 541
||||| |||||||

Db 586 GHEGTSASVGYQW 598

RESULT 6
 US-09-377-155-13
 : Sequence 13, Application us/09377155
 : Patent No. 6197312
 : GENERAL INFORMATION:
 : APPLICANT: PEAK, Ian Richard Anselm
 : APPLICANT: JENNINGS, Michael Paul
 : APPLICANT: MOMON, E. Richard
 : TITLE OF INVENTION: NOVEL SURFACE ANTIGENE
 : FILE REFERENCE: 065064/0128
 : CURRENT APPLICATION NUMBER: US/09/377,155
 : CURRENT FILING DATE: 1999-08-19
 : PRIOR APPLICATION NUMBER: PCT/AU98/01031
 : PRIOR FILING DATE: 1998-12-14
 : PRIOR APPLICATION NUMBER: GB 9726398.2
 : PRIOR FILING DATE: 1997-12-12
 : NUMBER OF SEQ ID NOS: 33
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 13
 : LENGTH: 598
 : TYPE: PRN
 : ORGANISM: Neisseria meningitidis
 US-09-377-155-13

Query Match	88.78;	Score 2426.5;	DB 3	Length 598;
Best Local Similarity	89.28;	Pred. No. 1.4e-183;		
Matches 493;	Conservative 11;	Mismatches 28;	Indels 21;	Gaps 5

```

Db          586 GHFGASASVGYGM 598

RESULT 7
US-09-669-974-5
: Sequence 5, Application US/09669974
: Patent No. 6333173
:
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/669, 974
: CURRENT FILING DATE: 2000-09-26
: PRIOR APPLICATION NUMBER: US 09/377,155
: PRIOR FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 5
: LENGTH: 598
: TYPE: PRN
: ORGANISM: Neisseria meningitidis
US-09-669-974-5

```

Query Match	88.7%	Score	2426.5	DB	4	Length	598
Best Local Similarity	89.0%	Pred. No.	14	Indels	183		
Matches	492	Conservative	12	Mismatches	28	Indels	21
						Gaps	5
0x	3	EDEEBEBSVOR-SVVGSIQASMECSVELEFITSMTNDKSEFDPYI-----VYT	52				

APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
FILE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 594
TYPE: PR
ORGANISM: Neisseria meningitidis
US-09-669-974-7

Query Match 88.6%; Score 2423.5; DB 4; Length 594;
Best Local Similarity 89.4%; Pred. No. 2.4e-183;
Matches 491; Conservative 10; Mismatches 31; Indels 17; Gaps 4;

QY 3 EDEEELESVOR-SVVGSIQASMEGSVELETISLSMTNDSKEFVDPI-----VVT 52
DB 53 DDDDDLYLEPYQRTAVVLSFRSDKEGEGEKE-----TEDSNNAV--YFDEKRVLKAGAIT 105
QY 53 LKAGNLKIKONTNENTNASSFTYSLSKDLTGLINVEFEKLSFGANGKRVNIISDTKGLN 112
DB 106 LKAGNLKIKONTNENTNASSFTYSLSKDLTGLTDLTSVEFEKLSFGANGKRVNIISDTKGLN 165
QY 113 FAKETAGTNGDPTVHLNGISLTDTMLNTGATNTVNDVNTDDEKRRASVADVLNMG 172
DB 166 FAKETAGTNGDPTVHLNGISLTDTMLNTGATNTVNDVNTDDEKRRASVADVLNMG 225
QY 173 NIKGVPKGTASDNDVFTVDTVEFLSADTKTTTVNVEKSKNGKRTVEKIGAKTSVIKE 232
DB 226 NIKGVPKGTASDNDVFTVDTVEFLSADTKTTTVNVEKSKNGKRTVEKIGAKTSVIKE 285
QY 233 KDGKLVTKGKGENSSSTDEGGLVTAKEVIDAVNKAQRMTTTTANGOTGADKFEYVT 292
DB 286 KDGKLVTKGKGENSSSTDEGGLVTAKEVIDAVNKAQRMTTTTANGOTGADKFEYVT 345
QY 293 SGTNYTFASGNGTTFATVSKDDOGNTTVKYDVNVGALANVNOLONSGMNIDSKAAVAGSSGK 352
DB 346 SGTNYTFASGNGTTFATVSKDDOGNTTVKYDVNVGALANVNOLONSGMNIDSKAAVAGSSGK 405
QY 353 VTSGVNPSKGMDETVINAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLSV 412
DB 406 VTSGVNPSKGMDETVINAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLSV 465
QY 413 DDEGALNNGSKDANKPVRTITNVAPEGKEDVTNVAOLKVAONLNRRIDNVGNARAGIA 472
DB 466 DDEGALNNGSKDANKPVRTITNVAPEGKEDVTNVAOLKVAONLNRRIDNVGNARAGIA 525
QY 473 QAIATAGLQVAVLTPKRSMAIGGTYLGEAGYAIIGYSSISAGGNMIIKGTASGNSRGHG 532
DB 526 QAIATAGLQVAVLTPKRSMAIGGTYLGEAGYAIIGYSSISAGGNMIIKGTASGNSRGHG 585
QY 533 ASASVGYOW 541
DB 586 ASASVGYOW 594

RESULT 11
US-09-377-155-9
Sequence 9, Application US/09377155
Patent No. 6197312
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul

APPLICANT: MOXON, E. Richard
FILE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 594
TYPE: PR
ORGANISM: Neisseria meningitidis
US-09-377-155-9

Query Match 87.9%; Score 2404.5; DB 3; Length 594;
Best Local Similarity 88.7%; Pred. No. 7.7e-182;
Matches 487; Conservative 15; Mismatches 34; Indels 13; Gaps 3;

QY 1 TDEEELESVOR-SVVGSIQASMEGSVELETISLSMTNDS-----KEFVDPIYVT 52
DB 51 TTDDDDLYLEPYQRTAVVLSFRSDKEGEGEKE-----VTEDSNMGVYEPDKKGVLLAGTIT 105
QY 53 LKAGNLKIKONTNENTNASSFTYSLSKDLTGLINVEFEKLSFGANGKRVNIISDTKGLN 112
DB 106 LKAGNLKIKONTNENTNASSFTYSLSKDLTGLTDLTSVEFEKLSFGANGKRVNIISDTKGLN 165
QY 113 FAKETAGTNGDPTVHLNGISLTDTMLNTGATNTVNDVNTDDEKRRASVADVLNMG 172
DB 166 FAKETAGTNGDPTVHLNGISLTDTMLNTGATNTVNDVNTDDEKRRASVADVLNMG 225
QY 173 NIKGVPKGTASDNDVFTVDTVEFLSADTKTTTVNVEKSKNGKRTVEKIGAKTSVIKE 232
DB 226 NIKGVPKGTASDNDVFTVDTVEFLSADTKTTTVNVEKSKNGKRTVEKIGAKTSVIKE 285
QY 233 KDGKLVTKGKGENSSSTDEGGLVTAKEVIDAVNKAQRMTTTTANGOTGADKFEYVT 292
DB 286 KDGKLVTKGKGENSSSTDEGGLVTAKEVIDAVNKAQRMTTTTANGOTGADKFEYVT 345
QY 293 SGTNYTFASGNGTTFATVSKDDOGNTTVKYDVNVGALANVNOLONSGMNIDSKAAVAGSSGK 352
DB 346 SGTNYTFASGNGTTFATVSKDDOGNTTVKYDVNVGALANVNOLONSGMNIDSKAAVAGSSGK 405
QY 353 VTSGVNPSKGMDETVINAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLSV 412
DB 406 VTSGVNPSKGMDETVINAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLSV 465
QY 413 DDEGALNNGSKDANKPVRTITNVAPEGKEDVTNVAOLKVAONLNRRIDNVGNARAGIA 472
DB 466 DDEGALNNGSKDANKPVRTITNVAPEGKEDVTNVAOLKVAONLNRRIDNVGNARAGIA 525
QY 473 QAIATAGLQVAVLTPKRSMAIGGTYLGEAGYAIIGYSSISAGGNMIIKGTASGNSRGHG 532
DB 526 QAIATAGLQVAVLTPKRSMAIGGTYLGEAGYAIIGYSSISAGGNMIIKGTASGNSRGHG 585
QY 533 ASASVGYOW 541
DB 586 ASASVGYOW 594

RESULT 12
US-09-669-974-9
Sequence 9, Application US/09669974
Patent No. 6333173
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
FILE OF INVENTION: NOVEL SURFACE ANTIGEN
CURRENT APPLICATION NUMBER: US/09/669,974

; PRIOR FILING DATE: 1997-12-12
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: Patentln Ver. 2.0
 ; SEQ ID NO 21
 ; LENGTH: 591
 ; TYPE: PRT
 ; ORGANISM: Neisseria meningitidis
 US-09-669-974-21

Query Match 85.2%; Score 2330.5; DB 4; Length 591;
 Best Local Similarity 86.8%; Pred. No. 5.4e-176;
 Matches 475; Conservative 22; Mismatches 35; Indels 15; Gaps 6;

QY	2	DEDEEE--LESVORSV-VGSIQASMEGSVELETISLMTNDSKEFEVDPIYV---VTLK	54
DB	53	NEDEEDLYLDPVQTFVAVLIYNSDKEGTGEKEVE-ENSDWAVYFNKGVLTAREITLK	111
QY	55	AGDNLIKIKONTNENTNASSFTYSLKKDLTGLINVEFEKLSFGANKKVNIIISDTKGLNFA	114
DB	112	AGDNLIKIKO-----NGTNFTYSLKKDLTGLSVGTEKLSFGANKKNITSDTKGLNFA	165
QY	115	KETAGTNGDTYVHLNGISSTLTDLMLNTGATTNTVNDVTDDEKKRAASVKDVLNAGNI	174
DB	166	KETAGTNGDTYVHLNGISSTLTDLMLNTGATTNTVNDVTDDEKKRAASVKDVLNAGNI	225
QY	175	KGVRPGTTASDNVDFRTYDVEFLSADTKTTTVNVEESKDKGKTEVIGAKTSYIKED	234
DB	226	KGVRPGTTASDNVDFRTYDVEFLSADTKTTTVNVEESKDKGKTEVIGAKTSYIKED	285
QY	235	GKLVYTKGKGENSGSTDEGEGLVTAKEVIDAVNKGWRRKTTTANGOTGQADKFEITYSG	294
DB	286	GKLVYTKGKGENSGSTDEGEGLVTAKEVIDAVNKGWRRKTTTANGOTGQADKFEITYSG	345
QY	295	TKVTFASGNGTTATYVSKDDOGNITVYDVNVGDALNVNOLONGNLDKSKAVAGSSGKYI	354
DB	346	TNVTTFASGKGTATYVSKDDOGNITVYDVNVGDALNVNOLONGNLDKSKAVAGSSGKYI	405
QY	355	SGNVSPSKGKDETVNINAGNIEITRNGKNIDITSMTPQSSVSLGAGADAPTLISYDD	414
DB	406	SGNVSPSKGKDETVNINAGNIEITRNGKNIDITSMTPQSSVSLGAGADAPTLISYDD	465
QY	415	EGALNVGSKDANKPVRTINVAAGVEGDVTNVAQLKGYAQNINNRIDVNVNGNARAGIAQA	474
DB	466	D-ALNVGSKDANKPVRTINVAAGVEGDVTNVAQLKGYAQNINNRIDVNVNGNARAGIAQA	524
QY	475	IATAGLVQAYLPGKSMMAIGGGTYLGEAGYALGYSSISAGNWIITKGTASGNSRGHFGAS	534
DB	525	IATAGLVQAYLPGKSMMAIGGGTYLGEAGYALGYSSISDGGNWITKGTASGNSRGHFGAS	584
QY	535	ASVGYQW 541	
DB	585	ASVGYQW 591	

RESULT 15
 US-09-377-155-11
 ; Sequence 11, Application US/09377155
 ; Patent No. 6197312
 ; GENERAL INFORMATION:
 ; APPLICANT: PEAK, Ian Richard Anselm
 ; APPLICANT: JENNINGS, Michael Paul
 ; APPLICANT: MOXON, E. Richard
 ; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
 ; FILE REFERENCE: 065064/0128
 ; CURRENT APPLICATION NUMBER: US/09/377,155
 ; CURRENT FILING DATE: 1999-08-19
 ; PRIOR APPLICATION NUMBER: PCT/AU98/01031
 ; PRIOR FILING DATE: 1998-12-14
 ; PRIOR APPLICATION NUMBER: GB 9726398.2
 ; PRIOR FILING DATE: 1997-12-12
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: Patentln Ver. 2.0
 ; SEQ ID NO 11

; LENGTH: 591
 ; TYPE: PRT
 ; ORGANISM: Neisseria meningitidis
 US-09-377-155-11

Query Match 85.0%; Score 2323.5; DB 3; Length 591;
 Best Local Similarity 86.7%; Pred. No. 1.9e-175;
 Matches 474; Conservative 22; Mismatches 36; Indels 15; Gaps 6;

QY	2	DEDEEE--LESVORSV-VGSIQASMEGSVELETISLMTNDSKEFEVDPIYV---VTLK	54
DB	53	NEDEEDLYLDPVLTAVLIYNSDKEGTGEKEVE-ENSDWAVYFNKGVLTAREITLK	111
QY	55	AGDNLIKIKONTNENTNASSFTYSLKKDLTGLINVEFEKLSFGANKKVNIIISDTKGLNFA	114
DB	112	AGDNLIKIKO-----NGTNFTYSLKKDLTGLSVGTEKLSFGANKKNITSDTKGLNFA	165
QY	115	KETAGTNGDTYVHLNGISSTLTDLMLNTGATTNTVNDVTDDEKKRAASVKDVLNAGNI	174
DB	166	KETAGTNGDTYVHLNGISSTLTDLMLNTGATTNTVNDVTDDEKKRAASVKDVLNAGNI	225
QY	175	KGVRPGTTASDNVDFRTYDVEFLSADTKTTTVNVEESKDKGKTEVIGAKTSYIKED	234
DB	226	KGVRPGTTASDNVDFRTYDVEFLSADTKTTTVNVEESKDKGKTEVIGAKTSYIKED	285
QY	235	GKLVYTKGKGENSGSTDEGEGLVTAKEVIDAVNKGWRRKTTTANGOTGQADKFEITYSG	294
DB	286	GKLVYTKGKGENSGSTDEGEGLVTAKEVIDAVNKGWRRKTTTANGOTGQADKFEITYSG	345
QY	295	TKVTFASGNGTTATYVSKDDOGNITVYDVNVGDALNVNOLONGNLDKSKAVAGSSGKYI	354
DB	346	TNVTTFASGKGTATYVSKDDOGNITVYDVNVGDALNVNOLONGNLDKSKAVAGSSGKYI	405
QY	355	SGNVSPSKGKDETVNINAGNIEITRNGKNIDITSMTPQSSVSLGAGADAPTLISYDD	414
DB	406	SGNVSPSKGKDETVNINAGNIEITRNGKNIDITSMTPQSSVSLGAGADAPTLISYDD	465
QY	415	EGALNVGSKDANKPVRTINVAAGVEGDVTNVAQLKGYAQNINNRIDVNVNGNARAGIAQA	474
DB	466	D-ALNVGSKDANKPVRTINVAAGVEGDVTNVAQLKGYAQNINNRIDVNVNGNARAGIAQA	524
QY	475	IATAGLVQAYLPGKSMMAIGGGTYLGEAGYALGYSSISAGNWIITKGTASGNSRGHFGAS	534
DB	525	IATAGLVQAYLPGKSMMAIGGGTYLGEAGYALGYSSISDGGNWITKGTASGNSRGHFGAS	584
QY	535	ASVGYQW 541	
DB	585	ASVGYQW 591	

Search completed: October 6, 2003, 09:35:55
 Job time : 16.4674 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:05:45 : Search time 44.0542 Seconds
(without alignments)
1848.329 Million cell updates/sec

Title: US-09-771-382-24

Perfect score: 2602

Sequence: 1 MNKRYRIMWSALNMAWAVS.....TASGNSNGHFGASASVGYCW 513

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2602	100.0	513	22 AAU06183	N. meningitidis H4
2	2552.5	98.1	592	22 AAY3744	A surface protein
3	2552.5	98.1	592	22 AAU06172	N. meningitidis H4
4	2472	95.0	599	20 AAY3743	A surface protein
5	2472	95.0	599	22 AAU06176	N. meningitidis H3
6	2460.5	94.6	598	20 AAY3742	A surface protein
7	2460.5	94.6	598	22 AAU06177	N. meningitidis H1
8	2456.5	94.4	512	22 AAU06182	N. meningitidis PM
9	2451.5	94.2	598	20 AAY3738	A surface protein

10	2451.5	94.2	598	22 AAU06178	N. meningitidis BZ
11	2448.5	94.1	594	22 AAY3739	A surface protein
12	2448.5	94.1	594	22 AAU06179	N. meningitidis BZ
13	2409.5	92.6	594	20 AAY3740	A surface protein
14	2409.5	92.6	594	21 AAY57044	BASB029 amino acid
15	2409.5	92.6	594	22 AAU06174	N. meningitidis EG
16	2408	92.5	591	21 AAY57045	BASB029 amino acid
17	2407	92.5	591	20 AAY37202	Amino acid sequenc
18	2407	92.5	591	20 AAY37346	A surface protein
19	2407	92.5	591	22 AAU06171	N. meningitidis PM
20	2402.5	92.3	592	20 AAY3737	A surface protein
21	2395	92.0	591	22 AAY3741	A surface protein
22	2395	92.0	591	22 AAU06175	N. meningitidis EG
23	2351.5	90.4	592	22 AAU06180	N. meningitidis BZ
24	2315.5	89.0	592	20 AAY27203	Amino acid sequenc
25	2314	88.9	589	20 AAY3745	A surface protein
26	2314	88.9	589	22 AAU06173	N. meningitidis P2
27	2255.5	86.7	589	22 AAU06186	N. meningitidis PM
28	2106.5	81.0	604	22 AAU06181	N. meningitidis su
29	2055	79.0	433	22 AAU06185	N. meningitidis PM
30	1909	73.4	407	22 AAU06184	N. meningitidis PM
31	981.5	37.7	1094	21 AAB23858	Haemophilus influe
32	966.5	37.1	1098	17 AAR9392	Haemophilus adhesi
33	941.5	36.2	2411	21 AAB33860	Haemophilus influe
34	939.5	36.1	2353	17 AAR9393	Haemophilus adhesi
35	761	29.2	679	21 AAR9394	Haemophilus adhesi
36	761	29.2	679	21 AAB23855	Haemophilus influe
37	728.5	28.0	245	20 AAY27201	Amino acid sequenc
38	685.5	26.3	1002	21 AAB23854	Haemophilus influe
39	668.5	25.7	1004	21 AAB23857	Haemophilus influe
40	580	22.3	116	21 AAB37832	Neisserial conserv
41	562.5	21.6	1104	21 AAB23856	Haemophilus influe
42	562.5	21.6	1104	21 AAB37859	Haemophilus influe
43	526.5	20.2	298	24 AAB30477	Haemophilus influe
44	379	14.6	2314	22 AAB69136	M. catarrhalis les
45	378.5	14.5	2139	24 AAB71294	M. catarrhalis sur

ALIGNMENTS

RESULT 1	AAU06183	standard; Protein; 513 AA.
ID	AAU06183	
AC	AAU06183;	
XX	24-OCT-2001 (first entry)	
DT		
XX		
DE	N. meningitidis H41 Nhma deletion mutant.	
XX		
KW	Surface antigen Nhma; meningococcal disease; meningitis vaccine;	
KW	mutant; muten.	
XX		
OS	Neisseria meningitidis strain H41.	
XX		
FT	Synthetic.	
FT		
FT	Key	Location/Qualifiers
FT	Peptide	1..51
FT	Protein	/label= signal_peptide
FT		52..513
FT		/label= Mature_Nhma_deletion_mutant
FT		/note= "Predicted mature protein, specifically claimed in claim 12"
FT		
FT		
PN	WO200155182-A1.	
XX		
XX	02-AUG-2001.	
PD		
XX		
XX	25-JAN-2001; 2001WO-AU00069.	
PF		
XX	25-JAN-2000; 2000US-0177917.	
PR		
XX		

PA (UYOU) UNIV QUEENSLAND.
XX
PI Peak IRA, Jennings MP;
XX
XX
DR WPI: 2001-488774/53.
DR N-PSDB; AAS09173.
XX
XX New Nhma surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 12, Fig 6: 91pp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhma
CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence represents N. meningitidis strain H41 surface
CC antigen Nhma deletion mutant.
XX
XX

SQ Sequence 513 AA;

Query Match 100.0%; Score 2602; DB 22; Length 513;
Best Local Similarity 100.0%; Pred. No. 4, 7e-153;
Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKTYRIINMSALNANAVASELNRNHTKRASATVKTAVLATLLFATVQANATDETGILNV 60
DB 1 MNKTYRIINMSALNANAVASELNRNHTKRASATVKTAVLATLLFATVQANATDETGILNV 60
QY 61 ETEKLSFGANGKAKVNIISDTKGLNFAKETAGTNGDTTVHLNGISLTLDMLNTGATTNV 120
DB 61 ETEKLSFGANGKAKVNIISDTKGLNFAKETAGTNGDTTVHLNGISLTLDMLNTGATTNV 120
QY 121 TNDNVVDDEKKRAASKVDYLNAGMNIKGVPCTTASNDVFVETVDFEFLSADTKTNY 180
DB 121 TNDNVVDDEKKRAASKVDYLNAGMNIKGVPCTTASNDVFVETVDFEFLSADTKTNY 180
QY 181 NVESKDNKGKTEYKIGAKTSVIEKDKLVTGKKGENGSSSTDEGEGLVTAKEVIDAVNK 240
DB 181 NVESKDNKGKTEYKIGAKTSVIEKDKLVTGKKGENGSSSTDEGEGLVTAKEVIDAVNK 240
QY 241 AGARMKTTTANGTGQADKFEYTSCTKYTFASGNGTTATVSKDDGNTITVKYDVNGDA 300
DB 241 AGARMKTTTANGTGQADKFEYTSCTKYTFASGNGTTATVSKDDGNTITVKYDVNGDA 300
QY 301 LANNQLONSGWNIDSLAAGSSSGKVIISGKMGKDETVNINAGNNIEITRNKNIDI 360
DB 301 LANNQLONSGWNIDSLAAGSSSGKVIISGKMGKDETVNINAGNNIEITRNKNIDI 360
QY 361 AFSMTPQFSSSVISLIGAGADAPTLISVDEGALNVGSKDANKPVRTTNVAPGVKEGDVTNVAQ 420
DB 361 AFSMTPQFSSSVISLIGAGADAPTLISVDEGALNVGSKDANKPVRTTNVAPGVKEGDVTNVAQ 420
QY 421 LKGVANQNLNRIDNVGNARAGIAQALATAGLVQATLPKGSMAIGGGITLGAGTAIGY 480
DB 421 LKGVANQNLNRIDNVGNARAGIAQALATAGLVQATLPKGSMAIGGGITLGAGTAIGY 480
QY 481 SSSAGCNMIITKGTASGNSRGHFGASASYGYOW 513
DB 481 SSSAGCNMIITKGTASGNSRGHFGASASYGYOW 513

RESULT 2
AAZ3744
ID AAZ3744 standard; protein; 592 AA.
XX

AC AAZ3744;
XX
XX 08-SEP-1999 (first entry)
XX
XX
DE A surface protein of Neisseria meningitidis.
XX
XX
XX Surface protein; surface glycoprotein; infection; vaccine;
KM Immunoreactive peptide.
XX
XX Neisseria meningitidis.
XX
XX WO9931132-A1.
XX
XX 24-JUN-1999.
XX
XX 14-DEC-1998; 98WO-AU01031.
XX
XX 12-DEC-1997; 97GB-0026398.
XX
XX (ISIS-) ISIS INNOVATION LTD.
PA (UYOU) UNIV QUEENSLAND.
XX
XX Jennings MP, Moxon ER, Peak IRA;
PI
XX
XX WPI: 1999-418754/35.
DR N-PSDB; AAX85796.
XX
XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
PT
XX Claim 1; Page 118-120; 132pp; English.
XX

CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
XX

SQ Sequence 592 AA;

Query Match 98.1%; Score 2552.5; DB 20; Length 592;
Best Local Similarity 86.7%; Pred. No. 6, 4e-150;
Matches 513; Conservative 0; Mismatches 0; Indels 79; Gaps 1;

QY 1 MNKTYRIINMSALNANAVASELNRNHTKRASATVKTAVLATLLFATVQANATDE----- 54
DB 1 MNKTYRIINMSALNANAVASELNRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
QY 55 ----- 54
DB 55 ----- 54
QY 61 ESVQRSVGSIQASMEGSELEETISLMTNDSKEPDPYIVYTLKAGDNLIKQNTNENT 120
DB 61 ESVQRSVGSIQASMEGSELEETISLMTNDSKEPDPYIVYTLKAGDNLIKQNTNENT 120
QY 55 -----TGLINVEETKLSFGANGKAKVNIISDTKGLNFAKETAGTNGDTTVHLN 101
DB 55 -----TGLINVEETKLSFGANGKAKVNIISDTKGLNFAKETAGTNGDTTVHLN 101
QY 102 GIGSTLTLDMLNTGATTNTVNDVTDDEKKRAASVDYLNAGNNIKGVKPGTTASDNVDF 161
DB 102 GIGSTLTLDMLNTGATTNTVNDVTDDEKKRAASVDYLNAGNNIKGVKPGTTASDNVDF 161
QY 181 GIGSTLTLDMLNTGATTNTVNDVTDDEKKRAASVDYLNAGNNIKGVKPGTTASDNVDF 240
DB 181 GIGSTLTLDMLNTGATTNTVNDVTDDEKKRAASVDYLNAGNNIKGVKPGTTASDNVDF 240
QY 162 VRTDYVVEFLSAPTCTTNTVNESKDNKTEYKIGAKTSVIEKDKLVTGKKGENGSS 221
DB 162 VRTDYVVEFLSAPTCTTNTVNESKDNKTEYKIGAKTSVIEKDKLVTGKKGENGSS 221
QY 241 VRTDYVVEFLSAPTCTTNTVNESKDNKTEYKIGAKTSVIEKDKLVTGKKGENGSS 300
DB 241 VRTDYVVEFLSAPTCTTNTVNESKDNKTEYKIGAKTSVIEKDKLVTGKKGENGSS 300
QY 222 TDEGEGLVTAKEVIDAVNKRAGMRKTTTANGTGQADKFEYTSCTKYTFASGNGTTATYV 281
DB 222 TDEGEGLVTAKEVIDAVNKRAGMRKTTTANGTGQADKFEYTSCTKYTFASGNGTTATYV 281
QY 301 TDEGEGLVTAKEVIDAVNKRAGMRKTTTANGTGQADKFEYTSCTKYTFASGNGTTATYV 360
DB 301 TDEGEGLVTAKEVIDAVNKRAGMRKTTTANGTGQADKFEYTSCTKYTFASGNGTTATYV 360
QY 282 SKDDGNTITVKYDVNGDALNVNQLONSGWNIDSLAAGSSSGKVIISGKMGKDETV 341
DB 282 SKDDGNTITVKYDVNGDALNVNQLONSGWNIDSLAAGSSSGKVIISGKMGKDETV 341

```
Db      361 SKDDGNTIVKDYVNVGALNVNQLONGSGWNLDSKAVAGSSGKVISGNVSPSKGMDPTV 420
Oy      342 NINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSVDEGALNYSKRNKPNV 401
Db      421 NINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSVDEGALNYSKRNKPNV 480
Oy      402 RITNVAPGVKEGDVTNVNQLKGVAQNLNRRIDNVNGNARAGIAQAIAATAGLVQAVLPKGS 461
Db      481 RITNVAPGVKEGDVTNVNQLKGVAQNLNRRIDNVNGNARAGIAQAIAATAGLVQAVLPKGS 540
Oy      462 MMAIGGTYLGBAGYAIGYSSISAGGNMIITKTASGNSRGHFGASASVGYQM 513
Db      541 MMAIGGTYLGBAGYAIGYSSISAGGNMIITKTASGNSRGHFGASASVGYQM 592

RESULT 3
AAU06172
ID      AAU06172 standard; Protein: 592 AA.
AC      AAU06172;
XX      24-OCT-2001 (first entry)
XX      N. meningitidis H41 surface antigen NhbA polypeptide sequence.
XX      Surface antigen NhbA; meningococcal disease; meningitis vaccine.
XX      Neisseria meningitidis strain H41.
XX      Key
FH      Location/Qualifiers
FH      Peptide
FT      1..51
FT      /label= Signal_peptide
FT      1..50
FT      /label= C1
FT      /note= "Conserved region 1"
FT      51..102
FT      /label= V1
FT      /note= "Variable region 1"
FT      52..592
FT      /label= Mature_NhbA
FT      /note= "Predicted mature protein, specifically
FT      claimed in claim 12"
FT      103..114
FT      /label= C2
FT      /note= "Conserved region 2"
FT      115..124
FT      /label= V2
FT      /note= "Variable region 2"
FT      125..188
FT      /label= C3
FT      /note= "Conserved region 3"
FT      189..210
FT      /label= V3
FT      /note= "Variable region 3"
FT      211..229
FT      /label= C4
FT      /note= "Conserved region 4"
FT      230..236
FT      /label= V4
FT      /note= "Variable region 4"
FT      237..592
FT      /label= C5
FT      /note= "Conserved region 5"
XX      WO20015182-A1.
XX      02-AUG-2001.
XX      25-JAN-2001; 2001WO-AU00069.
XX      25-JAN-2000; 2000US-0177917.
```

```
PA      (UYOU ) UNIV QUEENSLAND.
XX      PI      Peak IRA, Jennings MP;
XX      DR      WPI: 2001-488774/53.
XX      N-PSDB: AAS09162.
XX      PT      New NhbA surface antigen polypeptides and polynucleotides from
XX      PT      Neisseria meningitidis, useful in producing vaccines for treating or
XX      PT      preventing broad spectrum of Neisseria meningitidis -
XX      PS      Claim 9; Fig 1; 91pp; English.
XX      CC      The present invention relates to the isolation of novel Neisseria
XX      CC      meningitidis mutant polypeptides of the surface antigen NhbA
XX      CC      (AAU06182-AAU06186). The modified or mutant NhbA polypeptides are
XX      CC      characterised by deletions of non-conserved amino acids, particularly
XX      CC      the deletion of variable regions. The deletion mutants are useful in
XX      CC      diagnostics, therapeutic and prophylactic vaccines against a broader
XX      CC      spectrum of N. meningitidis, and in designing and/or screening of
XX      CC      immunisations. The mutant proteins when used as a vaccine can effectively
XX      CC      immunise against a broader spectrum of N. meningitidis strains than
XX      CC      would be expected from a corresponding wild-type surface antigen.
XX      CC      The present sequence representing the wild type surface antigen NhbA
XX      CC      from N. meningitidis strain H41 is 1 of 10 NhbA polypeptide sequences
XX      CC      (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX      CC      the present invention.
XX      SO      Sequence 592 AA:
XX      Query Match 98.1%; Score 2552.5; DB 22; Length 592;
XX      Best Local Similarity 86.7%; Pred. No. 6.4e-150;
XX      Matches 513; Conservative 0; Mismatches 0; Indels 79; Gaps 1;
Oy      1 MNKIYRIIWSNALNMAVAVSELTFRNHRKASATVKTAVLATLLEATVOANATDF----- 54
Db      1 MNKIYRIIWSNALNMAVAVSELTFRNHRKASATVKTAVLATLLEATVOANATDEDEEEL 60
Oy      55 ----- 54
Db      61 ESVQRSVVGSIQASMEGSEVELETTISLMTNDSKEFVDPYIVVTLKAGNLIKONTNENT 120
Oy      55 -----TGLINVEETEKLSEFGANGKRVNIISDTKGLNFAKETAGTNGDTVHLN 101
Db      121 NASSFTYSLEKKDLTGLINVEETEKLSEFGANGKRVNIISDTKGLNFAKETAGTNGDTVHLN 180
Oy      102 GIGSTLTDMLNTGATTVNTDNDVTDDEKKRAASYKDVNLNAGWNIKGVKPGTTASDNDVF 161
Db      181 GIGSTLTDMLNTGATTVNTDNDVTDDEKKRAASYKDVNLNAGWNIKGVKPGTTASDNDVF 240
Oy      162 VRTYDVEFLSADPFTTVNVNESKONGKKEVKKIGAKSVYKEKKGKLVTKGGENSS 221
Db      241 VRTYDVEFLSADPFTTVNVNESKONGKKEVKKIGAKSVYKEKKGKLVTKGGENSS 300
Oy      222 TDEGGLVTAKEVIDAVNKAQWPKTKTANGOTGADPFEVTSCTKYTFASGNGTATV 281
Db      301 TDEGGLVTAKEVIDAVNKAQWPKTKTANGOTGADPFEVTSCTKYTFASGNGTATV 360
Oy      282 SKDDGNTIVKDYVNVGALNVNQLONGSGWNLDSKAVAGSSGKVISGNVSPSKGMDPTV 341
Db      361 SKDDGNTIVKDYVNVGALNVNQLONGSGWNLDSKAVAGSSGKVISGNVSPSKGMDPTV 420
Oy      342 NINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSVDEGALNYSKRNKPNV 401
Db      421 NINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSVDEGALNYSKRNKPNV 480
Oy      402 RITNVAPGVKEGDVTNVNQLKGVAQNLNRRIDNVNGNARAGIAQAIAATAGLVQAVLPKGS 461
Db      481 RITNVAPGVKEGDVTNVNQLKGVAQNLNRRIDNVNGNARAGIAQAIAATAGLVQAVLPKGS 540
Oy      462 MMAIGGTYLGBAGYAIGYSSISAGGNMIITKTASGNSRGHFGASASVGYQM 513
Db      541 MMAIGGTYLGBAGYAIGYSSISAGGNMIITKTASGNSRGHFGASASVGYQM 592
```

```
RESULT 4
AA023743
ID   AAY23743 standard; protein, 599 AA.
XX
XX   AAY23743;
XX
XX   08-SEP-1999 (first entry)
XX
XX   A surface protein of Neisseria meningitidis.
DE
XX
XX   Surface protein; surface glycoprotein; infection; vaccine;
KW   immunoreactive peptide.
XX
XX   Neisseria meningitidis.
OS
XX
XX   WO931132-A1.
XX
XX   24-JUN-1999.
XX
XX   14-DEC-1998; 98WO-AU01031.
XX
XX   12-DEC-1997; 97GB-0026398.
XX
XX   (ISIS-) ISIS INNOVATION LTD.
PA   (UYOU) UNIV QUEENSLAND.
XX
XX   Jennings MP, Moxon ER, Peak IRA;
PI   WPI, 1999-418754/35.
XX
XX   N-PSDB; AAX85795.
DR
XX
XX   Neisseria meningitidis surface proteins useful for treating N.
PT   meningitidis infections
XX
XX   Claim 1; Page 114-115, 132pp; English.
PS
XX
XX   The present sequence represents a surface protein of Neisseria
CC   meningitidis which is approximately 62 kDa. The N. meningitidis
CC   surface glycoproteins, nucleic acids, the primers and optionally
CC   a thermostable polymerase, or antibodies are useful in a kit for
CC   the detection or diagnosis of N. meningitidis infection in humans.
CC   The N. meningitidis surface glycoproteins can also be used to
CC   prevent or treat N. meningitidis infection in humans, especially
CC   in the form of vaccines. The proteins and antibodies can also
CC   be used to identify immunoreactive peptides.
XX
XX
XX   Sequence 599 AA;
SQ
XX
XX   Query Match 95.0%; Score 2472; DB 20; Length 599;
XX   Best Local Similarity 83.1%; Pred. No. 6, 2e-145;
XX   Matches 498; Conservative 5; Mismatches 10; Indels 86; Gaps 1;
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XX   1 MNKIYIINNSALINAVAVSELTRNHTKRASATVKAVALATLLFATVQANATDE----- 54
DB   1 MNKIYRIINNSALINAVAVSELTRNHTKRASATVKAVALATLLFATVQANATDEDEEEL 60
XX
XX   55 -----
DB   61 EPIVRSALVLOEMIDKEGNGENESTGNIGMSIYYDNHNTLHGATVTLKAGDNLKIKONTN 120
XX
XX   55 -----TGLINETERKLSFGANGKKVNIISDPRKGLNFAKETAGTNG 94
DB   121 KMTNENTNDSSTFYSLKDLTDLTSVETEKLSFGANGKNVNIISDPRKGLNFAKETAGTNG 180
XX
XX   95 DTTVHLNGIGSTLTDMLTNGATNTVNDVTDDEKKRAASVQVNLNAGNNIKGVKPGTT 154
DB   181 DTTVHLNGIGSTLTDLTLNTGATNTVNDVTDDEKKRAASVQVNLNAGNNIKGVKPGTT 240
XX
XX   155 ASDNVDFVRYTDFVEFLSADFTKTTYNVESKONGKTEYVIGAKTSVIREKDKLVYGGK 214
DB   241 ASDNVDFVRYTDFVEFLSADFTKTTYNVESKONGKTEYVIGAKTSVIREKDKLVYGGK 300
```

```
XX
XX   215 KGENGSSTDEGEGLVYAKAEVIDAVNKGMRMKTTTTANGQTGQADKEFEYVTSKTVTFASG 274
DB   301 KGENGSSTDEGEGLVYAKAEVIDAVNKGMRMKTTTTANGQTGQADKEFEYVTSKTVTFASG 360
XX
XX   275 NGTTATVSKDDGCGNTTKYDYNVGDALNNQLONSGMNLDKRAVASSGKVIISGNVSPSK 334
DB   361 KGTATATVSKDDGCGNTTKYDYNVGDALNNQLONSGMNLDKRAVASSGKVIISGNVSPSK 420
XX
XX   335 GKMDETVNIINAGNIEITRNGKNIDATSWTPQESSVSLGAGADPTLSYDDEGALNVGS 394
DB   421 GKMDETVNIINAGNIEITRNGKNIDATSWTPQESSVSLGAGADPTLSYDDEGALNVGS 480
XX
XX   395 KDANKPVRITNVAAPGVKEGDVTNVAQLKGYAQNLRNIDVNGMARAGIAQAATATAGLVQ 454
DB   481 KDANKPVRITNVAAPGVKEGDVTNVAQLKGYAQNLRNIDVNGMARAGIAQAATATAGLVQ 540
XX
XX   455 AYLPGRKSMAIGGGITLGEAGTAIGYSSISAGSNMIIKGTASGNSGHHGASASVGYOW 513
DB   541 AYLPGRKSMAIGGGITRGEAGTAIGYSSISDGGNWIIRKGTASGNSGHHGASASVGYOW 599
XX
XX
XX   RESULT 5
XX   ID   AAU06176 standard; Protein, 599 AA.
XX
XX   AAU06176;
XX
XX   24-OCT-2001 (first entry)
XX
XX   N. meningitidis H38 surface antigen NhbA polypeptide sequence.
DE
XX
XX   Surface antigen NhbA; meningococcal disease; meningitis vaccine.
XX
XX   Neisseria meningitidis strain H38.
OS
XX
XX   Location/Qualifiers
FH   Key
FT   Region
FT   /label= C1
FT   /note= "Conserved region 1"
FT   51..105
FT   /label= V1
FT   /note= "Variable region 1"
FT   106..117
FT   /label= C2
FT   /note= "Conserved region 2"
FT   118..131
FT   /label= V2
FT   /note= "Variable region 2"
FT   132..195
FT   /label= C3
FT   /note= "Conserved region 3"
FT   196..217
FT   /label= V3
FT   /note= "Variable region 3"
FT   218..236
FT   /label= C4
FT   /note= "Conserved region 4"
FT   237..243
FT   /label= V4
FT   /note= "Variable region 4"
FT   244..599
FT   /label= C5
FT   /note= "Conserved region 5"
XX
XX   WO200155182-A1.
XX
XX   02-AUG-2001.
XX
XX   25-JAN-2001; 2001MO-AU00069.
XX
XX   25-JAN-2000; 2000US-0177917.
XX
```

PA (UYOU) UNIV QUEENSLAND.
 XX
 XX Peak IRA, Jennings MP;
 XX
 DR WPI: 2001-488774/53.
 DR N-PSDB: AAS09166.
 XX
 XX New Nhha surface antigen polypeptides and polynucleotides from
 PT Neisseria meningitidis, useful in producing vaccines for treating or
 PT preventing broad spectrum of Neisseria meningitidis -
 XX
 XX Claim 9, Fig 1; 91pp; English.
 PS
 XX
 CC The present invention relates to the isolation of novel Neisseria
 CC meningitidis mutant polypeptides of the surface antigen Nhha
 CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
 CC characterised by deletions of non-conserved amino acids, particularly
 CC the deletion of variable regions. The deletion mutants are useful in
 CC diagnostics, therapeutic and prophylactic vaccines against a broader
 CC spectrum of N. meningitidis, and in designing and/or screening of
 CC medicaments. The mutant proteins when used as a vaccine can effectively
 CC immunise against a broader spectrum of N. meningitidis strains than
 CC would be expected from a corresponding wild-type surface antigen.
 CC The present sequence representing the wild type surface antigen Nhha
 CC from N. meningitidis strain H38 is 1 of 10 Nhha polypeptide sequences
 CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
 CC the present invention.
 CC
 XX
 SQ Sequence 599 AA:
 Query Match 95.0%; Score 2472; DB 22; Length 599;
 Best Local Similarity 83.1%; Pred. No. 6-2e-145;
 Matches 498; Conservative 5; Mismatches 10; Indels 86; Gaps 1;
 QY 1 MNKIYRIIWSALNMAVAVSELTNRHTRASATVATAVLATLLEFATVOANATDE----- 54
 DB 1 MNKIYRIIWSALNMAVAVSELTNRHTRASATVATAVLATLLEFATVOANATDEEBEL 60
 QY 55 ----- 54
 DB 61 EPPVRSALVLOPMIDKEGENESGNGISYIYDNLHATLGATVYTLKAGDNLKQNTN 120
 QY 55 -----TGLINVEETKLSFGANGKRVNIISDTKGLNFAKETAGTNG 94
 DB 121 KNTNENTNDSSEFTYSLKKDLFDLTSVETEKLSFGANGKRVNITSDTKGLNFAKETAGTNG 180
 QY 95 DTYHLNGIGSTLTDMLNTGATNTVNDVNTDDEKRAASYKVDVLANGMNKGVPCTT 154
 DB 181 DTYHLNGIGSTLTDMLNTGATNTVNDVNTDDEKRAASYKVDVLANGMNKGVPCTT 240
 QY 155 ASDNVDFFVRYTDYVEFLSADTKRTTNTVNESKDNCKKTEVKIGAKTSVIREKDGKLVYTGK 214
 DB 241 ASDNVDFFVRYTDYVEFLSADTKRTTNTVNESKDNCKKTEVKIGAKTSVIREKDGKLVYTGK 300
 QY 215 KGENGSSTDEEGVLTAKEVIDAVNKAQMRKTTTANGOTGOADKFEETVTSQTVTFASG 274
 DB 301 KGENGSSTDEEGVLTAKEVIDAVNKAQMRKTTTANGOTGOADKFEETVTSQTVTFASG 360
 QY 275 NGTATVTSKDDOGNTVTVYDVNVDALNVNOLNSGMWLSKAAVAGSSGKVIISGNVSPSK 334
 DB 361 KGTATVTSKDDOGNTVTVYDVNVDALNVNOLNSGMWLSKAAVAGSSGKVIISGNVSPSK 420
 QY 335 GKMDFTVINAGNNNEITRNKKNIDIASMTPOSSVSLGAGADAPTLSTVDEGLANGS 394
 DB 421 GKMDFTVINAGNNNEITRNKKNIDIASMTPOSSVSLGAGADAPTLSTVDEGLANGS 480
 QY 395 KDANKPVRITNVAPGVEKEDYTNVAQLKVAONLNNDVNGNARAGIAAIAATAGLVQ 454
 DB 481 KDANKPVRITNVAPGVEKEDYTNVAQLKVAONLNNDVNGNARAGIAAIAATAGLVQ 540
 QY 455 AYLPEKSMMAIGGGYLGEGAGYAGYSSISAGGNWITIGTASGNSRHFAGSASGYOM 513
 DB 541 AYLPEKSMMAIGGGYLGEGAGYAGYSSISAGGNWITIGTASGNSRHFAGSASGYOM 599

RESULT 6
 AAU23742
 ID AAU23742 standard; Protein; 598 AA.
 XX
 XX AAU23742;
 AC
 XX 08-SEP-1999 (first entry)
 DT
 XX A surface protein of Neisseria meningitidis.
 DE
 XX Surface protein; surface glycoprotein; infection; vaccine;
 XX immunoreactive peptide.
 KW
 XX Neisseria meningitidis.
 OS
 XX WO931132-A1.
 PN
 XX 24-JUN-1999.
 PD
 XX 14-DEC-1998; 98WO-AU01031.
 PF
 XX 12-DEC-1997; 97GB-0026398.
 PR
 XX (ISIS-) ISIS INNOVATION LTD.
 PA (UYOU) UNIV QUEENSLAND.
 XX
 XX Jennings MP, Moxon ER, Peak IRA;
 PI
 DR WPI: 1999-418754/35.
 DR N-PSDB: AAX85794.
 XX
 PT Neisseria meningitidis surface proteins useful for treating N.
 PS meningitidis infections
 XX
 XX Claim 1; Page 108-110; 132pp; English.
 CC
 CC The present sequence represents a surface protein of Neisseria
 CC meningitidis which is approximately 62 kDa. The N. meningitidis
 CC surface glycoproteins, nucleic acids, the primers and optionally
 CC a thermostable polymerase, or antibodies are useful in a kit for
 CC the detection or diagnosis of N. meningitidis infection in humans.
 CC The N. meningitidis surface glycoproteins can also be used to
 CC prevent or treat N. meningitidis infection in humans, especially
 CC in the form of vaccines. The proteins and antibodies can also
 CC be used to identify immunoreactive peptides.
 CC
 XX
 SQ Sequence 598 AA:
 Query Match 94.6%; Score 2460.5; DB 20; Length 598;
 Best Local Similarity 82.9%; Pred. No. 3-2e-144;
 Matches 496; Conservative 4; Mismatches 13; Indels 85; Gaps 1;
 QY 1 MNKIYRIIWSALNMAVAVSELTNRHTRASATVATAVLATLLEFATVOANATDE----- 54
 DB 1 MNKIYRIIWSALNMAVAVSELTNRHTRASATVATAVLATLLEFATVOANATDDDDLYLE 60
 QY 55 ----- 54
 DB 61 PVORTAVVLSFRSDEKGTGEKEDTSNMVAVFDEKRVLLKAGATLTLKAGDNLKIKONTNE 120
 QY 55 -----TGLINVEETKLSFGANGKRVNIISDTKGLNFAKETAGTNGD 95
 DB 121 NTNENTNDSSEFTYSLKKDLFDLTSVETEKLSFGANGKRVNITSDTKGLNFAKETAGTNGD 180
 QY 96 TTVHLNGIGSTLTDMLNTGATNTVNDVNTDDEKRAASYKVDVLANGMNKGVPCTTA 155
 DB 181 PTVHLNGIGSTLTDMLNTGATNTVNDVNTDDEKRAASYKVDVLANGMNKGVPCTTA 240
 QY 156 SDNVDFFVRYTDYVEFLSADTKRTTNTVNESKDNCKKTEVKIGAKTSVIREKDGKLVYTGK 215
 DB 241 SDNVDFFVRYTDYVEFLSADTKRTTNTVNESKDNCKKTEVKIGAKTSVIREKDGKLVYTGK 300


```
RESULT 8
AAU06182
ID AAU06182 standard. Protein: 512 AA.
XX
XX AAU06182;
AC
XX
XX 24-OCT-2001 (first entry)
DT
XX
XX N. meningitidis PMC21 Nhma deletion mutant #1.
DE
XX
XX Surface antigen Nhma; meningococcal disease; meningitis vaccine;
KW mutant; mutein.
XX
XX Neisseria meningitidis strain PMC21.
OS Synthetic.
XX
XX
XX Key Location/Qualifiers
XX Peptide 1..51
XX Protein /label= Signal_peptide
XX /label= Mature_Nhma_deletion_mutant_#1
XX /note= "Predicted mature protein, specifically
XX claimed in claim 12"
XX
XX WO20015182-A1.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU00069.
XX
XX 25-JAN-2000; 2000US-0177917.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX
XX Peak IRA, Jennings MP;
XX
XX WPI: 2001-488774/53.
XX
XX N-PSDB: AAS09172.
XX
XX
XX New Nhma surface antigen polypeptides and polynucleotides from
XX Neisseria meningitidis, useful in producing vaccines for treating or
XX preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 12; Fig 5; 91pp; English.
XX
XX
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen Nhma
XX (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are
XX characterised by deletions of non-conserved amino acids, particularly
XX the deletion of variable regions. The deletion mutants are useful in
XX diagnostics, therapeutic and prophylactic vaccines against a broader
XX spectrum of N. meningitidis, and in designing and/or screening of
XX medicaments. The mutant proteins when used as a vaccine can effectively
XX immunise against a broader spectrum of N. meningitidis strains than
XX would be expected from a corresponding wild-type surface antigen.
XX The present sequence represents N. meningitidis strain PMC21 surface
XX antigen Nhma deletion mutant #1.
XX
XX Sequence 512 AA:
SQ
XX
XX Query Match 94.4%; Score 2456.5; DB 22; Length 512;
XX Best Local Similarity 95.3%; Pred No. 4.6e-144;
XX Matches 489; Conservative 5; Mismatches 16; Indels 1; Gaps 1;
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```
QY 121 TNDNVTDDKKRAASVKDYLNAGMNIKGYPGTTASDNDVFRVYDTVEFLSADTKTTTV 180
DB 121 TNDNVTDDKKRAASVKDYLNAGMNIKGYPGTTASDNDVFRVYDTVEFLSADTKTTTV 180
QY 181 NVESKDNKGKTEVKIGAKTSVIREKDKLVYTGKRGENGSSYDEEGELVTAKEVIDAVNK 240
DB 181 NVESKDNKGKTEVKIGAKTSVIREKDKLVYTGKRGENGSSYDEEGELVTAKEVIDAVNK 240
QY 241 AGMRKTTTANGQTOADKFEVYTGKVTAFPSGNGTTATVSKDDOGNTTVYDVNAGDA 300
DB 241 AGMRKTTTANGQTOADKFEVYTGKVTAFPSGNGTTATVSKDDOGNTTVYDVNAGDA 300
QY 301 LNVNOLONGMNLDSKAAVAGSSGKVTISGVNSPKKMPETVINAGNNIETRNKNIDI 360
DB 301 LNVNOLONGMNLDSKAAVAGSSGKVTISGVNSPKKMPETVINAGNNIETRNKNIDI 360
QY 361 ATSMTPPESSVSLGAGADAPTLSDVEGALNVGSKDANKPVRITNVAPGVKEGDYTNAAQ 420
DB 361 ATSMTPPESSVSLGAGADAPTLSDVEGALNVGSKDANKPVRITNVAPGVKEGDYTNAAQ 419
QY 421 LKGVANQNLNRRIDNVNNGNARRAGIAQAIATAGLVQAYLPKSKMAIIGGTYIGEAQYAI 480
DB 420 LKGVANQNLNRRIDNVNNGNARRAGIAQAIATAGLVQAYLPKSKMAIIGGTYIGEAQYAI 479
QY 481 SLSAGNMWIIKGTASGNSRGHFGASASVGYOW 513
DB 480 SLSIDGMWIIKGTASGNSRGHFGASASVGYOW 512
```

```
RESULT 9
AAU23738
ID AAU23738 standard. Protein: 598 AA.
XX
XX AAU23738;
XX
XX 08-SEP-1999 (first entry)
XX
XX A surface protein of Neisseria meningitidis.
XX
XX Surface protein; surface glycoprotein; infection; vaccine;
XX immunoreactive peptide.
XX
XX Neisseria meningitidis.
XX
XX WO9931132-A1.
XX
XX 24-JUN-1999.
XX
XX 14-DEC-1998; 98WO-AU01031.
XX
XX 12-DEC-1997; 97GB-0026398.
XX
XX (ISIS-) ISIS INNOVATION LTD.
XX (UYOU ) UNIV QUEENSLAND.
XX
XX Jennings MP, Moxon ER, Peak IRA;
XX
XX WPI: 1999-418754/35.
XX N-PSDB: AAX85790.
XX
XX Neisseria meningitidis surface proteins useful for treating N.
XX meningitidis infections
XX
XX Claim 1; Page 91-93; 132pp; English.
XX
XX
XX The present sequence represents a surface protein of Neisseria
XX meningitidis which is approximately 62 kDa. The N. meningitidis
XX surface glycoproteins, nucleic acids, the primers and optionally
XX a thermostable polymerase, or antibodies are useful in a kit for
XX the detection or diagnosis of N. meningitidis infection in humans.
XX The N. meningitidis surface glycoproteins can also be used to
XX prevent or treat N. meningitidis infection in humans, especially
```



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OY 96 TTVHLNGIGSTLTDLMLNTGATTNTNDNVTDDDEKKRAASYKDVNLNAGMNKGVAPGTTA 155
    |||||
Db 181 PTVHLNGIGSTLTDLTLNTGATTNTNDNVTDDDEKKRAASYKDVNLNAGMNKGVAPGTTA 240
OY 156 SDNVDFVRTYDVEFLSADTKTTTVNVESKDNKKTEVKGAKTSVIREKDKLVTKGKG 215
    |||||
Db 241 SDNVDFVRTYDVEFLSADTKTTTVNVESKDNKKTEVKGAKTSVIREKDKLVTKGKG 300
OY 216 GENSSDTEDEGGLVYAKFVIDAVNKGWRMKTNTTNGQTGQADKEFTVSGTKYTFASGN 275
    |||||
Db 301 GENSSDTEDEGGLVYAKFVIDAVNKGWRMKTNTTNGQTGQADKEFTVSGTKYTFASGN 360
OY 276 GTTATVSKDDGNITVYKDVVNGDALNVNOLNSGMNDSKRAVAGSSGKVISGNVSPSKG 335
    |||||
Db 361 GTTATVSKDDGNITVYKDVVNGDALNVNOLNSGMNDSKRAVAGSSGKVISGNVSPSKG 420
OY 336 KMDFTVNINAGNNIEITRNGKNIDIAISMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 395
    |||||
Db 421 KMDFTVNINAGNNIEITRNGKNIDIAISMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480
OY 396 DANKPVRTTNVAPGVKEGDVTNVNQLKGVAQNLNRRIDNVNGNARAGIAQAATAGLVQA 455
    |||||
Db 481 DANKPVRTTNVAPGVKEGDVTNVNQLKGVAQNLNRRIDNVNGNARAGIAQAATAGLVQA 540
OY 456 YLPGRKSMAAIGGCTYLGEGYGAIGYSSISAGGNWIIKGTASGNSRGHFGASASVGYQM 513
    |||||
Db 541 YLPGRKSMAAIGGCTYRGEGYGAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQM 598

```

RESULT 11

AAV23739

ID AAV23739 standard; Protein: 594 AA.

XX AC AAV23739;

DT 08-SEP-1999 (first entry)

DE A surface protein of Neisseria meningitidis.

KM Surface protein; surface glycoprotein; infection; vaccine;

OS Immunoreactive peptide.

XX OS Neisseria meningitidis.

PN W09931132-A1.

PD 24-JUN-1999.

PF 14-DEC-1998; 98MO-AU01031.

PR 12-DEC-1997; 97GB-0026398.

PA (ISIS-) ISIS INNOVATION LTD.

PA (UYOU) UNIV QUEENSLAND.

PI Jennings MP, Moxon ER, Peak IRA;

DR MPI: 1999-418754/35.

DR N-PSDB; AAX85791.

PT Neisseria meningitidis surface proteins useful for treating N.

PT meningitidis infections

PS Claim 1: Page 95-97; 132pp: English.

CC The present sequence represents a surface protein of Neisseria
 CC meningitidis which is approximately 62 kDa. The N. meningitidis
 CC surface glycoproteins, nucleic acids, the primers and optionally
 CC a thermostable polymerase, or antibodies are useful in a kit for
 CC the detection or diagnosis of N. meningitidis infection in humans.
 CC The N. meningitidis surface glycoproteins can also be used to
 CC prevent or treat N. meningitidis infection in humans, especially

CC in the form of vaccines. The proteins and antibodies can also
 CC be used to identify immunoreactive peptides.

SQ Sequence 594 AA:

Query Match 94.1%; Score 2448.5; DB 20; Length 594;
 Best Local Similarity 83.2%; Pred. No. 1.7e-143;
 Matches 494; Conservative 3; Mismatches 16; Indels 81; Gaps 1;

```

OY 1 MNKIRIITNSALNMAVASELIRNHTRASVTYATVALTLFFATVQANATDE----- 54
    |||||
Db 1 MNKIRIITNSALNMAVASELIRNHTRASVTYATVALTLFFATVQANATDDDLYLE 60
OY 55 ----- 54
Db 61 PVQRTAVVLSFRSDKEGTEGTEGSDSMWYVFEDEKRVLKACATILKAGDNLIKQNTNE 120
OY 55 -----TGLINWETEKLSFGANGKVNIIISDTRKGLNFAKETAGTNGDTTVH 99
    |||||
Db 121 NTNDSFTYSLKKDLDTLSVETEKLSFGANGKNVNIISDTRKGLNFAKETAGTNGDPTVH 180
OY 100 LMGISTLTDLMLNTGATTNTNDNVTDDDEKKRAASYKDVNLNAGMNKGVAPGTTASDNV 159
    |||||
Db 181 LMGISTLTDLMLNTGATTNTNDNVTDDDEKKRAASYKDVNLNAGMNKGVAPGTTASDNV 240
OY 160 DFTVTDVVEFLSADTKTTTVNVESKDNKKTEVKGAKTSVIREKDKLVTKGKGENG 219
    |||||
Db 241 DFTVTDVVEFLSADTKTTTVNVESKDNKKTEVKGAKTSVIREKDKLVTKGKGKDENG 300
OY 220 SSTDEGGLVYAKFVIDAVNKGWRMKTNTTANGQTGQADKEFTVSGTKYTFASGNGTTA 279
    |||||
Db 301 SSTDEGGLVYAKFVIDAVNKGWRMKTNTTANGQTGQADKEFTVSGTKYTFASGNGTTA 360
OY 280 TVSKDDGNITVYKDVVNGDALNVNOLNSGMNDSKRAVAGSSGKVISGNVSPSKGKDE 339
    |||||
Db 361 TVSKDDGNITVYKDVVNGDALNVNOLNSGMNDSKRAVAGSSGKVISGNVSPSKGKDE 420
OY 340 TVNINAGNNIEITRNGKNIDIAISMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANK 399
    |||||
Db 421 TVNINAGNNIEITRNGKNIDIAISMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANK 480
OY 400 PVRTTNVAPGVKEGDVTNVNQLKGVAQNLNRRIDNVNGNARAGIAQAATAGLVQAYLPG 459
    |||||
Db 481 PVRTTNVAPGVKEGDVTNVNQLKGVAQNLNRRIDNVNGNARAGIAQAATAGLVQAYLPG 540
OY 460 KSMAAIGGCTYLGEGYGAIGYSSISAGGNWIIKGTASGNSRGHFGASASVGYQM 513
    |||||
Db 541 KSMAAIGGCTYRGEGYGAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQM 594

```

RESULT 12

AAU06179

ID AAU06179 standard; Protein: 594 AA.

AC AAU06179;

DT 24-OCT-2001 (first entry)

DE N. meningitidis B2198 surface antigen Nhma polypeptide sequence.

KW Surface antigen Nhma; meningococcal disease; meningitis vaccine.

OS Neisseria meningitidis strain B2198.

XX Key Location/Qualifiers

FH 1..50

FT /label= C1

FT /note= "Conserved region 1"

FT Region 51..104

FT /label= V1

FT /note= "Variable region 1"

FT Region 105..116

FT /label= C2

FT		/note= "Conserved region 2"
ET	Region	117..126
FT		/label= V2
ET	Region	/note= "Variable region 2"
FT		127..190
ET	Region	/label= C3
FT		/note= "Conserved region 3"
ET	Region	191..212
FT		/label= V3
ET	Region	/note= "Variable region 3"
FT		213..231
ET		/label= C4
ET	Region	/note= "Conserved region 4"
FT		232..238
ET		/label= V4
ET	Region	/note= "Variable region 4"
FT		239..594
ET		/label= C5
ET		/note= "Conserved region 5"
XX		
PN	WO200155182-A1.	
PD	02-AUG-2001.	
PR	25-JAN-2001; 2001WO-AU00069.	
PA	(UYQU) UNIV QUEENSLAND.	
PL	Peak IRA, Jennings MP;	
DR	WPI; 2001-488774/53.	
DR	N-PSDB; AAS09169.	
PT	New Nhba surface antigen polypeptides and polynucleotides from	
PT	Neisseria meningitidis, useful in producing vaccines for treating or	
PT	preventing broad spectrum of Neisseria meningitidis -	
PS	Claim 9; Fig 1; 91pp; English.	
CC	The present invention relates to the isolation of novel Neisseria	
CC	meningitidis mutant polypeptides of the surface antigen Nhba	
CC	(AAU06182-AAU06186). The modified or mutant Nhba polypeptides are	
CC	characterised by deletions of non-conserved amino acids, particularly	
CC	the deletion of variable regions. The deletion mutants are useful in	
CC	diagnosis, therapeutic and prophylactic vaccines against a broader	
CC	spectrum of N. meningitidis, and in designing and/or screening of	
CC	medicaments. The mutant proteins when used as a vaccine can effectively	
CC	immunise against a broader spectrum of N. meningitidis strains than	
CC	would be expected from a corresponding wild-type surface antigen.	
CC	The present sequence representing the wild type surface antigen Nhba	
CC	from N. meningitidis strain B2198 is 1 of 10 Nhba polypeptide sequences	
CC	(AAU06171-AAU06180) from 10 different N. meningitidis strains given in	
CC	the present invention.	
XX		
SQ	Sequence 594 AA;	
OY	Query Match 94.1%; Score 2448.5; DB: 22; Length 594;	
Db	Best Local Similarity 83.2%; Pred. No. 1.7e-143;	
	Matches 494; Conservative 3; Mismatches 16; Indels 81; Gaps 1	
OY	1 MNKIRIIMNSALNMAVAVSELTNRHTRRASATVTAVALTLTLPFAVOANATDE-----	54
Db	1 MNKIRIIMNSALNMAVAVSELTNRHTRRASATVTAVALTLTLPFAVOANATDDDLYLE	60
OY	55 -----	54
Db	61 PVGRNAVVLSPRDSKEGTGEKEGTEEDSNMVAVFDEKRVLKAGATRLKAGDNLKIKONTNE	120
OY	55 -----TGILINVETELKLSGCANGKKNIISDPKGLMFACETAGNDGYTH	99
Db	121 NTINDSFTYSLLKDDLTLDTLTSVETEKLSPGANGKNVNITSIDPKGLMFACETAGNDGPVH	180

QY	100	LNIGSTFLIDMLNIGATTNVTNDVNTDDEKRRASVKKDVLNAGNNIKGVKPGTTASDNV	159
Db	181	LNIGSTFLIDPTLLNIGATTNVTNDVNTDDEKRRASVKKDVLNAGNNIKGVKPGTTASDNV	240
QY	160	DEVATYTFVEFLSADIKRTTTVANVESKDKTEVEIKGKTSYIKKDGKLVTKGKENG	219
Db	241	DEVATYTFVEFLSADIKRTTTVANVESKDKTEVEIKGKTSYIKKDGKLVTKGKENG	300
QY	220	SSTDEGEGLTAAKEVIDAIVNKAQWRRKTTTANGQGTGAADKFEYVTSQTKVTFASNGTTA	279
Db	301	SSTDEGEGLTAAKEVIDAIVNKAQWRRKTTTANGQGTGAADKFEYVTSQTKVTFASNGTTA	360
QY	280	TYSKDDGQNTTVYTDVNVGDAALNVNOLNSGNNEDSKVAASSGKVISGNNVSPKGMDE	339
Db	361	TYSKDDGQNTTVYTDVNVGDAALNVNOLNSGNNEDSKVAASSGKVISGNNVSPKGMDE	420
QY	340	TVNINAGNNIEIRNKKNDIDATSMTPQFSSVSLGAGADAPTLVSVDDEGALNVGSKDANK	399
Db	421	TVNINAGNNIEIRNKKNDIDATSMTPQFSSVSLGAGADAPTLVSVDDEGALNVGSKDANK	480
QY	400	PVRITNVAPVKKEGDTVNTAOLKGYAQNLMNRIDVNGNARAGIAQAATATGLVQAVLPG	459
Db	481	PVRITNVAPVKKEGDTVNTAOLKGYAQNLMNRIDVNGNARAGIAQAATATGLVQAVLPG	540
QY	460	KSMMAIIGGTYLGEAGYALGYSYSISAGGWWITTKGTASGNSGHHGASASVGYOW	513
Db	541	KSMMAIIGGTYLGEAGYALGYSYSISDQGNWIIKGTASGNSRGGHGFASASVGYOW	594
RESULT 13			
ID	AAI23740	standard; Protein; 594 AA.	
AC	AAI23740;		
XX	08-SEP-1999	(first entry)	
DE	A surface protein of Neisseria meningitidis.		
XX	Surface protein; surface glycoprotein; infection; vaccine;		
KW	immunoreactive peptide.		
XX	Neisseria meningitidis.		
XX	W09931132-A1.		
PD	24-JUN-1999.		
PF	14-DEC-1998;	98MO-AU01031.	
XX	12-DEC-1997;	97GB-0026398.	
PA	(ISIS-) ISIS INNOVATION LTD.		
XX	(UYOU) UNIV QUEENSLAND.		
PI	Jennings MP, Moxon ER, Peak IRA;		
DR	WPI; 1999-418754/35.		
DR	N-PSDB; AAX85792.		
PT	Neisseria meningitidis surface proteins useful for treating N.		
PT	meningitidis infections		
PS	Claim 1; Page 100-101; 132pp; English.		
CC	The present sequence represents a surface protein of Neisseria		
CC	meningitidis which is approximately 62 kDa. The N. meningitidis		
CC	surface glycoprotein, nucleic acids, the primers and optionally		
CC	a thermostable polymerase, or antibodies are useful in a kit for		
CC	the detection or diagnosis of N. meningitidis infection in humans.		
CC	The N. meningitidis surface glycoproteins can also be used to		
CC	prevent or treat N. meningitidis infection in humans, especially		

CC in the form of vaccines. The proteins and antibodies can also
 CC be used to identify immunoreactive peptides.

XX Sequence 594 AA:

Query Match 92.6%; Score 2409.5; DB 20; Length 594;
 Best Local Similarity 82.0%; Pred. No. 4.5e-141;
 Matches 487; Conservative 7; Mismatches 19; Indels 81; Gaps 1;

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   |||||
DB 481 PVRITNVAPGVKEDDVTVNAQLKGYAQNLMNRIDVNGNARAGIAQATATAGLVQAYLPG 540
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   |||||
DB 541 KSMALIGGGTYLGEAGYAIIGYSSISAGGNWITIKGTASGNSRGHFGASASVGTOW 594

```

RESULT 14

AA57044 ID AA57044 standard; Protein; 594 AA.

AC AA57044;

DE 21-FEB-2000 (first entry)

DE BASB029 amino acid sequence from N. meningitidis strain ATCC13090.

KW BASB029; *Neisseria meningitidis*; surface fibril protein; HSF; diagnosis;
 infection; treatment; prevent; antibacterial drug.

OS *Neisseria meningitidis*.

FH Key Location/Qualifiers

FT Misc-difference 104 /note= "Encoded by AATC"

PN WO9558683-A2.

PD 18-NOV-1999.

PF 07-MAY-1999; 99WO-EP03255.
 XX
 PR 13-MAY-1998; 98GB-0010276.
 XX

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

PI Ruelle J;

DR MPI: 2000-053103/04.

DR N-PSDB: AA239864.

PR New polypeptide from *Neisseria meningitidis* useful for diagnosis,
 treatment or prevention of bacterial infections in mammal
 PS Claim 4; Fig 2; 74pp: English.

This is the *Neisseria meningitidis* BASB029 amino acid sequence from serogroup B strain ATCC13090. The BASB029 protein is homologous to the *Haemophilus influenzae* surface fibril (HSF) protein. The invention relates to BASB029 polynucleotide sequences (AA239864-239865) and polypeptide sequences (AA57044-57045) and their immunogenic fragments. BASB029 polypeptides are useful in a method of diagnosing a *Neisseria meningitidis* infection in a mammal. Compositions containing BASB029 polynucleotides and polypeptides are useful for generating an antibody response in an animal. A therapeutic composition comprising an antibody directed against BASB029 is useful in treating humans with *Neisseria meningitidis* disease. The polynucleotide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASB029 polynucleotides and polypeptides are also useful for treating infections particularly bacterial infections. The protein is useful in the screening and development of antibacterial drugs. Fused recombinant protein is useful for the stimulation of the immune system of an organism receiving the protein.

XX Sequence 594 AA:

Query Match 92.6%; Score 2409.5; DB 21; Length 594;
 Best Local Similarity 82.0%; Pred. No. 4.5e-141;
 Matches 487; Conservative 7; Mismatches 19; Indels 81; Gaps 1;

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   |||||
DB 1 MKKIRIIMNSALNMAVAVSELTRHNRKASATVAVLATLLEFTVQANATDE----- 60
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OY 55 ----- 54
DB 61 PVQRTAVVLSFRSDEKGEKEVEDSNMGVYFDKKGVLTACTITLAKGDNLIKQNTNE 120
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DB 181 LKNGISSTLTDMLNLTGATNTNDVTDDEKRAASVDVYNAGNNIGVPGTASDNV 240
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DB 241 DFEVRYDVEFLSADTKTTTVNVEESKDKGKTEVIGAKTSYIKEDKGLVTKGKGEND 300
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DB 301 SSTDEGEGLVTAKEVIDAVNKRAGWRMKTATTANGOTGADKFEVTSGTKVTFASGNGTTA 360
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Db 421 TVINAGNNIETIRNKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNNGSKDANK 480
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 RESULT 15
 AAU06174
 ID AAU06174 standard; protein: 594 AA.
 AC AAU06174;
 XX
 DT 24-OCT-2001 (first entry)
 DE N. meningitidis EG327 surface antigen Nhma polypeptide sequence.
 XX Surface antigen Nhma; meningococcal disease; meningitis vaccine.
 KM
 OS Neisseria meningitidis strain EG327.
 XX
 FH Key
 FT Location/Qualifiers
 FT 1..50
 FT /label= C1
 FT /note= "Conserved region 1"
 FT 51..104
 FT /label= V1
 FT /note= "Variable region 1"
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 FT 213..231
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 FT 232..238
 FT /label= V4
 FT /note= "Variable region 4"
 FT 239..594
 FT /label= C5
 FT /note= "Conserved region 5"
 FT
 FT
 FT
 PN WO200155182-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 25-JAN-2001; 2001WO-AU00069.
 XX
 PR 25-JAN-2000; 2000US-0177917.
 XX
 PA (UYQU) UNIV QUEENSLAND.
 XX
 PI Peak IRA, Jennings MP;
 XX
 DR WPI; 2001-488774/53.
 XX
 DR N-PSDB; AAS09164.
 XX
 PT New Nhma surface antigen polypeptides and polynucleotides from
 PT Neisseria meningitidis, useful in producing vaccines for treating or
 PT preventing broad spectrum of Neisseria meningitidis -

PS Claim 9; Fig 1; 91pp; English.
 XX
 CC The present invention relates to the isolation of novel Neisseria
 CC meningitidis mutant polypeptides of the surface antigen Nhma
 CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are
 CC characterised by deletions of non-conserved amino acids, particularly
 CC the deletion of variable regions. The deletion mutants are useful in
 CC diagnostics, therapeutic and prophylactic vaccines against a broader
 CC spectrum of N. meningitidis, and in designing and/or screening of
 CC medicaments. The mutant proteins when used as a vaccine can effectively
 CC immunise against a broader spectrum of N. meningitidis strains than
 CC would be expected from a corresponding wild-type surface antigen.
 CC The present sequence representing the wild type surface antigen Nhma
 CC from N. meningitidis strain EG327 is 1 of 10 Nhma polypeptide sequences
 CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
 CC the present invention.
 XX
 SQ Sequence 594 AA;
 Query Match 92.6%; Score 2409.5; DB 22; Length 594;
 Best Local Similarity 82.0%; Pred. No. 4.5e-141;
 Matches 487; Conservative 7; Mismatches 19; Indels 81; Gaps 1;
 QY 1 MNKIRIYNSALNANAVASELNRNHTKRASATVAVATLTFATVQANATDE----- 54
 Db 1 MNKIRIYNSALNANAVASELNRNHTKRASATVAVATLTFATVQASTDDDDLYLE 60
 QY 55 ----- 54
 Db 61 PVORTAVVLSFRBDEKGTGKEVTEDSNMGVYDDKGVLTAGTITLTKAGDNLIKIKONTNE 120
 QY 55 -----TGLINVEETKLSFGANGKNNIISDTKGLNFAKETAGTNGDTYVH 99
 Db 121 NTNASSFTYSLKRDLDLTSVGTREKLSFSANSKNNVITSDTKGLNFAKKAETRNNGDTYVH 180
 QY 100 LINGISLTPLMLNTGATTNVTNDNTDDEKRAAASVQVLANGNMINKVKKPPTTASDNY 159
 Db 181 LINGISLTPLDLTNTGATTNVTNDNTDDEKRAAASVQVLANGNMINKVKKPPTTASDNY 240
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 Db 241 DFRVTDYVEFLSADRTTTVNVEKSKNGKKEVTKIGAKTSVKEKDKGLVTKGKGEND 300
 QY 220 SSTDEGEGLVTAKEVIDAVNKAAGRMKTTTANGOTQADKFEVTSCTVTFASNGGTGA 279
 Db 301 SSTDEGEGLVTAKEVIDAVNKAAGRMKTTTANGOTQADKFEVTSCTVTFASNGGTGA 360
 QY 280 TVSKDDOGNTTVYDVNVDGALVNOLONGSNMLDSKAVSGSGKVIISGNVSPSKGKME 339
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 Db 481 PVRITNVAPGKEDGYTNVAQLKGVANLNRRIDNVNGNARAGIAQAATAGLVQAYLPG 540
 QY 460 KSMMAIGGGTYLGEAGYATGSSISAGGNNIIGTASGNSRGHFGASASVGYOM 513
 Db 541 KSMMAIGGGTYRGEAGYATGSSISDGNNIIGTASGNSRGHFGASASVGYOM 594

Search completed: October 6, 2003, 09:22:27
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:14:45 ; Search time 13.7186 Seconds
(without alignments)
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Title: US-09-771-382-24

Perfect score: 2602

Sequence: 1 MNKIRIIMNSALNMAWAVS.....TAGSNRCHFGASASVGYOW 513

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2552.5	98.1	592	US-09-377-155-17	Sequence 17, Appl
2	2552.5	98.1	592	US-09-669-974-17	Sequence 17, Appl
3	2472	95.0	599	US-09-377-155-15	Sequence 15, Appl
4	2472	95.0	599	US-09-669-974-15	Sequence 15, Appl
5	2460.5	94.6	598	US-09-377-155-13	Sequence 13, Appl
6	2460.5	94.6	598	US-09-669-974-13	Sequence 13, Appl
7	2451.5	94.2	598	US-09-377-155-5	Sequence 5, Appl
8	2451.5	94.2	598	US-09-669-974-5	Sequence 5, Appl
9	2448.5	94.1	594	US-09-377-155-7	Sequence 7, Appl
10	2448.5	94.1	594	US-09-669-974-7	Sequence 7, Appl
11	2409.5	92.6	594	US-09-377-155-9	Sequence 9, Appl
12	2409.5	92.6	594	US-09-669-974-9	Sequence 9, Appl
13	2407	92.5	591	US-09-377-155-21	Sequence 21, Appl
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15	2402.5	92.3	592	US-09-377-155-2	Sequence 2, Appl
16	2402.5	92.3	592	US-09-669-974-2	Sequence 2, Appl
17	2395	92.0	591	US-09-377-155-11	Sequence 11, Appl
18	2395	92.0	591	US-09-669-974-11	Sequence 11, Appl
19	2314	88.9	589	US-09-377-155-19	Sequence 19, Appl
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23	966.5	37.1	1098	US-08-685-467-2	Sequence 2, Appl
24	966.5	37.1	1098	US-09-377-155-32	Sequence 32, Appl
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34	939.5	36.1	2353	US-09-669-974-33	Sequence 33, Appl
35	938.5	36.1	2354	US-09-268-347-47	Sequence 47, Appl
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ALIGNMENTS

RESULT 1					
US-09-377-155-17					
Sequence 17, Application US/09377155					
Patent No. 6197312					
GENERAL INFORMATION:					
APPLICANT: PEAK, Ian Richard Anselm					
APPLICANT: JENNINGS, Michael Paul					
APPLICANT: MOXON, E. Richard					
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN					
FILE REFERENCE: 065064/0128					
CURRENT APPLICATION NUMBER: US/09/377,155					
CURRENT FILING DATE: 1999-08-19					
PRIOR APPLICATION NUMBER: PCT/AU98/01031					
PRIOR FILING DATE: 1998-12-14					
PRIOR APPLICATION NUMBER: GB 9726398.2					
PRIOR FILING DATE: 1997-12-12					
NUMBER OF SEQ ID NOS: 33					
SOFTWARE: PatentIn Ver. 2.0					
SEQ ID NO 17					
LENGTH: 592					
TYPE: PRT					
ORGANISM: Neisseria meningitidis					
US-09-377-155-17					
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Best Local Similarity 98.1%; Score 2552.5; DB 3; Length 592;					
Matches 513; Conservative 0; Mismatches 0; Indels 79; Gaps 1;					
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Db 481 RITNVAPGVKEGVDVTVAOLKGVQNLNRRIDNVNNGNARAGIAQALATAGLVQAYLPGRS 540
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RESULT 2
US-09-669-974-17
; Sequence 17, Application US/09669974
; Patent No. 6331173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669, 974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; LENGTH: 592
; TYPE: PRF
; ORGANISM: Neisseria meningitidis
US-09-669-974-17
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Query Match 98.1%; Score 2552.5; DB 4; Length 592;
Best Local Similarity 86.7%; Pred. No. 8.8e-196;
Matches 513; Conservative 0; Mismatches 0; Indels 79; Gaps 1;
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Qy 282 SKDDQGNITVKYDVNVGDALNVQNLQNSGWNLDKSAVAGSSGKVIISGNVSPSKGKMDERV 341
Db 361 SKDDQGNITVKYDVNVGDALNVQNLQNSGWNLDKSAVAGSSGKVIISGNVSPSKGKMDERV 420
Qy 342 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPPLSYDDDEGALNVGSKDANKPV 401
Db 421 NINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPPLSYDDDEGALNVGSKDANKPV 480
Qy 402 RITNVAPGVKEGVDVTVAOLKGVQNLNRRIDNVNNGNARAGIAQALATATAGLVQAYLPGRS 461
Db 481 RITNVAPGVKEGVDVTVAOLKGVQNLNRRIDNVNNGNARAGIAQALATAGLVQAYLPGRS 540
Qy 462 MMAIGGTYLGEAGVAGYSSISAGGNWIIKGTASGNSRCHFGASASVGYOW 513
Db 541 MMAIGGTYLGEAGVAGYSSISAGGNWIIKGTASGNSRCHFGASASVGYOW 592
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RESULT 3
US-09-377-155-15
; Sequence 15, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; LENGTH: 599
; TYPE: PRF
; ORGANISM: Neisseria meningitidis
US-09-377-155-15
```

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Query Match 95.0%; Score 2472; DB 3; Length 599;
Best Local Similarity 83.1%; Pred. No. 2.4e-189;
Matches 498; Conservative 5; Mismatches 10; Indels 86; Gaps 1;
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Qy 1 MNKIYRIINMSALNANAVASELFRNHTKRASATVKTAVLATLTFATVOANATDE----- 54
Db 1 MNKIYRIINMSALNANAVASELFRNHTKRASATVKTAVLATLTFATVOANATDEDEBEEL 60
Qy 55 ----- 54
Db 61 EPVYRSALVQFMIDKEGNGENESTGNIGSIYYDNHNTLHGATVTLKAGDNLKIKONTN 120
Qy 55 -----TGLINVEETKLSFGANGKAYNIISDTKGLNPAKETAGTNG 94
Db 121 KNTNENTNDSFYSYSLKKDLTGLINVEETKLSFGANGKAYNIISDTKGLNPAKETAGTNG 180
Qy 95 DTVVHLNGTSTLTLMLNTGATTNVTNDVTDDEKKRAASVYKVDVNLNAGNNIKGVKPGTT 154
Db 181 DTVVHLNGTSTLTLMLNTGATTNVTNDVTDDEKKRAASVYKVDVNLNAGNNIKGVKPGTT 240
Qy 155 ASDNVDFVRTYDVEEFLSADTKTTTVNVESEKNGKTEVYKIGAKTSVIREKDGKLVYTGK 214
Db 241 ASDNVDFVRTYDVEEFLSADTKTTTVNVESEKNGKTEVYKIGAKTSVIREKDGKLVYTGK 300
Qy 215 KGENGSTDEGELVTAKEVIDAVNKAQRMKTTTANGOTGADKFEFTVSGTKVTFASG 274
Db 301 KGENGSTDEGELVTAKEVIDAVNKAQRMKTTTANGOTGADKFEFTVSGTKVTFASG 360
Qy 275 NGTTATVSKDDQGNITVKYDVNVGDALNVQNLQNSGWNLDKSAVAGSSGKVIISGNVSPSK 344
Db 361 NGTTATVSKDDQGNITVKYDVNVGDALNVQNLQNSGWNLDKSAVAGSSGKVIISGNVSPSK 420
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QY	335	GKMDTVINAGNNIEITPNGKNIDIATMTQFSSYSICAGADAPTLSDYDEGALNVGS	354
Db	421	GKMDTVINAGNNIEITRNGKNIDIATMTQFSSYSICAGADAPTLSDYDEGALNVGS	480
QY	395	KDANKPVITTNVAPGVBEEDYTNVAQLKQVAQNLNRRINDVNGNNAAGIAQAATATAGLVQ	454
Db	481	KDANKPVITTNVAPGVBEEDYTNVAQLKQVAQNLNRRINDVNGNNAAGIAQAATATAGLVQ	540
QY	455	AYLPKSMMAITGGGYTLCGAGYALTCSSYSAGGNWIKKTAASNSNGHGKASASVGYQW	513
Db	541	AYLPKSMMAITGGGYTLCGAGYALTCSSYSAGGNWIKKTAASNSNGHGKASASVGYQW	599

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: RESULT 4
: US-09-669-974-15
: Sequence 15, Application US/0966974
: Patent No. 6533173
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/669,974
: CURRENT FILING DATE: 2000-09-26
: PRIOR APPLICATION NUMBER: US 09/377,155
: PRIOR FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 15
: LENGTH: 599
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
: US-09-669-974-15

```

Query Match	95.0%	Score 2472;	DB 4;	Length 599;
Best Local Similarity	83.1%;	Pred. No. 2.4e-189;		
Matches 498;	Conservative 5;	Mismatches 10;	Indels 86;	Gaps 1;
Oy	1	MNKIIRIIMNSALNAWAVSELTRNHRKRAAFVKTAVLATILFLFAVQANATDE-----	54	
Db	1	MNKIIRIIMNSALNAWAVSELTRNHRKRAAFVKTAVLATILFLFAVQANATDEDEBEL	60	
Oy	55	-----	54	
Db	61	EPVVSALVLQFMIDKEGNGENESNIGMSIYYDHNHTLHGATVTLKAGDNLIKQNTN	120	
Oy	55	-----TGLINVEIERKISFGANGKKVNIISDTKLNINAKETACIANG	94	
Db	121	KNTNENTNDSSFYTSLKADLLDLTSVEIKKISFGANGKKVNIISDTKLNINAKETACIANG	180	
Oy	95	DTFVHLNIGSTLIDMLNLTGATTNVTNDANTDDEKKRAASVKVDVLNAGNMIKGVKPGTT	154	
Db	181	DTFVHLNIGSTLIDTLTLNLTGATTNVTNDANTDDEKKRAASVKVDVLNAGNMIKGVKPGTT	240	
Oy	155	ASDNVDFRYIYDVEELISADTKTYYYVESKDKNGKTEVKIGANTSVIIEKDGKLVYTKG	214	
Db	241	ASDNVDFRYIYDVEELISADTKTYYYVESKDKNGKTEVKIGANTSVIIEKDGKLVYTKG	300	
Oy	215	KGENSSSTDEEGLYTAKVEIDAVNKKGMKKKTTTANGTQOQADKFEFVTSGETVYTFASG	274	
Db	301	KGENSSSTDEEGLYTAKVEIDAVNKKGMKKKTTTANGTQOQADKFEFVTSGETVYTFASG	360	
Oy	275	NGTTATVSKDOGQNTYVYDVNVGDLVNVNDLQNSGWNMLDSKAAVSSSGKVIISGNVPSK	334	
Db	361	KGTTATVSKDOGQNTYVYDVNVGDLVNVNDLQNSGWNMLDSKAAVSSSGKVIISGNVPSK	420	
Oy	335	GKMDFTVINAGNNIETRNCKNIDIAVSMTPOFSSVSLGAGADAPTLISVDEGALNVS	394	

Db 421 GKMDETVAINAGNNIEITPNCNKINDIATSMTPQFSSVSLGAGADATLTVYDDKGALNVS 480

QY 395 KDANKPVRTTNVAPGYEGEDVYTNVAOLKCYAONLNRRINDVNGNNAAGTAQOATATAGLV 454

Db 481 KDANKPVRTTNVAPGYEGEDVYTNVAOLKCYAONLNRRINDVNDNNAAGTAQOATATAGLV 540

QY 455 AYLPEKSMALIGGTYLGEAGYAIGYSSISAGCNWILKGTASGNSKGFPGASAVGYQW 513

Db 541 AYLPEKSMALIGGTYRGEAGYAIGYSSISDGCNWLILKGTASGNSKGFPGASAVGYQW 599

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RESULT 5
US-09-377-155-13
; Sequence 13, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-13

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Query Match	94.6%	Score 2460.5	DB 3	Length 598
Best Local Similarity	82.9%	Prod. No. 2e-188		
Matches	Conservative	4	Mismatches 13	Indels 85
QY	1	MNKIYRIIMNSALNMAVAVSELTNRHTRKASATVATLALTLFATVOANNTDE-----	54	
DB	1	MNKIYRIIMNSALNMAVAVSELTNRHTRKASATVATLALTLFATVOANNTDDDDLYLE	60	
QY	55	-----	54	
DB	61	PVQRTAVVLSFSDEKGEKTEGEDNSMVAAYFDEKRVYLKAGAITLKAGDMLIKONTNE	120	
QY	55	-----TGLINETEKLSPGANGKRVNIIISDPKGLNPAKETAGTNGD	95	
DB	121	NTNEKNTDSSFTYSLKKDLIDLTTSVEIKLSFGAGKNKVNITSDTKGLNPAKETAGTNGD	180	
QY	96	TTVHLNGIGSTLTDLMLNTGATNTVNTDNDVTDDEKKRAASVDYVLAAGNITKGVKPGTTA	155	
DB	181	PTVHLNGIGSTLTDLMLNTGATNTVNTDNDVTDDEKKRAASVDYVLAAGNITKGVKPGTTA	240	
QY	156	SDNDVFATYTPVPELSADTKTYYNVESKNGKTEVIGAKTSVIEIKNGKLTGTGK	215	
DB	241	SDNDVFATYTPVPELSADTKTYYNVESKNGKTEVIGAKTSVIEIKNGKLTGTGK	300	
QY	216	GENGSSTDEGBELVAKEVIDAIVNKAQGRMKTTTANGOTGQADKFEYTSQTKVYFASGN	275	
DB	301	DENGSSSTDEGBELVAKEVIDAIVNKAQGRMKTTTANGOTGQADKFEYTSQTKVYFASGN	360	
QY	276	GTTATVSKDDOGNTITVKYDVAVNGALANNOLONSQWMLDSKRAVAGSSKVIISGNVSPSKG	335	
DB	361	GTTATVSKDDOGNTITVKYDVAVNGALANNOLONSQWMLDSKRAVAGSSKVIISGNVSPSKG	420	
QY	336	KMDETVNINAGNIEITRNGKNIDATSMTPQOFSSVSGAGADAPTLTVSDEGALNVGSK	395	
DB	421	KMDETVNINAGNIEITRNGKNIDATSMTPQOFSSVSGAGADAPTLTVSDEGALNVGSK	480	
QY	396	DANKPVRTTNVAPGVKEGDVTNVQALQVAGNQLNLRIDNVNGNARAGIAQATATAGLVQA	455	

Db 481 DANKPVRTINVAAGVEGDVTNVAOLKGYAQNINNRIDVNGNARAGIAOAIATAGLAQA 540
QY 456 YLPKGSMAAIGGGTYLGEAGYAIGYSSISAGNMIIKGTASGNSRGHFGASASVGYQW 513
|||||
Db 541 YLPKGSMAAIGGGTYLGEAGYAIGYSSISDPTGMNVIKGTASGNSRGHFGASASVGYQW 598

RESULT 6
US-09-669-974-13
; Sequence 13, Application US/0966974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669, 974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PRF
; ORGANISM: Neisseria meningitidis
US-09-669-974-13

Query Match 94.6%; Score 2460.5; DB 4; Length 598;
Best Local Similarity 82.9%; Pred. No. 2e-188;
Matches 496; Conservative 4; Mismatches 13; Indels 85; Gaps 1;

QY 1 MNKIYIIMNSALNANVAAYSELTRNHTKRASATVKTAVLATLLFAIVQANATDE----- 54
|||||
Db 1 MNKIYIIMNSALNANVAAYSELTRNHTKRASATVKTAVLATLLFAIVQANATDDDLYLE 60
55 ----- 54
Db 61 PVORTAVVLSFRSDEKGEKTEGEDSNNAAVYFDEKRVLKAGAITLKAGDNLIKONTNE 120
QY 55 -----TGLINVEETKLSFGANGKKNIIISDTGKLNPAKETAAGTNGD 95
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Db 121 NTNENTNDSEFTYSLKDDLTDLTSVETEKLSFGANGKKNIIISDTGKLNPAKETAAGTNGD 180
QY 96 TTVHLNGIGSTLTDMLNTGATTNVTNDVNTDDEKRRASVSKDVLNAGNMNIKGVKPGTTA 155
|||||
Db 181 PTVHLNGIGSTLTDLTGATTNVTNDVNTDDEKRRASVSKDVLNAGNMNIKGVKPGTTA 240
QY 156 SDNVDEVRYDYVEFLSADTKTTTVNVEESKDNKKTVEKIGAKTSYIKERDGLVYGK 215
|||||
Db 241 SDNVDEVRYDYVEFLSADTKTTTVNVEESKDNKKTVEKIGAKTSYIKERDGLVYGK 300
QY 216 GENGSSTDEGEGLVTAKEVIDAVNKAQNRKTTTANGQTGOADKFETVYSGTVTFASGN 275
|||||
Db 301 DEGSSSTDEGEGLVTAKEVIDAVNKAQNRKTTTANGQTGOADKFETVYSGTVTFASGN 360
QY 276 GTTATVSKDDQGNITVYDVNVDALNVNOLONGSNNLDSKAVAGSSGKVISGNVSPSKG 335
|||||
Db 361 GTTATVSKDDQGNITVYDVNVDALNVNOLONGSNNLDSKAVAGSSGKVISGNVSPSKG 420
QY 336 KMEETVINAANNIEITRNGKNIDTASMTPOFSSVSLGAGADAPTLVSDDEGALNVGSK 395
|||||
Db 421 KMEETVINAANNIEITRNGKNIDTASMTPOFSSVSLGAGADAPTLVSDDEGALNVGSK 480
QY 396 DANKPVRTINVAAGVEGDVTNVAOLKGYAQNINNRIDVNGNARAGIAOAIATAGLAQA 455
|||||
Db 481 DANKPVRTINVAAGVEGDVTNVAOLKGYAQNINNRIDVNGNARAGIAOAIATAGLAQA 540

QY 456 YLPKGSMAAIGGGTYLGEAGYAIGYSSISAGNMIIKGTASGNSRGHFGASASVGYQW 513
Db 541 YLPKGSMAAIGGGTYLGEAGYAIGYSSISDPTGMNVIKGTASGNSRGHFGASASVGYQW 598

RESULT 7
US-09-377-155-5
; Sequence 5, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRF
; ORGANISM: Neisseria meningitidis
US-09-377-155-5

Query Match 94.2%; Score 2451.5; DB 3; Length 598;
Best Local Similarity 82.6%; Pred. No. 1e-187;
Matches 494; Conservative 5; Mismatches 14; Indels 85; Gaps 1;

QY 1 MNKIYIIMNSALNANVAAYSELTRNHTKRASATVKTAVLATLLFAIVQANATDE----- 54
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Db 1 MNKIYIIMNSALNANVAAYSELTRNHTKRASATVKTAVLATLLFAIVQANATDDDLYLE 60
55 ----- 54
Db 61 PVORTAVVLSFRSDEKGEKTEGEDSNNAAVYFDEKRVLKAGAITLKAGDNLIKONTNE 120
QY 55 -----TGLINVEETKLSFGANGKKNIIISDTGKLNPAKETAAGTNGD 95
|||||
Db 121 NTNENTNDSEFTYSLKDDLTDLTSVETEKLSFGANGKKNIIISDTGKLNPAKETAAGTNGD 180
QY 96 TTVHLNGIGSTLTDMLNTGATTNVTNDVNTDDEKRRASVSKDVLNAGNMNIKGVKPGTTA 155
|||||
Db 181 PTVHLNGIGSTLTDLTGATTNVTNDVNTDDEKRRASVSKDVLNAGNMNIKGVKPGTTA 240
QY 156 SDNVDEVRYDYVEFLSADTKTTTVNVEESKDNKKTVEKIGAKTSYIKERDGLVYGK 215
|||||
Db 241 SDNVDEVRYDYVEFLSADTKTTTVNVEESKDNKKTVEKIGAKTSYIKERDGLVYGK 300
QY 216 GENGSSTDEGEGLVTAKEVIDAVNKAQNRKTTTANGQTGOADKFETVYSGTVTFASGN 275
|||||
Db 301 DEGSSSTDEGEGLVTAKEVIDAVNKAQNRKTTTANGQTGOADKFETVYSGTVTFASGN 360
QY 276 GTTATVSKDDQGNITVYDVNVDALNVNOLONGSNNLDSKAVAGSSGKVISGNVSPSKG 335
|||||
Db 361 GTTATVSKDDQGNITVYDVNVDALNVNOLONGSNNLDSKAVAGSSGKVISGNVSPSKG 420
QY 336 KMEETVINAANNIEITRNGKNIDTASMTPOFSSVSLGAGADAPTLVSDDEGALNVGSK 395
|||||
Db 421 KMEETVINAANNIEITRNGKNIDTASMTPOFSSVSLGAGADAPTLVSDDEGALNVGSK 480
QY 396 DANKPVRTINVAAGVEGDVTNVAOLKGYAQNINNRIDVNGNARAGIAOAIATAGLAQA 455
|||||
Db 481 DANKPVRTINVAAGVEGDVTNVAOLKGYAQNINNRIDVNGNARAGIAOAIATAGLAQA 540
QY 456 YLPKGSMAAIGGGTYLGEAGYAIGYSSISAGNMIIKGTASGNSRGHFGASASVGYQW 513
|||||
Db 541 YLPKGSMAAIGGGTYLGEAGYAIGYSSISDPTGMNVIKGTASGNSRGHFGASASVGYQW 598

RESULT 8
US-09-669-974-5
; Sequence 5, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-5

Query Match 94.2%; Score 2451.5; DB 4; Length 598;
Best Local Similarity 82.6%; Pred. No. 1e-187;
Matches 494; Conservative 5; Mismatches 14; Indels 85; Gaps 1;

QY 1 MNKIRIIMNSALNAAVAVSELTRNHRKASATVKTAVLATLLPATVOANATDE----- 54
DB 1 MNKIRIIMNSALNAAVAVSELTRNHRKASATVKTAVLATLLPATVOANATDDDLYLE 60
QY 55 ----- 54
DB 61 PVORTAVLSPRSDEKGEKEDTSNMNAVYFDEKRVLKAGATILKAGDMLKIKONTNE 120
QY 55 ----- 95
DB 121 NTNDSFTYSLKDLDTLTSVEFKLSFGANGKNVNITSDTKGINFAKETAGNDPTVH 180
QY 96 TTVHLNGISLTDLMLNTGATNTVNDNTDDEKRRASVYKVDLNAAGNIRKGVKPGTTA 155
DB 181 PTVHLNGISLTDLMLNTGATNTVNDNTDDEKRRASVYKVDLNAAGNIRKGVKPGTTA 240
QY 156 SDNVDFVRYDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIREKDKLVTGK 215
DB 241 SDNVDFVRYDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIREKDKLVTGK 300
QY 216 GENSSSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGADKFEYVTSCTKTFASGN 275
DB 301 GENSSSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGADKFEYVTSCTKTFASGN 360
QY 276 GTTAVSKDQGNITVYKDVVNGDALNNQLONSGMNDSKAVAGSSGKTVISGNVSPK 335
DB 361 GTTAVSKDQGNITVYKDVVNGDALNNQLONSGMNDSKAVAGSSGKTVISGNVSPK 420
QY 336 KMDFTVINAGNIIETRNKKNIDATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSK 395
DB 421 KMDFTVINAGNIIETRNKKNIDATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSK 480
QY 396 DANPVRTTNVAPGVKBEQDVTVNAQLKGVQNLNRRIDNVGNARAGIAQAIAATAGLVOA 455
DB 481 DANPVRTTNVAPGVKBEQDVTVNAQLKGVQNLNRRIDNVGNARAGIAQAIAATAGLVOA 540
QY 456 YLPKSMMAIGGTYLGEAGYAIIGSSISAGGNMIIKGTASGNSRGHFGASASVGYOW 513
DB 541 YLPKSMMAIGGTYLGEAGYAIIGSSISAGGNMIIKGTASGNSRGHFGASASVGYOW 598

RESULT 9

US-09-377-155-7
; Sequence 7, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-7

Query Match 94.1%; Score 2448.5; DB 3; Length 594;
Best Local Similarity 83.2%; Pred. No. 1.8e-187;
Matches 494; Conservative 3; Mismatches 16; Indels 81; Gaps 1;

QY 1 MNKIRIIMNSALNAAVAVSELTRNHRKASATVKTAVLATLLPATVOANATDE----- 54
DB 1 MNKIRIIMNSALNAAVAVSELTRNHRKASATVKTAVLATLLPATVOANATDDDLYLE 60
QY 55 ----- 54
DB 61 PVORTAVLSPRSDEKGEKEDTSNMNAVYFDEKRVLKAGATILKAGDMLKIKONTNE 120
QY 55 ----- 99
DB 121 NTNDSFTYSLKDLDTLTSVEFKLSFGANGKNVNITSDTKGINFAKETAGNDPTVH 180
QY 100 LNGISLTDLMLNTGATNTVNDNTDDEKRRASVYKVDLNAAGNIRKGVKPGTTASNV 159
DB 181 LNGISLTDLMLNTGATNTVNDNTDDEKRRASVYKVDLNAAGNIRKGVKPGTTASNV 240
QY 160 DFVRYDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIREKDKLVTGKGENG 219
DB 241 DFVRYDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIREKDKLVTGKGENG 300
QY 220 SSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGADKFEYVTSCTKTFASGN 279
DB 301 SSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGOTGADKFEYVTSCTKTFASGN 360
QY 280 TVSKDDQGNITVYKDVVNGDALNNQLONSGMNDSKAVAGSSGKTVISGNVSPK 339
DB 361 TVSKDDQGNITVYKDVVNGDALNNQLONSGMNDSKAVAGSSGKTVISGNVSPK 420
QY 340 TVNINAGNIIETRNKKNIDATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANK 399
DB 421 TVNINAGNIIETRNKKNIDATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANK 480
QY 460 KSMMAIGGTYLGEAGYAIIGSSISAGGNMIIKGTASGNSRGHFGASASVGYOW 513
DB 541 KSMMAIGGTYLGEAGYAIIGSSISAGGNMIIKGTASGNSRGHFGASASVGYOW 594

RESULT 10
US-09-669-974-7
; Sequence 7, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:

APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 594
TYPE: PR1
ORGANISM: Neisseria meningitidis
US-09-669-974-7

Query Match 94.1%; Score 2448.5; DB 4; Length 594;
Best Local Similarity 83.2%; Pred. No. 1.8e-187;
Matches 494; Conservative 3; Mismatches 16; Indels 81; Gaps 1;

QY 1 MNKIRIINNSALNMAVAVSELTNRHTRKASATVKTAVLATILFATVQANATDE----- 54
DB 1 MNKIRIINNSALNMAVAVSELTNRHTRKASATVKTAVLATILFATVQANATDDDDLYLE 60
QY 55 ----- 54
DB 61 PVQRTAVVLSFSDKSGTEGKEGEDSDSNMAYFEDEKRAASVKDVLNAGWNIKGVKPGTASDNV 120
QY 55 -----TGLINVEFEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTYH 99
DB 121 MNDSSEFTYSLKKDLTDLTSVEFEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTYH 180
QY 100 LNCIGSTLTDMLNLTGATTNVTNDVNTDDEKRAASVKDVLNAGWNIKGVKPGTASDNV 159
DB 181 LNCIGSTLTDMLNLTGATTNVTNDVNTDDEKRAASVKDVLNAGWNIKGVKPGTASDNV 240
QY 160 DFRRTDYVEFLSADTKTTTNNVESKDNKKEVKGATSVYKEKDKLVTKGKGENG 219
DB 241 DFRRTDYVEFLSADTKTTTNNVESKDNKKEVKGATSVYKEKDKLVTKGKGENG 300
QY 220 SSTDEBEGLVTAKEVIDAVNKAQWRRKTTTANGOTGOADKFEVTSGTVFASGNGTGA 279
DB 301 SSTDEBEGLVTAKEVIDAVNKAQWRRKTTTANGOTGOADKFEVTSGTVFASGNGTGA 360
QY 280 TVSKDDQGNITVYKDVNVDALNVLNOLQNSGWNLDKKAAGSSGKVISGNVSPSKGKMD 339
DB 361 TVSKDDQGNITVYKDVNVDALNVLNOLQNSGWNLDKKAAGSSGKVISGNVSPSKGKMD 420
QY 340 TVNINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLISVDEGALNVGSKDANK 399
DB 421 TVNINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLISVDEGALNVGSKDANK 480
QY 400 PVRTITVAVGVEGDDTVNVAOLKGVQONLNRIIDNVNNGARAGIAQAITAGIYQAYLP 459
DB 481 PVRTITVAVGVEGDDTVNVAOLKGVQONLNRIIDNVNNGARAGIAQAITAGIYQAYLP 540
QY 460 KSMMAIGGTYLGEAGYAIGYSSISAGWMIKGTASGNSRGHFGASASVGYOW 513
DB 541 KSMMAIGGTYLGEAGYAIGYSSISAGWMIKGTASGNSRGHFGASASVGYOW 594

RESULT 11
US-09-377-155-9
Sequence 9, Application US/09377155
Patent No. 6197312
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul

APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 594
TYPE: PR1
ORGANISM: Neisseria meningitidis
US-09-377-155-9

Query Match 92.6%; Score 2409.5; DB 3; Length 594;
Best Local Similarity 82.0%; Pred. No. 2.3e-184;
Matches 487; Conservative 7; Mismatches 19; Indels 81; Gaps 1;

QY 1 MNKIRIINNSALNMAVAVSELTNRHTRKASATVKTAVLATILFATVQANATDE----- 54
DB 1 MNKIRIINNSALNMAVAVSELTNRHTRKASATVKTAVLATILFATVQASTTDDDDLYLE 60
QY 55 ----- 54
DB 61 PVQRTAVVLSFSDKSGTEGKEGEDSDSNMAYFEDEKRAASVKDVLNAGWNIKGVKPGTASDNV 120
QY 55 -----TGLINVEFEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTYH 99
DB 121 MNASSFTYSLKKDLTDLTSVEFEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTYH 180
QY 100 LNCIGSTLTDMLNLTGATTNVTNDVNTDDEKRAASVKDVLNAGWNIKGVKPGTASDNV 159
DB 181 LNCIGSTLTDMLNLTGATTNVTNDVNTDDEKRAASVKDVLNAGWNIKGVKPGTASDNV 240
QY 160 DFRRTDYVEFLSADTKTTTNNVESKDNKKEVKGATSVYKEKDKLVTKGKGENG 219
DB 241 DFRRTDYVEFLSADTKTTTNNVESKDNKKEVKGATSVYKEKDKLVTKGKGENG 300
QY 220 SSTDEBEGLVTAKEVIDAVNKAQWRRKTTTANGOTGOADKFEVTSGTVFASGNGTGA 279
DB 301 SSTDEBEGLVTAKEVIDAVNKAQWRRKTTTANGOTGOADKFEVTSGTVFASGNGTGA 360
QY 280 TVSKDDQGNITVYKDVNVDALNVLNOLQNSGWNLDKKAAGSSGKVISGNVSPSKGKMD 339
DB 361 TVSKDDQGNITVYKDVNVDALNVLNOLQNSGWNLDKKAAGSSGKVISGNVSPSKGKMD 420
QY 340 TVNINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLISVDEGALNVGSKDANK 399
DB 421 TVNINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLISVDEGALNVGSKDANK 480
QY 400 PVRTITVAVGVEGDDTVNVAOLKGVQONLNRIIDNVNNGARAGIAQAITAGIYQAYLP 459
DB 481 PVRTITVAVGVEGDDTVNVAOLKGVQONLNRIIDNVNNGARAGIAQAITAGIYQAYLP 540
QY 460 KSMMAIGGTYLGEAGYAIGYSSISAGWMIKGTASGNSRGHFGASASVGYOW 513
DB 541 KSMMAIGGTYLGEAGYAIGYSSISAGWMIKGTASGNSRGHFGASASVGYOW 594

RESULT 12
US-09-669-974-9
Sequence 9, Application US/09669974
Patent No. 6333173
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974

;; CURRENT FILING DATE: 2000-09-26
;; PRIOR APPLICATION NUMBER: US 09/377,155
;; PRIOR FILING DATE: 1999-08-19
;; PRIOR APPLICATION NUMBER: PCT/AU98/01031
;; PRIOR FILING DATE: 1998-12-14
;; PRIOR APPLICATION NUMBER: GB 9726398.2
;; PRIOR FILING DATE: 1997-12-12
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 9
;; LENGTH: 594
;; TYPE: PRF
;; ORGANISM: Neisseria meningitidis
US-09-669-974-9

Query Match 92.6%; Score 2409.5; DB 4; Length 594;
Best Local Similarity 82.0%; Pred. No. 2,3e-184;
Matches 487; Conservative 7; Mismatches 19; Indels 81; Gaps 1;

QY 1 MNKIRIIMNSALNAAVAVSELTRNHTKRASATYKTAVALTLLFATVQANATDE----- 54
DB 1 MNKIRIIMNSALNAAVAVSELTRNHTKRASATYKTAVALTLLFATVQASTDDDLYLE 60
QY 55 ----- 54
DB 61 PVORTAVLSFRSDKEGTGEKEVTEEDSNMGVYFDKGVLTAGTITLAKGDNLIKONTNE 120
QY 55 ----- 54
DB 61 PVORTAVLSFRSDKEGTGEKEVTEEDSNMGVYFDKGVLTAGTITLAKGDNLIKONTNE 120
QY 55 ----- 54
DB 61 PVORTAVLSFRSDKEGTGEKEVTEEDSNMGVYFDKGVLTAGTITLAKGDNLIKONTNE 120
QY 121 NTAASFTYSLKDLDTLSVTEKLSFSANSKNVITSDTKGTFNFAKKAETNGDTVH 180
DB 121 NTAASFTYSLKDLDTLSVTEKLSFSANSKNVITSDTKGTFNFAKKAETNGDTVH 180
QY 100 LINGISLTLDMLNTGATNTVNDNTDDEKRRASAVKDYLNAGWNKGVKPGTTASDNV 159
DB 181 LINGISLTLDMLNTGATNTVNDNTDDEKRRASAVKDYLNAGWNKGVKPGTTASDNV 240
QY 160 DEVRTDYVEFLSADTKTTTVNVEESKDNKKTEVYKIGAKTSVYKEKDKLVYKGGENG 219
DB 241 DEVRTDYVEFLSADTKTTTVNVEESKDNKKTEVYKIGAKTSVYKEKDKLVYKGGENG 300
QY 220 SSVDEGLVTAKEVIDAVNKAAGWRKTTTANGOTGQADKFEPTVSGTXYTFASGNCTTA 279
DB 301 SSVDEGLVTAKEVIDAVNKAAGWRKTTTANGOTGQADKFEPTVSGTXYTFASGNCTTA 360
QY 280 TVSKDQDGNITVYDVNVGDALNVQNLQNSGWNLSKAVAGSSGKTVSGNVSPSKGMDE 339
DB 361 TVSKDQDGNITVYDVNVGDALNVQNLQNSGWNLSKAVAGSSGKTVSGNVSPSKGMDE 420
QY 340 TVNINAGNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANK 399
DB 421 TVNINAGNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANK 480
QY 400 PVRTTNAPGVKGGDVTNVAQLKGVANLNRRIDNVNGNARAGIAQAIATAGLYOATLPG 459
DB 481 PVRTTNAPGVKGGDVTNVAQLKGVANLNRRIDNVNGNARAGIAQAIATAGLYOATLPG 540
QY 460 KSMALGGGTLYGEGAGYAGYSSISAGNMIIKGTASGSRGHFGASASVGYOW 513
DB 541 KSMALGGGTLYGEGAGYAGYSSISAGNMIIKGTASGSRGHFGASASVGYOW 594

RESULT 13
US-09-377-155-21
;; Sequence 21, Application US/09377155
;; Patent No. 6197312
;; GENERAL INFORMATION:
;; APPLICANT: PEAK, Ian Richard Anselm
;; APPLICANT: JENNINGS, Michael Paul
;; APPLICANT: MOXON, E. Richard
;; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
;; FILE REFERENCE: 065064/0128
;; CURRENT APPLICATION NUMBER: US/09/377,155
;; CURRENT FILING DATE: 1999-08-19
;; PRIOR APPLICATION NUMBER: PCT/AU98/01031

;; PRIOR FILING DATE: 1998-12-14
;; PRIOR APPLICATION NUMBER: GB 9726398.2
;; PRIOR FILING DATE: 1997-12-12
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 21
;; LENGTH: 591
;; TYPE: PRF
;; ORGANISM: Neisseria meningitidis
US-09-377-155-21

Query Match 92.5%; Score 2407; DB 3; Length 591;
Best Local Similarity 82.6%; Pred. No. 3,7e-184;
Matches 489; Conservative 5; Mismatches 18; Indels 80; Gaps 2;

QY 1 MNKIRIIMNSALNAAVAVSELTRNHTKRASATYKTAVALTLLFATVQANATDE----- 54
DB 1 MNKIRIIMNSALNAAVAVSELTRNHTKRASATYKTAVALTLLFATVQASANNEDDEL 60
QY 55 ----- 54
DB 61 YLDPVORTAVLVNLSKKEGTGEKEVENSMAVYFNEKGVLTAREITLAKGDNLIKIKO 120
QY 55 ----- 54
DB 61 YLDPVORTAVLVNLSKKEGTGEKEVENSMAVYFNEKGVLTAREITLAKGDNLIKIKO 120
QY 121 NGTFNFTYSLKDLDTLSVTEKLSFSANSKNVITSDTKGTFNFAKKAETNGDTVH 180
DB 181 GIGSTLTLDMLNTGATNTVNDNTDDEKRRASAVKDYLNAGWNKGVKPGTTASDNVDF 240
QY 162 VRTDYVEFLSADTKTTTVNVEESKDNKKTEVYKIGAKTSVYKEKDKLVYKGGENGSS 221
DB 241 VRTDYVEFLSADTKTTTVNVEESKDNKKTEVYKIGAKTSVYKEKDKLVYKGGENGSS 300
QY 222 TDEGEGLVTAKEVIDAVNKAAGWRKTTTANGOTGQADKFEPTVSGTXYTFASGNCTTA 281
DB 301 TDEGEGLVTAKEVIDAVNKAAGWRKTTTANGOTGQADKFEPTVSGTXYTFASGNCTTA 360
QY 282 SKDDQDGNITVYDVNVGDALNVQNLQNSGWNLSKAVAGSSGKTVSGNVSPSKGMDETV 341
DB 361 SKDDQDGNITVYDVNVGDALNVQNLQNSGWNLSKAVAGSSGKTVSGNVSPSKGMDETV 420
QY 342 NINAGNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPV 401
DB 421 NINAGNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLSDVGD-ALNVGSKDKMPV 479
QY 402 RITNVAPGVKGGDVTNVAQLKGVANLNRRIDNVNGNARAGIAQAIATAGLYOATLPKS 461
DB 480 RITNVAPGVKGGDVTNVAQLKGVANLNRRIDNVNGNARAGIAQAIATAGLYOATLPKS 539
QY 462 MMAIGGTLYGEGAGYAGYSSISAGNMIIKGTASGSRGHFGASASVGYOW 513
DB 540 MMAIGGTLYGEGAGYAGYSSISAGNMIIKGTASGSRGHFGASASVGYOW 591

RESULT 14
US-09-669-974-21
;; Sequence 21, Application US/09669974
;; Patent No. 633173
;; GENERAL INFORMATION:
;; APPLICANT: PEAK, Ian Richard Anselm
;; APPLICANT: JENNINGS, Michael Paul
;; APPLICANT: MOXON, E. Richard
;; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
;; FILE REFERENCE: 065064/0128
;; CURRENT APPLICATION NUMBER: US/09/669,974
;; CURRENT FILING DATE: 2000-09-26
;; PRIOR APPLICATION NUMBER: US 09/377,155
;; PRIOR FILING DATE: 1999-08-19
;; PRIOR APPLICATION NUMBER: PCT/AU98/01031
;; PRIOR FILING DATE: 1998-12-14
;; PRIOR APPLICATION NUMBER: GB 9726398.2

;; PRIOR FILING DATE: 1997-12-12
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 21
;; LENGTH: 591
;; TYPE: PRF
;; ORGANISM: Neisseria meningitidis
US-09-669-974-21

Query Match 92.5%; Score 2407; DB 4; Length 591;
Best Local Similarity 82.6%; Pred. No. 3.7e-184;
Matches 489; Conservative 5; Mismatches 18; Indels 80; Gaps 2;

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QY 1 MKKIRIINWSALNMAVAVSELTNRHNRKASATVTAVALTLLFATVQANATDE----- 54
DB 1 MKKIRIINWSALNMAVAVSELTNRHNRKASATVTAVALTLLFATVQASANNRBEEDL 60
QY 55 ----- 54
DB 61 YLDPVQRTVAVLIVNSDKEGTEKEKEVEENSDMAVYFNEKGVLTAREITLAKADNLKIK 120
QY 55 -----TGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTVHLN 101
DB 121 NGTNFTYSLKDLTDLTSVTEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTVHLN 180
QY 102 GIGSTLFDMLNTGATTNTNDNTDDEKRRASAVKDVNLNAGWNIKGVKPGTTASDNVD 161
DB 181 GIGSTLFDMLNTGATTNTNDNTDDEKRRASAVKDVNLNAGWNIKGVKPGTTASDNVD 240
QY 162 VRTYDVEFLSADTKRTTYNVESKONGKTEVKIGAKTSVIEKEDKLVYTGKDGKENGSS 221
DB 241 VRTYDVEFLSADTKRTTYNVESKONGKTEVKIGAKTSVIEKEDKLVYTGKDGKENGSS 300
QY 222 TDEBEGLYTAKEVIDAVNKAQRMTTANQOTGADKFEFVTSGTXYTFASGNGTATV 281
DB 301 TDEBEGLYTAKEVIDAVNKAQRMTTANQOTGADKFEFVTSGTXYTFASGNGTATV 360
QY 282 SKDDOGNITVYKDYVNVGDLNVLNOLNSGMNLDKRAVSSGKVIISGNVSPSKGMDFTV 341
DB 361 SKDDOGNITVYKDYVNVGDLNVLNOLNSGMNLDKRAVSSGKVIISGNVSPSKGMDFTV 420
QY 342 NINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLVSVDDEGALNVSGSKDANKP 401
DB 421 NINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLVSVDG-ALNVSGSKDANKP 479
QY 402 RITNVAPEGKEDVTNVAQLKGVAQNLNRRIDNVNNGNARAGIAQAIATAGLVQAYLPKGS 461
DB 480 RITNVAPEGKEDVTNVAQLKGVAQNLNRRIDNVNNGNARAGIAQAIATAGLVQAYLPKGS 539
QY 462 MMAIGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSRGHFGASASVGYOW 513
DB 540 MMAIGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 591

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RESULT 15
US-09-377-155-2
; Sequence 2, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0.
; SEQ ID NO 2

;; LENGTH: 592
;; TYPE: PRF
;; ORGANISM: Neisseria meningitidis
US-09-377-155-2

Query Match 92.3%; Score 2402.5; DB 3; Length 592;
Best Local Similarity 82.3%; Pred. No. 8.4e-184;
Matches 488; Conservative 5; Mismatches 19; Indels 81; Gaps 2;

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QY 1 MKKIRIINWSALNMAVAVSELTNRHNRKASATVTAVALTLLFATVQANATDE----- 54
DB 1 MKKIRIINWSALNMAVAVSELTNRHNRKASATVTAVALTLLFATVQASANNRBEEDL 60
QY 55 ----- 54
DB 61 YLDPVQRTVAVLIVNSDKEGTEKEKEVEENSDMAVYFNEKGVLTAREITLAKADNLKIK 120
QY 55 -----TGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTVHLN 100
DB 121 NGTNFTYSLKDLTDLTSVTEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDTVHLN 180
QY 101 NGIGSTLFDMLNTGATTNTNDNTDDEKRRASAVKDVNLNAGWNIKGVKPGTTASDNVD 160
DB 181 NGIGSTLFDMLNTGATTNTNDNTDDEKRRASAVKDVNLNAGWNIKGVKPGTTASDNVD 240
QY 161 FVRTYDVEFLSADTKRTTYNVESKONGKTEVKIGAKTSVIEKEDKLVYTGKDGKENGSS 220
DB 241 FVRTYDVEFLSADTKRTTYNVESKONGKTEVKIGAKTSVIEKEDKLVYTGKDGKENGSS 300
QY 221 STDEBEGLYTAKEVIDAVNKAQRMTTANQOTGADKFEFVTSGTXYTFASGNGTATV 280
DB 301 STDEBEGLYTAKEVIDAVNKAQRMTTANQOTGADKFEFVTSGTXYTFASGNGTATV 360
QY 281 VSKDDOGNITVYKDYVNVGDLNVLNOLNSGMNLDKRAVSSGKVIISGNVSPSKGMDFT 340
DB 361 VSKDDOGNITVYKDYVNVGDLNVLNOLNSGMNLDKRAVSSGKVIISGNVSPSKGMDFT 420
QY 341 VNINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLVSVDDEGALNVSGSKDANKP 400
DB 421 VNINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLVSVDG-ALNVSGSKDANKP 479
QY 401 VRTNVAPEGKEDVTNVAQLKGVAQNLNRRIDNVNNGNARAGIAQAIATAGLVQAYLPK 460
DB 480 VRTNVAPEGKEDVTNVAQLKGVAQNLNRRIDNVNNGNARAGIAQAIATAGLVQAYLPK 539
QY 461 SMAAIGGTYLGEAGYAIGYSSISAGGNWIIKGTASGNSRGHFGASASVGYOW 513
DB 540 SMAAIGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 592

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Search completed: October 6, 2003, 09:35:42
Job time : 15.7186 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:35 ; Search time 14.6847 Seconds
(without alignments)
3359.577 Million cell updates/sec

Title: US-09-771-382-24

Perfect score: 2602

Sequence: 1 MNKIYRIIWSALNANWAVS.....TASGNSRGHPGASGVGYQW 513

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2407	92.5	591	2 G81133	adhesin NMB0992 [i
2	2351.5	90.4	592	2 A81888	probable surface f
3	526.5	20.2	298	2 I64138	adhesin homolog HI
4	371	14.3	1588	2 A86036	probable adhesin z
5	371	14.3	1588	2 H91188	probable adhesin z
6	365	14.0	1190	2 A82615	surface protein XF
7	361	13.9	1107	2 AC0976	probable autotrans
8	359.5	13.8	2059	2 D82671	surface protein XF
9	333.5	12.8	638	2 AH0110	probable surface p
10	241	9.3	1091	2 G64964	hypothetical prote
11	231.5	8.9	1004	2 C82672	surface-exposed ou
12	231	8.9	1325	2 A64905	yvek protein - Esc
13	222.5	8.6	949	2 D90803	Aida-I adhesin-lik
14	222.5	8.6	1005	2 H85611	probable adhesin z
15	220.5	8.5	1286	2 S28634	adhesin Aida-I pre
16	211	8.1	1343	2 E90893	hypothetical prote
17	209	8.0	3705	2 AD0123	probable autotrans
18	208	8.0	1343	2 D85724	hypothetical prote
19	207.5	8.0	1018	2 H83135	probable adhesin p
20	206	7.9	1910	2 AF0384	probable adhesin h
21	201	7.7	2249	2 A41477	100k surface anlig
22	198	7.6	5188	2 B85547	probable RTX fami
23	198	7.6	5291	2 F90696	hypothetical prote
24	197.5	7.6	1536	2 A43855	high-molecular-we
25	197.5	7.6	3029	2 S76109	hypothetical prote
26	193	7.4	4919	2 T31105	hypothetical prote
27	192.5	7.4	936	2 I40711	sapB protein - Cam
28	191.5	7.4	1651	2 J01340	outer membrane pro
29	191	7.3	1477	2 B43855	high-molecular-we

30	189.5	7.3	2468	2 A83412	hypothetical prote
31	188	7.2	2020	2 C48399	ABC-type transport
32	187.5	7.2	365	2 AB3486	cell surface prote
33	187	7.2	961	2 AD0548	putative autotransp
34	187	7.2	3013	2 AB0480	probable invasin x
35	185	7.1	4152	2 T31102	filamentous hemagg
36	184.5	7.1	1417	2 A83080	hypothetical prote
37	184	7.1	2551	2 B98047	hypothetical prote
38	182.5	7.0	1004	2 T00046	surface layer prot
39	182.5	7.0	1109	2 A56143	surface-array prot
40	182	7.0	1655	2 E97835	hypothetical prote
41	181.5	7.0	1275	2 T33369	hypothetical prote
42	181	7.0	1366	2 S57664	IgA-specific metal
43	180.5	6.9	893	2 A37284	surface-array/hemo
44	180.5	6.9	1268	2 B99789	hemagglutinin/hemo
45	180.5	6.9	1270	2 E85649	hypothetical prote

ALIGNMENTS

RESULT 1

G81133
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: G81133
R:Retelijn, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. et al., H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masigian, V.; Pizzia, M. Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: G81133
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-591 <RT>
A:Cross-references: GB:AE002450; GB:AE002098; NID:97226229; PID:AAF41395.1; PID:9722
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0992

Query Match	92.5%	Score 2407;	DB 2;	Length 591;
Best Local Similarity	82.6%	Pred. No. 2,7e-118;		
Matches 489;	Conservative	5;	Mismatches 18;	Indels 80;
Gaps				2;
QY	1	MNKIYRIIWSALNANWAVSELTNNHTKRASATVATVATLLEFATVQANATDE-----	54	
DB	1	MNKIYRIIWSALNANWVAVSELTNNHTKRASATVATVATLLEFATVQANNEDEEDL	60	
QY	55	-----	54	
DB	61	YLDPEORTVAVLIVNSDKEGTEGEKVEENSDMAVYENKGVLTAREITLLAKGDNLIKQ	120	
QY	55	-----	101	
DB	121	NGTNYTSLKKDLTDLISVGETKLSFSANGKAVVITSDTKLNAKETAAGNGDTYHNL	180	
QY	102	GIGSTLMDLNTGATTTNTNDVTDDEKRRASVSKDVLANGMNKGKPGPTASDVNDF	161	
DB	181	GIGSTLMDLNTGATTTNTNDVTDDEKRRASVSKDVLANGMNKGKPGPTASDVNDF	240	
QY	162	VRTDYVEFLSADPKTTTNNVESDNGKTEVKGATSVYKEDGKLVYKGGENGSS	221	
DB	241	VRTDYVEFLSADPKTTTNNVESDNGKTEVKGATSVYKEDGKLVYKGGENGSS	300	
QY	222	TDEEGGLVTAKEVDAVNAKGMKKTATANGQTGADKFETVSGTAVTFASGAGTATV	281	
DB	301	TDEEGGLVTAKEVDAVNAKGMKKTATANGQTGADKFETVSGTAVTFASGAGTATV	360	
QY	282	SKDDGNITVYKYDVNVGDALNVNOLNSGNWLDKRAVAGSSGKVISGNVSPSKMDETV	341	


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Db 361 SKDDGNTVTADVAVGALNVNQLQNSGWNIDSKAVAGSSGKVTISGVNPSFKMDETV 420
Oy 342 NINAGNNIETIRNGKNIDIASMTPOFSSVSLGAGADAPTSLVDEGALNVGSKDANKPV 401
Db 421 NINAGNNIETIRNGKNIDIASMTPOFSSVSLGAGADAPTSLVDEGALNVGSKDANKPV 479
Oy 402 RTTNVAPGVKESDVTNVAOLKGVAAONLNRRIDNVGNARAGIAQAIAATAGLVQAVLPGRS 461
Db 480 RTTNVAPGVKESDVTNVAOLKGVAAONLNRRIDNVGNARAGIAQAIAATAGLVQAVLPGRS 539
Oy 462 MMAIGGTYLGEAGYALIGYSSISAGNNITKGTASGNSRHHGASASVGYQW 513
Db 540 MMAIGGTYLGEAGYALIGYSSISAGNNITKGTASGNSRHHGASASVGYQW 591

RESULT 2
A:1888
probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain Z249)
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: A81888
R:Parthill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel,
N.; Holroyd, S.; Jørgensen, K.; Leather, S.; Mølle, S.; Mungall, K.; Quail, M.A.; Rajandream,
N.; et al. 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:2022556; PMID:10761919
A:Accession: A81888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-592 <PAR>
A:Cross-References: GB:A162755; GB:A157959; NID:g7379742; PIDN:CAB84461.1; PID:g737985
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1200

Query Match 90.4%; Score 2351.5; DB 2; Length 592;
Best Local Similarity 80.8%; Pred. No. 2.1e-115;
Matches 480; Conservative 9; Mismatches 22; Indels 83; Gaps 3;

Oy 1 MNKIRIITNSALNMAVAVSELTRNHRKASATVTAVALTLFATVQANATDE----- 54
Db 1 MNKIRIITNSALNMAVAVSELTRNHRKASATVTAVALTLFATVQANATDEDEDEEL 60
Oy 55 ----- 54
Db 61 ESVQSVVGSIOASMEGSELETTISLMTNDSKEFVPIYVTLKAGDMLKIKONTNENT 120
Oy 55 -----TGLINVERPEKLSFGANGKRVNIISDTKGNLPAKETAAGTGTTHLN 101
Db 121 NASSSTYSILKDLTGLINVERPEKLSFGANGKRVNIISDTKGNLPAKETAAGTGTTHLN 180
Oy 102 GIGSTLTMDLNTGATTVTNDVTDDEKRAASVQVYLNAGNIIKGVKPGTTA--SDNV 159
Db 181 GIGSTLTMDLNTGATTVTNDVTDDEKRAASVQVYLNAGNIIKGVKPGTTA--SDNV 238
Oy 160 DFRVTYDVEELSDTKTTTVNVEKSKDNGKTEVKIGAKTSYIKERDGLVTKGKGENG 219
Db 239 DFRVTYDVEELSDTKTTTVNVEKSKDNGKTEVKIGAKTSYIKERDGLVTKGKGENG 298
Oy 220 SSTDGDELVNAKEVIDAVNKGWMMKTTTANGQGOADKFTVYSGTAVTASGNGTTA 279
Db 299 SSTDGDELVNAKEVIDAVNKGWMMKTTTANGQGOADKFTVYSGTAVTASGNGTTA 358
Oy 280 TVSKDDGNTITVYKVVYVNGDALNVNQLQNSGWNIDSKAVAGSSGKVTISGVNPSFKMDE 339
Db 359 TVSKDDGNTITVYKVVYVNGDALNVNQLQNSGWNIDSKAVAGSSGKVTISGVNPSFKMDE 418
Oy 340 TVNINAGNNIETIRNGKNIDIASMTPOFSSVSLGAGADAPTSLVDEGALNVGSKDANK 399
Db 419 TVNINAGNNIETIRNGKNIDIASMTPOFSSVSLGAGADAPTSLVDEGALNVGSKDANK 478
Oy 400 PYRTINVAPGVKESDVTNVAOLKGVAAONLNRRIDNVGNARAGIAQAIAATAGLVQAVLP 459
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Db 479 PYRTINVAPGVKESDVTNVAOLKGVAAONLNRRIDNVGNARAGIAQAIAATAGLVQAVLP 538
Oy 460 KSMAIGGTYLGEAGYALIGYSSISAGNNITKGTASGNSRHHGASASVGYQW 513
Db 539 KSMAIGGTYLGEAGYALIGYSSISAGNNITKGTASGNSRHHGASASVGYQW 592

RESULT 3
A:16138
adhesin homolog H11732 - Haemophilus influenzae (strain Rd Kw20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997
C:Accession: I64138
R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage,
J.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.L.; Glodek, A.; Kelley, J.M.; Weidman,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A.; et al. 1995
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: I64138
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-298 <TIG>
A:Cross-References: GB:U32846; GB:I42023; NID:g1574588; PID:g1574589; TIGR:H11732

Query Match 20.2%; Score 526.5; DB 2; Length 298;
Best Local Similarity 43.1%; Pred. No. 1.1e-20;
Matches 129; Conservative 28; Mismatches 63; Indels 79; Gaps 7;

Oy 1 MNKIRIITNSALNMAVAVSELTRNHRKASATVTAVALTLFATVQANATDE----- 49
Db 1 MNKIRIITNSALNMAVAVSELTRNHRKASATVTAVALTLFATVQANATDE----- 60
Oy 50 -----NATDETGL-----INVEREK 64
Db 61 STEDIEDSAATKDDNKQALKAQTLTLTKACKNLKAKIDGCGKSVTALAKDLVKTAK 120
Oy 65 LS-----FGANGKRVNIISDTKGNLPAKETAAGTGTTHLNGLSTLMDLN 113
Db 121 VSDTLTIGNTPAAGATPKVSIITSDADGLAKA---GNGDGVNHLNGLASTLDVPTN 177
Oy 114 TGATTNVTNDVTDDEKRAASVQVYLNAGNIIKGVKPGTTASDNDVFRYTYDEFLSA 173
Db 178 TGASTSVT-FSPSDIEKTRAAIKDYLNAGNIIKGVKPGTTASDNDVFRYTYDEFLSA 236
Oy 174 DFKTTTVNVEKSKDNGKTEVKIGAKTSYIKERDGLVTKGKGENG-----GKGENG-SSTDE 224
Db 237 DKNTLDVYLTAKENKTEVKFTPKTSYIKDNGKLLTGKQLKDANTGATATNATEDTDE 295

RESULT 4
A:86036
probable adhesin 25029 [imported] - Escherichia coli (strain O157:H7, substrain EDL93)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: A86036
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May,
J.L.; Fajer, L.; Grobbeck, E.J.; Davis, N.W.; Linn, A.; Dimalanta, E.; Potamousis, K.; Apoda,
N.; et al. 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A86036
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1588 <STO>
A:Cross-References: GB:AE005174; NID:g12518349; PIDN:AAG58749.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: 25029

Query Match 14.3%; Score 371; DB 2; Length 1588;
Best Local Similarity 23.5%; Pred. No. 1.2e-11;
```


A:Contents: annotation
C:Genetics:
A:Gene: XF1981

Query Match 14.0%; Score 365; DB 2; Length 1190;
Best Local Similarity 24.8%; Pred. No. 1.7e-11;
Matches 141; Conservative 83; Mismatches 213; Indels 132; Gaps 20;

```
QY 17 VAVSELRNHTKRASATVKTAVLATLFLATVQANATDEGLINVEFKLSFGAN-----70
DB 682 VTSSSISAGNOKITVAVGATADTDAVNFSQLOAVSSTASKGNL-----LASANSNNAP 737
QY 71 GKKNVVISDTGKLNFAKETAG-----TNGDTVHLNIGISGTLTDLMLNT 114
DB 738 GESVDLKTMDGNIVISKESGNDVLENTSSSLKLDKLFTVGDVTMTNGV-----TVGS 790
QY 115 GATTNVTNDNTDDEKKRAASKVDLNG-NNIKGVKPGTASD-----157
DB 791 GTTLAGSMGLVITDGPSTVSSGI---NAGSOKITVAVGATADTDAVNLSQLTAMAGSGA 846
QY 158 -NVDEVRTYDVEFLSADTKTTTVNVESSKNGKTEVKIGAKTSYIKEDGKLVYTGKKG 216
DB 847 KSVHYSTYD-----GGTGGGNTNGDAGTGTFRSLAVGGLASA-----EGATAVGSGGA 896
QY 217 ENG-SSTDEBEGLVAKAYIDAANKAGMRMKTATTANGOTGADKFTVTSCTKTPASGN 275
DB 897 ASGKSTAIGRNAVASADGSVALGD-GAKDGARGAESYTGKYSGLQNNVTGTVSYVDASK 955
QY 276 GTTAVVSKDDGNTIVKYDVNVGDALNVNOL-----QNSGMNLDKRAVAGSSGKTVSGNS 331
DB 956 GETRTVVS-----NVADAKEAT--DAVNLRLDRVADANRYVDANKIESLSEGOTF-----1003
QY 332 PSKGMDEVTNINAGNNIEITRNGKNIDITATSMTPFSSVSISAGADA-----P 380
DB 1004 -----YKYNLSLN-----SAPPLIAGVATAIGCATASGADSIAMGNKA 1043
QY 381 TLSVDEGAL-----NNGSKDANKPVRTTNVAPGYKEGDVTNVNOLKQVONL 428
DB 1044 SASADNAVALIGNHSAVDANRATVSVGSAGSER--QVTNNAAGTADDAVNVSQLNGLTJA 1101
QY 429 NNRIDNVGNAR-----AGTAAIATAGLVQAVLPCKSMKAIIGGTYLGEAGVAIGYSIS 484
DB 1102 KQYTDGVVGSRLRRDIDGGVAAAIATANLPQATITPERGMTSVGVSSIRGOSAIATAGVSVS 1161
QY 485 AGGNMIIGKTASGNSRGHFGASASVGYOW 513
DB 1162 ESGRWVFKFSGSANTRSQVIGAGVGYOW 1190
```

RESULT 7

AC0976
Probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serovar Typhimurium
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: This species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AC0976
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Parkhill, J.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AC0976
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1107 <PAR>
A:Cross-References: GB:AL513382; PIDN:CAD03303.1; PID:g16504923; GSPDB:GN00176
C:Genetics:
A:Gene: sapB

Query Match 13.9%; Score 361; DB 2; Length 1107;
Best Local Similarity 21.7%; Pred. No. 2.5e-11;

Matches 171; Conservative 94; Mismatches 222; Indels 302; Gaps 29;

```
QY 9 WNSALNAN-----VAVSELRNHTKRASATVKTAVLATLFLAT---VOANA 51
DB 337 WNETNSTSASGSSSTTKKITVAVAGELSEEST-----DAVNSOLFENNEVDONT 388
QY 52 TD-----EGLINVEF-----EKLSGAN--GKKNV 77
DB 389 TDIAANTNITONSATNENLNTSVSDINTSITGLTDMALMDDEDAFASANGGSTSKIT 448
QY 78 SDPTKLNFAKETAGNG-----DTVHLNIGISGTLTDLMLNTGATNVNNDVTDEKKRA 133
DB 449 NVAGALSSEDSTDAVNSQLETKNOKVDONTSAID--INT-SITNLGTDALSDWDEBA 505
QY 134 ASVKDVLNAGMNIKGVKGTTPASDVDPV---RTVDT-----VEFLSADTKTTTV 180
DB 506 FSASHGTSCTKNTITVAVAGELASDSTDAINSQLETKNMLLSQVNESISQLAGDTSERYI 565
QY 181 N-----VESKNGKTEVKIGAKTSYIKEDGKLVYTGK--KGNGSSTDEG---225
DB 566 TENGTVKRYIRINDGLEGODAYATNGATAYGDVAVASGAGCLALGONSSSIEGSIATL 625
QY 226 -----EGLY-----TAKEVIDAVNKA---GMRMKTTPANGGTG 255
DB 626 GSGSTSNRAITTGIRETSATSDGVYIGYNTTDRLLGLSLGTDEESTROTINWADGSEA 685
QY 256 Q-----ADKFTVTSCTKTVFASGNGTTPATVSKDDGNTVYKYDVNV 297
DB 686 QDAVTVROLQNAIGAVTTTPTKYHANSTBEDSLAVGTDLSLMAKAK-----TIVNADAGI 740
QY 298 GDALVNVNOLN--SGWMLDSKAVAGSSGKTVSGNSP-----332
DB 741 GIGLTLVMAIDAINGIAISNARAHANSIANGNSQTTGCAQDTYATVNMPTPONSVE 800
QY 333 -SKGMD--ETVNIINAGN-----NIEITRNGKNI-----358
DB 801 FSVSGEDGORTITNAAGSADTDAVNVGOLKATDQVSRNTOITNLTOVSNLDTRTN 860
QY 359 -----DIATSMTPPF-----SSVSLGAGADAP-----TLSVDE-G 388
DB 861 IENGIGDVTGTSSTYFPTNTDGDADANQAGDSVALIGSSITAAEANSVALGTNSVADBAN 920
QY 389 ALNNGSKANKPVRTTNVAPGYKEGDVTNVNOLK-----422
DB 921 TVSVGSSTQOR--RITNVAAGVNNPDVAVNVLKASEAGSVRYETNADGSVNSVYLNLDG 978
QY 423 -----GVAO-----NLNRIIDNVGNARAGIA 444
DB 979 GSGGTRIGNVSAVNDIDAVNVADLKRKSVBEANTYTDQKGEHNSKIKIGENKKSITA 1038
QY 445 QAIATAGLVQAVLPCKSMKAIIGGTYLGEAGVAIGYSISAGGNMIIGKTASGNSRGHFG 504
DB 1039 SAMAAVAGLPQAVAPGANTSTIGTFNGESAAVAIGVSVSEGGVYKLGTSNSGQDYS 1098
QY 505 ASASVGYOW 513
DB 1099 AAIAGAGQW 1107
```

RESULT 8

DB2671
Surface protein XF1529 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: DB2671
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: AB2515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number AS9328 below
A:Accession: DB2671
A:Status: preliminary
A:Molecule type: DNA

science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: G64964
A:Status: nucleic acid sequence+not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1091 <BLAST>
A:Cross-references: GB:AE000291; GB:U00096; NID:g1788298; PIDN:AACT5061.1; PID:g1788309,
A:Experimental source: Strain K-12, substrain M6165
C:Keywords: nucleotide binding; P-loop
F:683-690/Region: nucleotide-binding motif A (P-loop)

Query Match 9.3%, Score 241; DB 2; Length 1091;
Best Local Similarity 21.5%, Pred. No. 4.4e-05;
Matches 131; Conservative 92; Mismatches 236; Indels 150; Gaps 29;

QY 1 MNKYYRIIWNALNAAVAVSELTRNHHKRSATYKTAVALATLATATQAN-----ATDE 54
DB 57 LNTYRIIRLVNMTGAFVAVASELARGRGVAAVSLAAVTSPLVLAADIVHPEGTVN 116
QY 55 TGLINVEETKLSFG-ANGKKVNIISDTKGLNFAKET-----AGTNGDTTHLNG 102
DB 117 GGTLANNDNQVFEFTTNGMTI-----STGLETGPDNEANTGGQVAVODGTANKTTVYISGG 171
QY 103 I-----GSTLDMLNTGATTNV-----TNDNVTDDEK---KRAASVKDVLN-AGNINIKV 149
DB 172 LQRYNPGSVSDYFISAGGSLOGRAVNTTLNGEOMHMGALATGTVINDKGMQV--V 229
QY 150 KPGTTASNDVFEVT-----YPTVEFLSADTKTTTVN-----VESKDGKRTVEY 193
DB 230 KPGVVAIDTV--VATGABGGPDANGDTGCPVRGDAAVKTITNKKGRQIVRAEGTANTTV 287
QY 194 KIGAKTSV-----IKEDGKLVTGKGGENGSSYDEGEGL 228
DB 288 YAGDDQYVHGHALDTTLNGGYQYVHNGCTASDTVANSDDQIVKNG--GVAGNTTVNQGGR 346
QY 229 VTAKEVIDAVN---KAGRMKTTTANGOT-----GQADKEPTVSGSKYVFAAS 273
DB 347 LQYDAGGTAIVTLKQGALVTSTAATVYTGIRLGAPSVYEGKADNV-VLENGGRDLVLT 405
QY 274 GNGTTATVSKDQGNITVYKYDVNVDALNVAQLONSQGNLDSKAVAGSSGVISGVNSPS 333
DB 406 GHTATNT- RYVDDGDTLDR---NGCTATTVS-MENGG-----VLLADSGAASVGTISDG 454
QY 334 K-----GKMDETVINAGNNIETTRNGKNIDIAFSMPQSSSVSLGACADAPTSLVDDEG 388
DB 455 KAFSIGGQADALMLEKSSFTLNAG---DTADDTYVNGGLFTFARGGTLLAGTTLLNCA 510
QY 389 ALANGSKDANKPVRITVAVPGVKEGDVTNVQLGVAQNLNRRIDNVNNGNARAGIAQIA 448
DB 511 ILTISGKTVN-----MDTLTIRGSD-----ALLGGSLITGSGVYEK-SGSGTLTVSNTLL 559
QY 449 TAGIVQAVLPKSKMAIGGGT---YLGEAGYAIAGYS-----SISAGNWI 490
DB 560 TOKAVNL---NEGTLITNDSTVTTDVIAIGRGTALKLGSFTVNLGAIDPTVNTLASGATWN 616
QY 491 IKGTASGNS 499
DB 617 IPDNATVOS 625

RESULT 11
C82672
Surface-exposed outer membrane protein Xrl516 [imported] - *Xylella fastidiosa* (strain 96
C:Species: *Xylella fastidiosa*
C:Date: 18-Aug-2000 #sequence,revision 20-Aug-2000 #text,change 20-Aug-2000
C:Accession: C82672
A:Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: C82672

[illegible]

RESULT 12

ydek protein - Escherichia coli (strain K-12)

A64905

N:Alternate names: protein T

C:Species: Escherichia coli

C>Date: 12-Sep-1997 #sequence,revision 17-Sep-1997 #text_change 01-Mar-2002

C:Accession: A64905; 152440; S54315

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: A64905

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1325 <BLAT>

A:Cross-references: GB:AE000248; GB:U00096; NID:g1787783; PIDN:AAC74583.1; PID:g1787788;

A:Experimental source: strain K-12, substrain MG1655

R:Cartwright, P.; Tjims, M.; Lithgow, T.; Hoj, P.; Hoogenraad, N.

Biochim. Biophys. Acta 1153, 345-347, 1993

A:Title: An Escherichia coli gene showing a potential ancestral relationship to the gene

A:Reference number: 152440; MUID:94100243; PMID:8274505

A:Accession: 152440

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 689-883, 'K', 885-1316, 'S', 1318-1325 <RES>

A:Cross-references: EMBL:X73295; NID:g312392; PIDN:CA51730.1; PID:g312393

A:Note: the difference in length is due to a frameshift error at pos 653

C:Genetics:

A:Gene: ydek

A:Function:

A:Description: probably involved in protein translocation apparatus

C:Keywords: nucleotide binding; P-loop

F:172-179/Region: nucleotide-binding motif A (P-loop)

Query Match 8.9%; Score 231; DB 2; Length 1325;

Best Local Similarity 24.4%; Pred. No. 0.00019;

Matches 146; Conservative 65; Mismatches 245; Indels 142; Gaps 29;

QY 1 MNKRIITMNSALNMAVAVSELTR-----NHTKRASATVKTAVLATLFAVQANAT 52

DB 1 MNRIYIMNCTLOVQACSELTFRRAKSTVNLKRSGLTFRSLTLGLVLLASGSAS 60

QY 53 -----DETGLINVEFE-----KLISGANGKKNVNIISDRKGLNFAKETA 90

DB 61 GASLEVDNDQITMIDVDVAYDAYLVGWYGTGVLNIIAAGNASLTTITTSVIGAN--EDSE 118

QY 91 GTNGDFTVHLNGIGST--LTD-----MLNTG-----ATTNVTNDNVTDDEKKRAASVKDV 139

DB 119 GT-----VNVIGGTMRLLYDSGNMARPILAVGOSGTILNKKQGHVDS-----GY 162

QY 140 LNAAGNIKGVKPGTTASDNVDVRYVDTEFLSADTKTTTVNESKDKNGKTE----- 192

DB 163 LRLGSSSTGV--GTAVNEGEDSVLTLEFETGSGTSLNIT--DKGYTSSVAILG 216

QY 193 VKIGARTSVYKEDGK-LVYTK-----GKGENGSTDEGBGLYAKVYDAVNAKAGW 243

DB 217 YQAGSNGQVYVEGGEVLINNDSSLEFOIGNOGTGATIREGGLVTAENTYIIGSNATG- 275

QY 244 RMTTANGOTGADKEFEVYSGKVFASGNGTAVTAVSKDDOGNITVK-YD-VNVDAL 301

DB 276 ----IGTLNVO-----DDSVITVRLRLNGYFGNG---TVNLSNGLINNKKEISLVGVDDGS 325

QY 302 N--VNOLQNSGWL-----DSKAVAGSSGKVIISGNVSPSKGKMDFTVNI 343

DB 326 HGVVNVYTDKGMHMFELTGEAFRTYIGDADGELNVSSEKGVDSGIITAG---MKER--- 379

QY 344 NAGN-----NIETTRNGKNIDTATSMTPPOFSSVSLGAGADAPTLVYDEGALNV----- 392

DB 380 GTGNITVYKDNKSVITNLTGTLNLYDGHGEMNISNOGLVAVSNGSSLGGETGVGNVSYTTG 439

RESULT 13

Aida-I adhesin-like protein [imported] - Escherichia coli (strain 0157:H7, substrain

D90803

C:Species: Escherichia coli

C>Date: 18-Jul-2001 #sequence,revision 18-Jul-2001 #text_change 18-Jul-2001

C:Accession: D90803

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C

gasawara, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and 9

A:Reference number: A99629; MUID:2156231; PMID:11258796

A:Accession: D90803

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-949 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA834819.1; PID:g13360856; GSPDB:GN00154

A:Experimental source: strain 0157:H7, substrain RMD 0509952

C:Genetics:

A:Gene: Ecs1396

Query Match 8.6%; Score 222.5; DB 2; Length 949;

Best Local Similarity 21.7%; Pred. No. 0.00034;

Matches 131; Conservative 80; Mismatches 224; Indels 169; Gaps 28;

QY 1 MNKRIITMNSALNMAVAVSELTRNHTKRASATVYK-----TAVLATLFAVQANATDE 54

DB 5 LNTSYRLVNMHITGTLVVASSELARSRGKRAVAVALSIAVTSVALADKVVQAGETVN 64

QY 55 TGLINVTETKLSFG-ANGKKNVNIISDRKGLNFAKET-----AGTNGDFTVLLNG 102

DB 65 DGTLLNHDNIVETGTANGMTT-----STGELGLPDSSENTGGMTONGIAGNTVYTTNG 119

QY 103 -----IGSTLLDMLNTG-----ATTNVTNDNVTDDEK 130

DB 120 ROVLVEGTFASDPIYRBDGGGSLNGLAVNTLNNRGEQWHEGAVATGTLINRBDGYGVK 179

QY 131 KRAASVDVILNAGNINIGVAPGTTASDNVDVRYVDTEFLSADTKTTTVNESKDKGK 190

DB 180 SGLATGTIINTG-----AEGGPDSDN-----SY-TGQRYOGTAESTTIN---KNGRQ 223

QY 191 TEVKIG-AKTSVYKEDGKLVYTKGKQ--ENGSTDEGBGLYAKVYDAVNAKAGRM- 245

DB 224 TILFSLAROTLIYAGDQSYHGKALMTTLNGYQYHROGLA-----LNTYINSGNQVY 279

QY 246 -----KTTTANGQT-----GQADKEFEVYSGKVFASGNGTAVTAVSKDDQ-GNITV 291

DB 280 KAGGAGNTTINQNGELRVHAGGEATAVTOFTGALVT-----STAATVIGTNLGNFTV 334

QY 292 KYDVNVBDALNVNOLQNSGWLDSKAVAGSSGKVI--SGNVSPSKGKMDFTVNIAGNNI 349

DB 335 ENGRADSVVL-----ESGRDLVDLESHSAQNTLVLDGGTLVAVSAGAKASVYITISGAL 388

QY 350 EITRNGKNIDTATSMTPPOF-----SVLSIGAGADAPTLVYDEGALNV 392

DB 389 -IADSGATVE-GTINASGKFSIDTSGQASGLLENGSFTVNAAGQAGNTTVGHRGTL 446

QY 393 -----GSKDANKPVYITTVAVGVKEDGVYTNNAQLKGVANQNLNRIDNVGNARAGIAQ 445

DB 447 AAGSLSGRQOLSGAGAMVNLGVDVSTGDIYNAGEI-----RDN-QTPNMAISR 496

QY 446 AATAG-----LVQAYLPDK-----SMAAGGTYLCEAGYA---IG 479

DB 497 AVAKSNSRPVTFHKLTTTLNLGOGGTIMRVRVLDGSNASDQVLVINGGQATGKTWLAFTNVG 556

OY 480 YSSI 483
Db 557 NSNL 560

RESULT 14

probable adhesin Z1211 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: H85611; B85663
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Hiller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H85611
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1005 <STO>
A:Cross-References: GB:AE005174; NID:g12514025; PIDN:AG55356.1; GSPDB:GN00145; UMG:212
A:Experimental source: strain O157:H7, substrain EDL933
A:Accession: B85663
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1005 <ST2>
A:Cross-References: GB:AE005174; NID:g12514546; PIDN:AG55766.1; GSPDB:GN00145; UMG:216
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z1211; Z1651

Query Match 8.6%; Score 222.5; DB 2; Length 1005;
Best Local Similarity 21.7%; Pred. No. 0.0037;
Matches 131; Conservative 80; Mismatches 224; Indels 169; Gaps 28;

OY 1 MNKIRITWNSALNMAVAVSELTNRHTRKASATVK-----TAVLATLTFATVQANANDE 54
Db 61 LMTSTRLVNHNHTGLVVAASELARSGRKAGVAVALSIAAIVSVPLAADKVVQAQETVN 120
OY 55 TGLINVEETKLSFG-ANGKKVNIISDTKGLNFAKET-----AGTNGDTVHLNG 102
Db 121 DGLTNHNDQIYFGTANGMTI-----STGLELGPSEENTGGQWONGSIACTTYTNG 175
OY 103 -----IGSTLDMMLNTG-----ATTNVTNDVNTDEK 130
Db 176 ROYVLEGGTASDPTVRIDGGGSLNGLAVTTLNNGEQWHEBGVATGIIINRDGYQSVK 235
OY 131 KRAASVKYVLANGMWIKVKKPCTASDNVDFRTDYVEFLSADTKRTTVNVEKDNKK 190
Db 236 SGGLATGTITLNTG-----ABSGPDSN-----ST-TGQKVGCTAESTTIN---KNGRQ 279
OY 191 TEVKIG-AKTSVKEKDKLVTGKGGK--ENGSSSTDEEGGLVTAKEVIDAVNKKAGRM- 245
Db 280 IILFSGLRDLITLVAGGQSVHGRALNLTTLNGCYVYHNDGLA-----LNTVINEGMOVY 335
OY 246 -----KTTTANGQT-----GQADKEFTVSGTKVTFASGNGTTAIVSKDDQ-GNTIV 291
Db 336 KAGGAAGTITINQNELRVHAGGEATVYONTGALVT-----STAAFTVIGTNRILGNFTV 390
OY 222 KYDVAVGALNVAQNQNSGMNLDKAVVAGSSGKVI--SGNVSPSKGKMDFTVNNANNNI 349
Db 391 ENGRKADGYVL-----ESGGRLDVLESHSAQNTLVDDGGLTAVSAGKATSVTITSGAL 444
OY 350 EITRNGKIDATSMTPQFS-----SVSLGADAPTLISVDDGALNV 392
Db 445 -IADSGATVE-CTNNSGKFSIDGTSGQASGLLENGSFTVNAAGQAGTTVGHGHTLTL 502
OY 333 -----GSKDANKVRITTNVAPGVKEDGVTVNAOLKGYAONLNRRIDVNCNARAGIAQ 445
Db 503 AAGGSLSGRTOLSKSGASVNLNGDVSTGDIYVAGEI-----RFDN-QTTPAALSR 552
OY 446 AATATG-----LVQATLPK-----SMAIGGTYIGEAGYA---IG 479
Db 446 AATATG-----LVQATLPK-----SMAIGGTYIGEAGYA---IG 479

Db 553 AVAKNSPVTEFHKLTITNLTGCGGTTINMRVRLDGSNASDQVINGQATGKTWLAFTNG 612
OY 480 YSSI 483
Db 613 NSNL 616

RESULT 15

adhesin AIDA-I precursor - Escherichia coli plasmid pIB6
s28634
C:Species: Escherichia coli
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 08-Oct-1999
C:Accession: S28634; S22680; S28681; S72657
R:Benz, I.
submitted to the EMBL Data Library, March 1992
A:Reference number: S28634
A:Accession: S28634

A:Molecule type: DNA

A:Residues: 1-1286 <BEN>
A:Cross-References: EMBL:X65022; NID:g42254; PIDN:CAA46156.1; PID:g42255

A:Reference number: S22680
A:Accession: S22680

A:Status: nucleic acid sequence not shown
A:Molecule type: DNA

A:Residues: 839-1286 <BE2>
A:Cross-References: EMBL:X65022

A:Experimental source: strain 2787
A:Accession: S28881

A:Molecule type: Protein
A:Residues: 50-56 <BE3>

A:Experimental source: strain 2787
A:Reference number: S72657; MUID:97055419; PMID:8899706

A:Title: Processing of the AIDA-I precursor: removal of AIDA and evidence for the out
Mo. Microbiol. 22, 31-42, 1996

A:Reference number: S72657; MUID:97055419; PMID:8899706
A:Accession: S72657

A:Molecule type: protein
A:Residues: 847-856 <SUH>

A:Experimental source: DAEC strain 2787
C:Genetics:
A:Genome: plasmid pIB6

C:Keywords: membrane protein
F:1-49/Domain: signal sequence #status predicted <SIG>

F:50-1286/Product: adhesin AIDA-I #status predicted <MAI>

Query Match 8.5%; Score 220.5; DB 2; Length 1286;
Best Local Similarity 21.7%; Pred. No. 0.0064;
Matches 128; Conservative 78; Mismatches 204; Indels 179; Gaps 29;

OY 1 MNKIRITWNSALNMAVAVSELTNRH-----TRKASATVKA--VLATLTFATVQANA 51
Db 1 MNKAVSILMSHSRQMIYVASELARGHFLANLTLLVAVSTIGNAFVNISGTVSSGG 60
OY 52 TDETLINVEETKLSFGANGKRVNIISDTKGLNFAKETAGTNGDTVHLNGISTLDM 111
Db 61 TVSSG-----ETQ-----IVYSGRG-----NSNATVNSG-----TQIV 89
OY 112 LMTGATTNVT-NDNVTDEKRAASVKDYVLANGMWIKVKKPCTAS-----DNV-DF 161
Db 90 NNGGKTATATVNSSGSONVGTSGATISTVNSG-GIORYSSGVSATFNLSCGAONINYL 148
OY 162 VRTDYVEFLSADTK-----TTVNVESKDKNGKTEVYIGAKTSV-----IKEDGK 208
Db 149 GHASNTVIFSGNQITIFSGCITDSINISSGGQORVSSGVSANTTIINSSGAONILSEBA 208
OY 209 IYTGKKGGEN-----GSSSTDEEGGLVTAKEVIDAVNKKAGWRMKT-----TTANGQT-- 254
Db 209 ISTHISGNGOYISAGANATE-----TIYNSGGFQVNSGAVATGTVLGGGTGN 257
OY 255 -----GQADKEFTVSGTKVTFASGNGTTATVSKD-----DQGNITVKKDYVNVGALNVA 305

```

Db      258  VSSGSAISTSVYNSGVQTFVAGATVDTFTVNSGNGNQNISSGIVSEETVNVSGTONIX- 316
QY      306  LQNSGWNLDKAVAGSSGKVIISGNVSPSKMDETVNIN--AGNNIETRNKNIDIAF 362
Db      317  -----SGSALSANIKGSOIVNSEGTALTIVSDGYOHIRNG--GIAS 358
QY      363  -SMTPOFSSVSLGAGADAPTLVYDEGALNVGSKDANKPVRITNVAPGVEGDPVTVNAOL 421
Db      359  GTIVNOSGYVNISSGVAESTIINSGLIRV-----LSDGYARGTILN----- 401
QY      422  KGYAQNLRNIDNVNGNARAGIAQAIAIAGLVQAYLPKSMMAIGGTYL--GEAGYAI 478
Db      402  -----NSGREVV--SNGGVSY-----NAMINTGNGNOYIYSDGEATAAI 437
QY      479  ----GYSSISAGG-----NWITKGTASGNSRGHFGASASVG-----YOW 513
Db      438  VNTSGFORINSGLTAPVQNSVVTFTVSSAAKPFDAEYVSGKQTVYIWM 486

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Search completed: October 6, 2003, 09:33:17
 Job time : 18.6847 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:06:20 : Search time 7.92203 Seconds

(without alignments)
3045.266 Million cell updates/sec

Title: US-09-771-382-24

Perfect score: 2602

Sequence: 1 MNKIRITIMNSALNMAVVS.....TASGNSRGHFGASASVGYW 513

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	241	9.3	1039	1 AG43_ECOLI	P39180 <i>Escherichia</i>
2	231	8.9	1325	1 YDEK_ECOLI	P32051 <i>Escherichia</i>
3	220.5	8.5	1286	1 AIDA_ECOLI	Q03155 <i>Escherichia</i>
4	201	7.7	2249	1 OMPA_RICRI	P15921 <i>Rickettsia</i>
5	188	7.2	2003	1 YDBA_ECOLI	P33666 <i>Escherichia</i>
6	182.5	7.0	1656	1 OMPB_RICCU	O06653 <i>r</i> outer mem
7	182	7.0	1655	1 OMPB_RICCN	O9KXa3 <i>r</i> outer mem
8	180	6.9	1654	1 OMPB_RICRI	O53047 <i>r</i> outer mem
9	179.5	6.9	737	1 ALYS_ENTFA	P37710 <i>enterococcu</i>
10	178.5	6.9	1567	1 ICEN_XANCT	P18127 <i>xanthomonas</i>
11	178	6.8	1953	1 BIGA_SALTY	P25827 <i>salmonella</i>
12	177.5	6.8	2021	1 OMPA_RICCN	O52857 <i>Rickettsia</i>
13	176.5	6.8	933	1 SLAP_CAMEE	P33827 <i>campylobact</i>
14	175	6.7	1025	1 SLAP_CAUDE	P35828 <i>caulobacter</i>
15	175	6.7	1645	1 OMPB_RICRY	P96989 <i>r</i> outer mem
16	174.5	6.7	1643	1 OMPB_RICPR	O53020 <i>r</i> outer mem
17	173.5	6.7	1300	1 120K_RICRI	P14914 <i>Rickettsia</i>
18	173.5	6.7	1577	1 HUYA_PROMI	P16466 <i>proteus mir</i>
19	170	6.5	1569	1 YPOA_ECOLI	P52143 <i>Escherichia</i>
20	168	6.5	1608	1 HUYA_SERMA	P15320 <i>serratia ma</i>
21	165	6.3	1861	1 APU_THETU	P38536 <i>t amylopull</i>
22	165	6.2	2660	1 YEBJ_ECOS7	O8X8V7 <i>Escherichia</i>
23	162.5	6.2	3591	1 FHAB_BORPE	P12255 <i>bordetella</i>
24	158	6.1	1034	1 ICEN_PANAN	O47879 <i>panthoe ana</i>
25	158	6.1	1258	1 ICEN_ERWHE	P16539 <i>erythra ana</i>
26	158	6.1	1322	1 ICEN_PANAN	P20469 <i>panthoe ana</i>
27	157	6.0	1148	1 ICEN_PSESX	O30611 <i>pseudomonas</i>
28	156.5	6.0	1007	1 Y7A1_CHLMU	O9P16 <i>chlamydia m</i>
29	156	6.0	550	1 FLIC_C_SHIFL	O08860 <i>shigella fl</i>
30	155.5	6.0	504	1 FLIC_SALBU	O06869 <i>salmonella</i>
31	155	6.0	948	1 HP11_DEIRA	P06667 <i>deinococcus</i>
32	155	6.0	1210	1 ICEN_PSEFL	P09815 <i>pseudomonas</i>
33	155	6.0	2358	1 YEBJ_ECOLI	P76347 <i>Escherichia</i>

34	154.5	5.9	1005	1 Y456_CHLTR	O84462 <i>chlamydia t</i>
35	152.5	5.9	918	1 YWJB_CAEEL	P34487 <i>caenorhabd1</i>
36	152	5.8	1694	1 IGA2_HAEIN	P44969 <i>haemophilus</i>
37	152	5.8	1702	1 IGA2_HAEIN	P45384 <i>haemophilus</i>
38	150.5	5.8	928	1 PM11_CHLPP	O86164 <i>chlamydia p</i>
39	150.5	5.8	3178	1 YS89_CAEEL	O09624 <i>caenorhabd1</i>
40	149.5	5.7	484	1 P60_LISMO	P21171 <i>listeria mo</i>
41	149.5	5.7	1150	1 APMU_PIG	P12021 <i>sus scrofa</i>
42	149	5.7	1196	1 ICEN_PSESX	O33479 <i>pseudomonas</i>
43	149	5.7	1200	1 ICEN_PSEST	P06629 <i>pseudomonas</i>
44	148	5.7	537	1 TE66_STRPY	P18481 <i>streptococc</i>
45	148	5.7	1036	1 HP12_DEIRA	P13126 <i>deinococcus</i>

ALIGNMENTS

RESULT 1
ID AG43_ECOLI STANDARD: PRT: 1039 AA.
AC P39180; P75614; P76360; P97241; Q46771;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 43 precursor (AG43) (Fluiffing protein).
GN FLU OR B2000.
OS *Escherichia coli*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; *Escherichia*.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of *Escherichia coli* K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitagawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,
RA Sivasubram S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horiiuchi T.;
RT "A 460-kb DNA sequence of the *Escherichia coli* K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-ML 308-225;
RX STRAIN-ML 308-225;
RA Henderson I.R., Owen P.;
RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PRELIMINARY SEQUENCE OF 53-78.
RC STRAIN-ML 308-225;
RX MEDLINE=89291704; PubMed=2661530;
RA Caffrey P., Owen P.;
RT "Purification and N-terminal sequence of the alpha subunit of antigen
43, a unique protein complex associated with the outer membrane of
Escherichia coli.";
RL J. Bacteriol. 171:3634-3640(1989).
RN [5]
RP SEQUENCE OF 53-63.
RC STRAIN-K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded

RT in the genome of *Escherichia coli* K-12. ";
 RT Electrophoresis 18:1259-1313(1997).
 RN [6]
 RP GENE NAME.
 RX MEDLINE=97257509; PubMed=9103983;
 RA Henderson I.R., Meenan M., Owen P.;
 RT "Antigen 43, a phase-variable bipartite outer membrane protein,
 RT determines colony morphology and autoaggregation in *Escherichia coli*
 RT K-12. ";
 RL FEMS Microbiol. Lett. 149:115-120(1997)
 CC -1- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION. MAY
 CC FUNCTION AS AN ADHESIN.
 CC -1- SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA
 CC CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA
 CC CHAIN).
 CC -1- SUBCELLULAR LOCATION: Outer membrane-associated.
 CC -1- SIMILARITY: TO ADHESIN AIDA-1 AND TO BORDETELLA PERTACTIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 DR EMBL; AE000291; AAC75061.1; ALT_INIT.
 DR EMBL; D90838; BAAL5825.1; ALT_INIT.
 DR EMBL; D90839; BAAL5832.1; ALT_INIT.
 DR EMBL; U24429; ABA47869.1; -.
 DR HSSP; P07505; ISRd.
 DR Ecogene; EGI2686; flu.
 DR InterPro; IPR006315; Autotransport.
 DR InterPro; IPR005546; Autotransporter.
 DR InterPro; IPR004899; Pertactin.
 DR Pfam; PF03797; Autotransporter; 1.
 DR Pfam; PF03212; Pertactin; 1.
 DR TIGRFAMS; TIGR01414; autotrans_bar1. 1.
 KM Outer membrane; Signal; Complete proteome.
 FT SIGNAL 1 52
 FT CHAIN 53 551
 FT CHAIN 552 1039
 FT VARIANT 2 2
 FT VARIANT 41 42
 FT VARIANT 46 46
 FT VARIANT 157 157
 FT VARIANT 188 188
 FT VARIANT 303 305
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 FT VARIANT 1025 1025
 FT CONFLICT 61 63
 SQ SEQUENCE 1039 AA; 106841 MW; 5170D647C8DBEDB0 CRC64;
 Query Match 9.3%; Score 241; DB 1; Length 1039;
 Best Local Similarity 21.5%; Pred. No 5e-05;
 Matches 131; Conservative 92; Mismatches 236; Indels 150; Gaps 29;
 1 MNKLYRTIWNLSALNMAVAVSELTNRNHRKRASATYKTAVALTLATPATVQAN-----ATDE 54

Db	5	LMTGCVRLVNMHNTGAFVVAASELARARCRKRGVVAALSLAATVSLPVLADIAVHPGETVVA	64
QY	55	TGLINVEETKLSFG-ANGKKVNIISDTRGLNFAKET-----AGTNGDTYHNLG	102
Db	65	GGTLNHDNDQIYFEGTNGMTI-----STGEYGDNEANTGGQWVODGGTANTTYVTSQV	119
QY	103	I-----GSTLTMLNLTGATTNV-----TNDVTPDEK-----KRAASVKEVLN-AGMNIKGV	149
Db	120	LQRYNPGGSVSPVTSASGGGSLQGRVAVNTLNLNGEOMHEGALATATVINDGMQV--V	177
QY	150	KPGTTASDNVDFVPT-----YDVEELSLDFTKTVV-----VESKDNKTEY	193
Db	178	KEGTVAATDIV--VNTGAEAGGPDANGDYGQFVREDDAVKTTINKNGROIYAEAGTANTVYV	235
QY	194	KIGAKTSV-----IKKDKGLVYTGKGGKGENSGSTDESEGL	228
Db	236	YAGDGTATGHALLDTTLNGGIQYVHNGSTASDITYVNSDGMQIVYNG-VGAGNTTYVNOGR	294
QY	229	YTAKEVIDAVN--RAGMRKMTTANQGT-----GQADKEFTVTSCTRYTFAS	273
Db	295	LQVDAGCATNTVTLKQGGALVYSTAATVGTINRLGAFSVBGRADNV-VLENGGRDLDTLT	353
QY	274	GNGTATYVSKDQGNITKYVDNVGDALNAVQDLONSGNINDSKRVASSSGKVSIGANVSPS	353
Db	354	GHTAINT-RVDDGTLTVR--NGSTATTVS-MGNGG-----VLADSGAAVSGTRSDG	402
QY	334	K-----GKDEFTVINAGNIEITPFGKNIDIAISMTPOFSSVSIAGADAPTLVSDDEG	388
Db	403	KAFSIGGGADALMLEKSSFTLNG-----DTATDTYVNGSLPTARGTLAGTTTLNNGA	458
QY	389	ALNVGSKDANKRVRTTNAPGVKEDDTVNAVQLGVAONLNKRIDNVNGNARAGIAQATA	448
Db	459	ILTLSEKTYN-----NDTLTIREGD-----ALLQGSGLTNGSVK-SGSGTTLVSNVTL	507
QY	449	TAGLVQAVYLPGRSMAIGGT-----YLGEAGYAIAYS-----SISAGNMV	490
Db	508	TOKAVLV-----NEGTLTINDSYTTVYIAQRGTALKLTCISYVLNCAIDPTVNTLASGATWN	564
QY	491	IKGTASGNS	499
Db	565	IPDNATVQS	573

RESULT 2

YDEK_ECOLI

ID

YDEK_ECOLI

STANDARD:

PRT:

1325 AA.

AC

P32051; P76140; P77168;

AD

P32051; P76140; P77168;

AT

P32051; P76140; P77168;

BT

01-OCT-1993 (Rel. 27, Created)

DT

01-NOV-1997 (Rel. 35, Last sequence update)

ET

16-OCT-2001 (Rel. 40, Last annotation update)

DE

Hypothetical lipoprotein ydek precursor (ORF7).

GN

YDEK OR ORF7 OR BL510.

OS

Escherichia coli.

OC

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OX

Enterobacteriaceae; Escherichia.

OX

NCBI_Taxid=562;

RN

[1]

RP

SEQUENCE FROM N.A.

RC

STRAIN-K12 / MG1655;

RC

MEDLINE-9742617; PubMed-9278503;

RA

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA

Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

RA

Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA

Mau B., Shao Y.;

RT

"The complete genome sequence of Escherichia coli K-12.";

RL

Science 277:1453-1474(1997).

RN

[2]

RP

SEQUENCE FROM N.A.

RC

STRAIN-K12;

RC

MEDLINE-97251357; PubMed-9097039;

RA

Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,

RA

Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,

RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Sampel G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Mada C., Yamamoto Y., Horuchi T.,
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN (3)
RX SEQUENCE OF 595-1325 FROM N.A.
RP MEDLINE-94100243; Pubmed-8274505;
RA Cartwright P.J., Timms M.W., Litchow T., Hoef P.B., Hoogenraad N.J.,
RT "An Escherichia coli gene showing a potential ancestral relationship
RT to the genes for the mitochondrial import site proteins ISP42 and
RT MOM38.";
RL Blochim. Biophys. Acta 1153:345-347(1993).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential).
CC -1- SIMILARITY: TO E. COLI YFAL.
CC -1- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
CC ISP42 AND MOM38.
CC -1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 653.
CC -----
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CC -----
DR EMBL: AEO00248; AAC74583.1; -
DR EMBL: D90793; BAA15190.1; ALT_INIT.
DR EMBL: D90794; BAA15197.1; ALT_INIT.
DR EMBL: X73295; CAA51730.1; ALT_FRAME.
DR PIR: A64905; A64905.
DR Ecogene: E611780; ydek.
DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
DR Hypothetical protein; Membrane; Lipoprotein; Signal;
KW Complete proteome.
KM Complete proteome.
FT SIGNAL 1 18
FT CHAIN 19 1325 POTENTIAL.
FT LIPID 19 19 HYPOTHETICAL LIPOPROTEIN YDEK.
FT CONFLICT 884 884 N-ACYL DIGLYCERIDE (POTENTIAL).
FT CONFLICT 1317 1317 M -> S (IN REF. 3).
FT SEQUENCE 1325 AA; 136514 MW; 26A3A066FA1AD7D CRC64;
Query Match 8.9%; Score 231; DB 1; Length 1325;
Best Local Similarity 24.4%; Pred. No. 0.00021;
Matches 146; Conservative 65; Mismatches 245; Indels 142; Gaps 29;
QY 1 MNKTYIINNSALNAVAVSELNR-----NHTKASATVTAVALTLFTVQANAT 52
DB 1 MNRIVYINMCTLOVQACSELTRRAGKSTYVNLKSSGTLTFESRLTGLVLLALSGSAS 60
QY 53 -----DETGLINVEE-----KLSEFGANGKKVNIISDTKGLNFAKETA 90
DB 61 GASLEVDNDQITIDPDAVAVDAVGVGVLNLAGASLITTTISVIGAN--EDSE 118
QY 91 GTRNGDTVHLNGIGST--LTD-----MLNTG---ATTNVTNDNVTDDEKKRAASVKDY 139
DB 119 GT-----VNVIGGTWRLLYDSCNNARPLNVGSGGTGLNIKOKGHVDG-----GY 162
QY 140 LNAWNKIKGPKPTSDANVDFVRYDVEFLSADTKTTVNVESDNCKKTE----- 192
DB 163 LRLGSGTGV--GTAVNEGDSVLTLEFLIGSYGSLNT---DKGVTSSVAILG 216
QY 193 VKIGATSVYKEDKG-LVYTK-----GKGENSGSTDEGGLVTAKEVIDAVKAGW 243
DB 217 YQAGSGQYVVEKGEMLIKNNDSIEFOGNGGTGEATIREGIVTAETIIGGNATG- 275
QY 244 RAKTTTANGTGCADKFEVYTSCTKVTFRASGNGTLYTVSKDQGNITVK-YD-VNVGDAL 301

DB 276 -IGTLNVQ---DODSVTVRRLYNGYFGNG---TVNISNNGLIINNKESLVGVQDGS 325
QY 302 N--VNOLQNSGWL-----DSKAVAGSSGKVTSGNVSPSKAMDETVNI 343
DB 326 HGAVNTYDKGMHFLTGGEAFRTIYTDAGDGLNVSBEKVGSCIITAG---MKET--- 379
QY 344 MAGN-----NIEITRNGKNIDIAATSWTPQSSVSLSAGADAPTLVSDDGALNV----- 392
DB 380 GTGNTIYKDKNSVITNLGTNLGYDGHGEMNISQGLVNSGSSSLGGETGVGNVSLTTG 439
QY 393 GSKDANKPVRITVAAGYKGDVTVNVAQLKGVAQNLNRRIDVNVGNARAGIAQALATAGL 452
DB 440 GMEVEKNKNTYTTIGVAGVGLNLISDGG--KFVSQNTIFLDKASGIGITLMLDPTSSFDPT 497
QY 453 YQAVLP--GKSMMAIGGGTYLGEAGYAI-----GYSSISAGNMIIKGTASGNSR 500
DB 498 VGINVGNFSGGIYVNSGATLNSTGTFIGGNASGKGIYVNIISDLSMLNLK-TSTTNQ 554

RESULT 3

AIDA_ECOLI STANDARD; PRT; 1286 AA.

AC 003155;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Adhesin aida-I precursor.

GN AIDA-I.

OS Escherichia coli.

OG Plasmid pIB6.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-56.

RC STRAIN=0126:H27 / 2787;

RX MEDLINE=92326638; Pubmed=1625582;

RA Benz I., Schmidt M.A.;

RT "Aida-I, the adhesin involved in diffuse adherence of the

RT diarrhoeagenic Escherichia coli strain 2787 (O126:H27), is

RT synthesized via a precursor molecule.";

RL Mol. Microbiol. 6:1539-1546(1992).

CC -1- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE

CC ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI

CC TO EPITHELIAL CELLS.

CC -1- SUBCELLULAR LOCATION: Outer membrane.

CC -----
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DR EMBL: X65022; CAA46156.1; -
DR PIR: S28634; S28634.
DR InterPro: IPR006315; Autotransport.
DR InterPro: IPR005546; Autotransporter.
DR InterPro: IPR004899; Peractin.
DR Pfam: PF03797; Autotransporter; 1.
DR Pfam: PF03212; Peractin; 1.
DR TIGRfams: TIGR01414; autotrans_bar1; 2.
KW Cell adhesion; Signal; Outer membrane; Plasmid.

FT SIGNAL 1 49

FT CHAIN 50 1286

FT PROPEP ? 1286

FT PROPEP ? 1286

FT PROPEP ? 1286

FT PROPEP ? 1286

FT PROPEP ? 1286

FT PROPEP ? 1286

FT PROPEP ? 1286

FT PROPEP ? 1286

FT PROPEP ? 1286

FT PROPEP ? 1286

FT PROPEP ? 1286

FT PROPEP ? 1286

FT PROPEP ? 1286

FT PROPEP ? 1286

FT PROPEP ? 1286

FT PROPEP ? 1286

FT PROPEP ? 1286

Query Match 8.5%; Score 220.5; DB 1; Length 1286;
Best Local Similarity 21.7%; Pred. No. 0.00066;
Matches 128; Conservative 78; Mismatches 204; Indels 179; Gaps 29;

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0Y      MNKYTRIMNSALNANVAASELJRNH-----TKRASATKTA--VLATLLFPTVOANA 51
Db      1 MNAYSTISHSHKQAMIVASELARGHGYLAKNTLLVLAVSTIGMAFVANSSTVSSGG 60
QY      52 TDETCJLINETEKLISFGANGKKRYNIISDPKGLNFAKETAGNCDPTVHLNIGSTLMDL 111
Db      61 TVSSG-----ETO-----IYSSRG-----NSNATVSSG-----TOIV 89
QY      112 LNTGATTNT--NDNVTDEKKRAASYKYDLNAGNINIKCYKPGTAS-----DNV-DF 161
Db      90 NNGKTTATTVNSSGSGONJTGATISTIVNSG-GIOHVVSSGAVASATNLSGAGNIYNL 148
QY      162 VRRYDVEEPLSADTK-----TTYVNEKDKMGKTEYKIAKSV-----IKEDGK 208
Db      149 GHASNTIYFEGGNOTIFSGGJTDSTNISGGGOORVSSGVSANNTTINSAGNILLSEGA 208
QY      209 LVTKGCKGEN-----GSSTDEGEGLVTAKEVIDANNAKGMWRKT-----TJANGOT- 254
Db      209 ISTHISGGQIYISAANATE-----TIYNSGFPORVNSGAVATGTIVLSGCTON 254
QY      255 ----GQADKEEYVTSCTKYTVFASGNGTATVSKD-----DOGNITVKYDVNWGALNVNO 305
Db      258 VSSGGSLSITSVYNSGVQIVFAGATVTDPTVNSGNGNIISSGGLVSETTVWVGTONIY- 316
QY      306 LQNSGNWLDKAVAGSSGKVISSGNSPSKGMKDEYVNI--AGNNIETTNKGNIDIAT 362
Db      317 -----SGGSLASNLKISGOIVNSECTAINTLVSDGQYOHING--GIAS 358
QY      363 -SMTPOESSYLACAGADPTLVSDEDEGALNVGSKDANKPVRTNVAPEVKGDTVNAQL 421
Db      359 GTIYNOSGVIYNISSGGYAESTIINSGLTV-----LSDCYANGTILN---- 401
QY      422 KGYAONLNNEIDNVNGNARAGIAQALATAGLVQAVLPEKSMMAJGGCTYL--GEAGYAI 478
Db      402 -----NSGRENV--SNCGVSY-----NAMINTGNGQIYISDEATAAI 437
QY      479 ----GYSSISAG-----NWILKIGLASGNSRKHFGASASVG-----YOW 513
Db      438 VMTSGFORINSGGTAPONSVVYVTRTVSSAAKPPFAEYVSGKGQOTVYLM 486

```

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RESULT 4
OMPA_RICRI
ID OMPA_RICRI STANDARD: PRF: 2249 AA.
AC P15921:
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (r ompA) (comp A).
GN OMPA.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-R:
RX MEDLINE=90354033; PubMed=2117568;
RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;
RT repeated, near-identical sequences.
RL Infect. Immun. 58:2760-2765(1990).
SC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
SC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.
CC -1- PTM: GLYCOSYLATED (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
CC -----
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DR	InterPro: IPR006315; Autotransport.
DR	InterPro: IPR005546; Autotransporter.
DR	Pfam: PF03797; Autotransporter; 1.
DR	TIGRFAMs: TIGR01414; autotrans_bar1; 3.
KW	Antigen; Repeat; signal; Cell wall; s-layer; Glycoprotein.
FT	SIGNAL 1 28
FT	CHAIN 29 2249
FT	DOMAIN 212 1180
FT	REPEAT 212 286
FT	REPEAT 287 358
FT	REPEAT 359 430
FT	REPEAT 431 505
FT	REPEAT 506 577
FT	REPEAT 578 652
FT	REPEAT 653 724
FT	REPEAT 725 799
FT	REPEAT 800 874
FT	REPEAT 875 949
FT	REPEAT 950 1021
FT	REPEAT 1022 1093
FT	REPEAT 1094 1165
FT	REPEAT 1166 1180
SO	SEQUENCE 2249 AA; 224333 MW; A9Db64cC089DF087 CRC64;

Query Match	7.7%	Score 201	DB 1	Length 2249
Best Local Similarity	22.98%	Pred. No.	0.012	
Matches 137	Conservative 65	Mismatches 229	Indels 168	Gaps 29

```

OY 13 NMNVAWSLELRRN--HHRKRAATKATVALLELFAVQANNTDEGLINVEEKLISGAN 70
    || :||:|::: :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 787 LNLGALSOQVGDJGDNQNSLATSISVGATGATLGGVATKATTKLPMNASVLT---LTMN 843
OY 71 GKRYNIIISDTFGLNEFAKETAGTNGDT--TVHANGISGFLPEMLNT----- 114
Db 844 AVLIVGAVDNT-----TGDDNGVVLNLMGALSQVTDIGNTNSLATSISVGAGAT 892
OY 115 --GATTNVNDNVTDDEKKRAASVQVDLWAGMNIKGVPGTTASDNDVEFTYPTVEFLS 172
    || :||:|::: :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 893 LGGAVIKATTKTLTN-----AASVLTLMNAAVLTGALDNTTGGDNGVLMNGALSQVT 947
OY 173 ADFTKT-----VWNESKD--NG--KTEVKIGAKTSVIEKKOKIVTG--KKGGEN 218
    || :||:|::: :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 948 GDIGNTNSLATSISVGATGATLGGVATKATTKLIDASAFAVFTPEVVVTAIDNTGMANN 1007
OY 219 GSSTDEGEGLYTAK-----EVIDAVNKA-----GMRKKTJTAN-----GQ 253
Db 1008 GIVFTGSIYTTGAVNGNTNALTATVNVGAGLLQYOGGVKANTIMLTDBASAVFTTNPVV 1067
OY 254 TGOADKEFTVTSGRKVFPAFASGNGTTATVSKDDGQNIYKYDVNVGDAL-----N 302
    || :||:|::: :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1068 TGAIDNTGMANNGI-VFETGNSVTVGN-----GNTNALATVNVGAGLLQYOGGVKANT 1121
OY 303 VN-----OLOMSGMMUDSKAAVAGSSGKVIISGNVPSKCKMDETYNIN 344
    || :||:|::: :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1122 INLFDNASAVFTPEVNVVVTGAIDNTG--NANGNIYFTGNSVTVDGI-----GNTNALATVN 1176
OY 345 AGNNIEIETRRNG---KNIDIATSMTPOFSSVSLGADAP-----TLSVDEGALNVGSK 395
    || :||:|::: :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1177 VGAGITLLOAGSSLANANNIDFGARSTLEHNGLDGGRKAIPIYFPGALANGNALLNVMTK 1236
OY 396 DANK-----PVRTTNAAPG-----YKSGDVTVAOLKGVQOULNNR-----IDNVN 436
    || :||:|::: :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1237 LLTASHLTLGTVAEINIGAGNMLFTIDASGVDTILN-----AQMIFRARDSVLVLNLT 1291
OY 437 GNARAGTQOATATAGLVQAVIPLGKSMAAGCGTGLGEGVIAIGVSSISAGNMIIKGTGA 495
    || :||:|::: :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1292 G--GVGNIIILADLV--APGDE-----GTVVFENGVNGLVGSN--VAGTGA 1333

```

```
RESULT 5
YDBA_ECOLI
ID YDBA_ECOLI STANDARD; PRT: 2003 AA.
AC P33666; P76087; P76088; P76856; P76857; P76859;
DT 01-FEB-1994 (Rel. 28, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ydba.
GN YDBA OR B1401/B1405.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.,
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kishimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Salto N.,
RA Sempel K., Seki Y., Sivasubraman S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horuchi T.;
RT "A 370-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map."
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 464-2003 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92190338; PubMed=1665988;
RA Moszer I., Glaeser P., Danchin A.;
RT "Multiple insertion sequences near the replication terminus in
RT Escherichia coli K-12."
RL Biochimie 73:1361-1374(1991).
CC -1- SIMILARITY: TO S.TYPHIMURUM ORF NEAR CYS6 (AC P25928).
CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR
CC THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT
CC BETWEEN AMINO ACIDS 839 AND 840.
CC -----
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CC -----
DR EMBL: AE000237; AAC74483.1; ALT_SEQ.
DR EMBL: AE000237; AAC74487.1; ALT_SEQ.
DR EMBL: D90778; BAA15009.1; ALT_SEQ.
DR EMBL: D90778; BAA18880.1; ALT_SEQ.
DR EMBL: D90779; BAA18881.1; ALT_SEQ.
DR EMBL: X62680; NOT_ANNOTATED_CDS.
DR EcoGene; EG11307; ydba.
KM Hypothetical protein: Complete proteome.
FT CONFLICT 489 489 I -> V (IN REF. 2).
FT CONFLICT 495 495 I -> V (IN REF. 2).
SQ SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220EE CRC64;
Query Match 7.2%; Score 188; DB 1; Length 2003;
Best Local Similarity 24.9%; Pred. No. 0.045;
```

```
Matches 138; Conservative 74; Mismatches 212; Indels 130; Gaps 33;
QY 46 TVQANATDEGLINLV-ETKLSFGANGKKNIIISD-----TKG-----LMPAKETACTNG 94
DB 269 TQDSATVNDKNGKMTVTDPESMGIQIDGDKAIVNEGSESTTNGTGQINGDDATANNNG 328
QY 95 DTVVHLNGISGTLTMDLNTGAT-----TNYTNDVTDDEKKRAASVDVL 140
DB 329 KTVV--DGKSTGEIENGNGKVIQDDDLVDSGGGHIDITGDSATVD-NKGITVTVDPE 385
QY 141 MAGNIVKVRPGTTASDNDVDFRTYDVEFLSADTKTTVVNESKONGK--TEVKIGA 197
DB 386 SIQIVDVG-DQAVVNNDESAITNGCTGTQINGDDATANNNGKTTVDGKSTGEI-AGN 443
QY 198 KTVYVKKDKKL-VTGKKG---ENGSTDEGEIYAKK-----VIDA---VYKAGW 243
DB 444 NGKVI--QDGDLDVSGGGHIDITGDSATVNDKNGKMTVTDPEISIGIIDDQAIVNEG- 500
QY 244 RMKTTTANGOTGOADKFEFTVTSCTKYVFASGNGTATVSKDD-----QGNITVYDVNVG 298
DB 501 --ESTITNGTG-----TQINGNDAT-ANNKGTIVDGKDSGTGKTAIGNIGI---VNLD 548
QY 299 DALNV-----NQLONGNN--LDSK-----AVAGSSGKVIIGNVSPSKGKDETVINAGN 347
DB 549 GSLVTVGAGVGENIGNGTNNKGDIVSDTSGISGLINGEGATVSNITGDVNVG-NEAT 607
QY 348 NIETTRGNKNDIATSM-TPOFSS-VSLAGADAPTVSYVD-----EGALNVSKDAN 398
DB 608 GFSITTNISGKVSILASQVQDFSTGVDLGNNNNSVTLAAKDLKVGOKATGINV-SDAN 666
QY 399 KPVRIIVAVGVEGDDTVNVAQL--KGVAQNLNIRIDYVNGNARAGI----- 443
DB 667 -TNYITNGVNLVYDNDKTDADNAEYFEDPSVGINYGSNNNTLQGLKLVSDSEVTSRQSN 725
QY 444 ---AQAIATGLVOATLPKSMWAIIGGTYLGE-----AGTAI-----G 479
DB 726 LFDGSAEKTSGLV-VIGDGMTVNMNGLELIEKKNALADSGQVSLRTGYSTSVIVVSG 784
QY 480 YSSISAGCNWILKG 493
DB 785 ESSVYLVNGDTTISG 798
RESULT 6
OMPB_RICIA STANDARD; PRT: 1656 AA.
AC O06635;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scas) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB.
OS Rickettsia japonica.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_Taxid=35790;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YH;
RA Uchiyama T.;
RT "Sequencing of the gene encoding the protein rOmp B of Rickettsia
RT japonica."
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
CC SIMILARITY).
CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
```

LAYER WITH HEXAGONAL SYMMETRY.
 CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AB003681; BAA20138.1; -
 CC InterPro: IPR006315; Autotransport.
 CC InterPro: IPR005546; Autotransporter.
 CC Pfam: PF03797; Autotransporter; 1.
 CC TIGRFAMs: TIGR01414; autotrans_bar1; 2.
 CC Antigen: S-layer; Cell wall.
 CC CHAIN 1 1338 120 kDa SURFACE-EXPOSED PROTEIN.
 CC CHAIN 1339 1656 32 kDa BETA PEPTIDE.
 CC DOMAIN 528 533 POLY-GLY.
 CC SEQUENCE 1656 AA; 168097 MW; 3132A69CD5999F CRC64;
 SO
 Query Match 7.0%; Score 182.5; DB 1; Length 1656;
 Best Local Similarity 22.7%; Pred. No. 0.068; Mismatches 217; Indels 211; Gaps 32;
 Matches 144; Conservative 63;
 Oy 37 AVLTLLFAFYQAN-ATDEGLINVEKLSFGANG-----KKVNI 76
 Db 179 AAATLIVFDL--ANPTQKAPLILADNALIYANGNLNTNGFIQVSDKSFATVKAIN- 235
 Oy 77 ISDTKGLNFAKETGNTN-----GDTYVHLNGISLTLDMLN-TGATNTNTNDNVDD 129
 Db 236 IGDGQGFMTNATNATNALNLQAGTTINFGTGTGRLVLLSKNGATDF--NVYG-- 290
 Oy 130 KKRAASVDVLNAGMNKGVKPGTTASDNVDFVLYDVEFLSDTKTNTN----- 181
 Db 291 -----SLGCKLKITELNTVALNGQLINAG-----PANAVIGTNGGKRAAGF 334
 Oy 182 VESKDNKRTVEV--KIGAKTSVIRE-----KDGKLYTGKKG 216
 Db 335 VVSYDNGKAATIDQVYAKDMVYIOSANANGOVNFRHIVDGIIDGTAFKTAASIVATLON 394
 Oy 217 ENGSGTDEGEGLYAKELYDAVYNKAGMKTTTANGOGADKRETVTSGTKVFASNG 276
 Db 395 SNFGTTDFG-NLAAQVTVPTM-----TLTGN-FTGDANN-PGNTAGV-ITFAA-NG 441
 Oy 277 TTATVSKDDGNTIVKYDVNVDALNVLNQLNSGMNLSKAV--AGSSGKYSGVSPSK 334
 Db 442 TLASASAD--ANAVTNNITAIKASGVGVVQLSGTHFELRLGNAGSVFKLADGIV--IN 497
 Oy 335 GKMDTV----- 341
 Db 498 GKVQGVTVLVGVLAAAGATTLDGSAITIDGNGGGGAAIQTILANDATKTLTGANII 557
 Oy 342 -----NINA-GNNIETTRNGKNI-----DIATSMTPQFSSVSLGAGADATLSVDD- 387
 Db 558 SANGTINFGANGGTIKLTSTONNIIVDCDLAIA-TDQTVGVADSLTMAOTLTISGTIG 616
 Oy 388 -----GALNFGSKDA--NRPVRIITNAPGVKEEDV-----TVAQLKGVAAQ 426
 Db 617 IIGANNITLGGFNIGSSKTTILNGSNVAINELVIG--NNGSVQFAHNTYILTFTNAAGGK 675
 Oy 427 NLNRRIDVNGNARAGIAQATATAGLVQAYLPGK-----SMAAIGGGTYLGEAGYA--- 477
 Db 676 IIFPVVNNNTTTLAAGTNLGSAAAPLAIINFGSKGARADTVLNVGEGVNL-----YATNIT 731
 Oy 478 -----IGSSISAGGNMIIKGTASGNSNGHFGASA 507
 Db 732 TTDAVNGSFVNAGKNIQVSGVGGQGNKKNPTVA 766

OMP, R1CCN STANDARD; PRT: 1655 AA.
 AC O9KKA3; O9KKA98; O9XC45.
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Outer membrane protein B precursor (168 kDa surface-layer protein)
 DE (Surface protein antigen) (Cell surface antigen 5) (Scas) (rOMP B)
 DE (omp B) [Contains: 120 kDa surface-exposed protein (Surface protein
 DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
 GN OMPB OR R1085.
 OS Rickettsia conorii.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 OX NCBI_TaxID=781;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Malish 7;
 RX MEDLINE=21442074; PubMed=11557893;
 RA Ogata H., Audic S., Renseto-Audifren P., Fournier P.-E., Barbe V.,
 RA Samsom D., Roux V., Cossart P., Weissendach J., Claverie J.-M.,
 RA Raoult D.;
 RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
 RL Science 293:2093-2098(2001).
 RN [2]
 RP SEQUENCE OF 33-1649 FROM N.A.
 RC STRAIN=Indian tick typhus, and Malish 7;
 RX MEDLINE=20393643; PubMed=10939649;
 RA Roux V., Raoult D.;
 RT "Phylogenetic analysis of members of the genus Rickettsia using the
 RT gene coding the outer-membrane protein rOMP B (ompB)." ;
 RL Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
 RN [3]
 RP SEQUENCE OF 353-1655 FROM N.A.
 RC STRAIN=Malish 7;
 RA Stenos J., Walker D.;
 RT "The rickettsial outer membrane protein A and B genes of Rickettsia
 RT australis: the most divergent rickettsia of the spotted fever group." ;
 RL Submitted (May-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
 CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
 CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
 CC SIMILARITY).
 CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
 CC LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.
 CC -----
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 CC -----
 CC EMBL: AE008659; AAL03623.1; -
 CC EMBL: AF123721; AAF34124.1; -
 CC EMBL: AF123726; AAF34129.1; -
 CC EMBL: AF149110; AAD39533.1; -
 CC PIR: E97835; E97835.
 CC InterPro: IPR006315; Autotransport.
 CC InterPro: IPR005546; Autotransporter.
 CC Pfam: PF03797; Autotransporter; 1.
 CC TIGRFAMs: TIGR01414; autotrans_bar1; 2.
 CC Antigen: S-layer; Cell wall; Complete proteome.
 CC CHAIN 1 1334 120 kDa SURFACE-EXPOSED PROTEIN.
 CC CHAIN 1335 1655 32 kDa BETA PEPTIDE.
 CC VARIANT 61 61 G -> A (IN STRAIN INDIAN TICK TYPHUS).
 CC VARIANT 75 75 G -> S (IN STRAIN INDIAN TICK TYPHUS).
 CC VARIANT 78 78 V -> N (IN STRAIN INDIAN TICK TYPHUS).
 CC VARIANT 251 251 K -> A (IN STRAIN INDIAN TICK TYPHUS).
 CC VARIANT 413 413 N -> D (IN STRAIN INDIAN TICK TYPHUS).
 FT RESULT 7
 OMPB_R1CCN

QY 416 TNVAQLKVAQNLRNLRDNRVNG-NARAGIAQAIATAGLVQ-----AYLPKSMMAIG 467
 DB 728 TMTTDTDA---NVGSEFVENAGFNIVSG-----TVGGQGNKRENTALENGTIVKFLGN 778
 QY 468 GTYLGAGYATGYSISAGNMWIKGTASGNSRG 501
 DB 779 ATFNNGTTTAA-NSTLQIGNGYNTADCVASADGTG 811

RESULT 9
 AYS_ENTFA STANDARD: PRT: 737 AA.
 AC P37710:
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Autolysin precursor (EC 3.2.1.-) (Peptidoglycan hydrolase)
 DE (Beta-glycosidase).
 GN EF0799.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=91338349; PubMed=1679432;
 RA Bellevue C., Potvin C., Trudel J., Asselin A., Bellemare G.;
 RT "Cloning, sequencing, and expression in *Escherichia coli* of a
 RT *Streptococcus faecalis* autolysin."
 RL J. Bacteriol. 173:5619-5623(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=V583 / ATCC 700802;
 RX MEDLINE=22550857; PubMed=12663927;
 RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
 RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
 RA Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
 RA Vannethan S., Deboy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
 RA Vanthek T., Rade D., Upton J., Hansen T., Shetty J., Khouli H.,
 RA Usterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
 RT "Role of mobile DNA in the evolution of vancomycin-resistant
 RT *Enterococcus faecalis*."
 RL Science 299:2071-2074(2003).
 CC -!- FUNCTION: Hydrolyzes the cell wall of *E. faecalis* and
 CC M. lysodeikticus. May play an important role in cell wall growth
 CC and cell separation.
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -!- DOMAIN: LYSM REPEATS ARE THOUGHT TO BE INVOLVED IN PEPTIDOGLYCAN
 CC BINDING.
 CC -!- SIMILARITY: BELONGS TO FAMILY 73 OF GLYCOSYL HYDROLASES.
 CC -!- SIMILARITY: Contains 6 lysm repeats.
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 CC -----
 DR EMBL: M58002: AAA67325.1: -
 DR EMBL: AE016949: AA080613.1: -
 DR PIR: A38109; A38109.
 DR TIGR: EF0799; -
 DR InterPro: IPR002901; Amidase_4.
 DR InterPro: IPR002482; LysM.
 DR Pfam: PF01832; Amidase_4; 1.
 DR Pfam: PF01476; LysM; 5.
 DR SMART: SM00257; LysM; 6.
 DR SMART: SM00047; Lys2; 1.
 KW Hydrolyase; Glycosidase; Bacteriolytic enzyme; Cell wall;
 KM Cell division; Septation; Repeat; Signal.
 FT SIGNAL 1 53 POTENTIAL.

FT CHAIN 54 737 AUTOLYSIN.
 FT REPEAT 363 405 LYSM 1.
 FT REPEAT 431 473 LYSM 2.
 FT REPEAT 499 541 LYSM 3.
 FT REPEAT 567 609 LYSM 4.
 FT REPEAT 633 675 LYSM 5.
 FT REPEAT 695 737 LYSM 6.
 FT REPEAT 85 85 T -> I (IN REF. 1).
 FT CONFLICT 118 118 A -> V (IN REF. 1).
 FT CONFLICT 143 143 A -> T (IN REF. 1).
 FT CONFLICT 417 417 S -> N (IN REF. 1).
 FT CONFLICT 449 449 S -> T (IN REF. 1).
 FT CONFLICT 476 476 A -> T (IN REF. 1).
 FT CONFLICT 484 484 N -> S (IN REF. 1).
 FT CONFLICT 567 632 MISSING (IN REF. 1).
 SQ SEQUENCE 737 AA; 77025 MW; ABB16BD506AC7507 CRC64;

Query Match 6.9%; Score 179.5; DB 1; Length 737;
 Best Local Similarity 23.0%; Pred. No. 0.038;
 Matches 111; Conservative 55; Mismatches 208; Indels 109; Gaps 21;

QY 66 SFGANGKRVNIISDTKGLNFA---KETAGTNGDTTVHLNGISLTPMLNTGATTVT 121
 DB 268 SFQDNHAYLKTTSFQAGYVYAGAKMSNTSSYRDATLFT--GRATDPSTNAKLNNTIT 325
 QY 122 NDNVTDEKKRAASYKDVLANGMWIKG--VKPGTTASDNVDFRTY-----DTVEFLSA 173
 DB 326 AYNLTQ-----YDTPSSGGNGTGGTVNPGTGSNNOSGTNTYTVKSGDTLNTKITA 376
 QY 174 DTKTTTVESKDNCKTEVKIGAKTSVKEKDGKLVTKGKKGNGSGSTDE--GEGLVYAK 232
 DB 377 QYGVSVANLRSMWNGISGDLIFVQGLIVKKGASGN--TG--DSGSGSNNOSGTNTYTV 433
 QY 233 EVIDAVNKRGMKTTTANSGTGQADKEFTVSGTKVTF---ASGN--GTTATVSKDDG 287
 DB 434 KSGDTLNTAQQYGVSVANLRSMWNGISGDLIFVQGLIVKKGASGNTGSGNNOS 493
 QY 288 NITVYDVNVGDALN-----VNQLNSGMNLDKAAVAGSSGKYI-----SGNVSPSKG 335
 DB 494 GTNTYTTKSGTTLNKIAQQYGVSVANLRSMWNGISGDLIFAGQKLIYKKGTSNGTGSS 552
 QY 336 KMDFTVNNMAGNIETIRNGKNIDATSMTPQFSSVSLGAGADAPTLTSV--DDEGAL--- 390
 DB 553 -----NGSGN--NNOSGTNTYTTKSGDTLNTKISQFQSVANLQAMNNISGLIFA 602
 QY 391 -----NVGSKDANKPVRTNVAPG-----VKEGDVYVNAQLKGVANLNLRIDN 434
 DB 603 GQKIIVKKGANGSNTNKP--TNNGGATTSTYIKSGDTLN-----K 643
 QY 435 VNGNARAGIAQAIATAGLVQAYLPKSMMAIGGTYLGEAGYATGYSISAGNMWIKGT 494
 DB 644 ISAPQGVSVANLRSMWNGI-----KGDLI FAGQTIIVKKG-----ASAGNASSTNS 689
 QY 495 ASG 497
 DB 690 ASG 692

RESULT 10
 ICEN_XANCT STANDARD: PRT: 1567 AA.
 AC P18127:
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ice nucleation protein.
 GN INAX.
 OS Xanthomonas campestris (pv. translucens).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 CC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=343;
 RN [1]
 RP SEQUENCE FROM N.A.

CC STRAIN-X56S;
 RX MEDLINE=9108059; PubMed=2259339;
 RA Zhao J., Orser C.S.;
 RT "Conserved repetition in the ice nucleation gene *inx* from
 RL *Xanthomonas campestris* pv. *translucens*.";
 CC -1- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
 CC CRYSTALLIZATION IN SUPERCOOLED WATER.
 CC -1- SUBCELLULAR LOCATION: Outer membrane (By similarity).
 CC -1- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
 CC OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
 CC REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
 CC -1- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE
 CC NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL; X52970; CAA37140.1; -;
 DR HSSP; P06620; INA;
 DR InterPro; IPR000258; Ice_nucleatn.
 DR Pfam; PF00818; Ice_nucleation; 81.
 DR PRINTS; PR00327; ICENDCLEATN.
 DR PROSITE; PS00314; ICE_NUCLEATION; 57.
 KM Ice nucleation; Repeat; Outer membrane.
 SQ SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;

Query Match 6.9%; Score 178.5; DB 1; Length 1567;
 Best Local Similarly 20.2%; Pred. No. 0.1;
 Matches 103; Conservative 82; Mismatches 246; Indels 79; Gaps 20;
 QY 20 SELTRNRTKRASAVKAVLATLTLFATVQANATDET---GLINTEKLSGANGKRYNI 76
 DB 808 SDITAGTGTAGADSTLLAG-YGSTQYSGSSSLTAGYGSTQAR---EGSDV-- 858
 QY 77 ISDTKGLNFAKETAGTDTVHLNGISLTLDMLTNGATTNTNNVTDEKKRASY 136
 DB 859 ---TAGY-----STGTAGADSTLLSGYSTQY---AGSSSLTAGYGSTQARKSDV 906
 QY 137 KDVLNAGMNITKVAKPGTTASDNDFVRYTVEFLADTKTTVNVESKDKGKTEVKIG 196
 DB 907 ---TAGYGSTG---TAGADSTLLAGYGSTQSGSSSLTAGYGSTQARKSDMTAG 957
 QY 197 AKTSVIREKDKGLVTGKKGKENGSSDTDEGLVYAKVEDIVANVKNAGRMKTTTANGQTQ 256
 DB 958 YGSGTGTAGADSTLLAGYGSTQSGS-----DSLTAGYGSTQTAEGSDVT 1003
 QY 257 ADKEFYVSGTKYTFASNGTATATVSKDQGNITVKYDVNVGDLANTNOLNSGMNIDSK 316
 DB 1004 AGGSGTGTAGADSTLLAGYGSTQAGSD--SLTAGY-----GSTQTAQGSDVYAGYST 1057
 QY 317 AVAGSGSKVTSQNVSPSKGMDETVINAGNNIEITRNKNIDITATSMTPQFSSVSLGAG 376
 DB 1058 GTAGADSTLLAGYGSTQAGSDSSLTAGYGST-QTARQGSPI-----TAGYGSTGT-AG 1109
 QY 377 ADAPTLSVDEGALNVSSKDKANKPVRTTNAAPGVKEDVDYNNVLOLKGVANLNRRIDNVN 436
 DB 1110 ADSSSLIA--GYSGTQGTAGIDSNLTAGYGSTQTAREDSSLTAGYGSTTAGDSSLLIAGYG 1167
 QY 437 GNAFAGIAQAIATA-GLVQAYLPGKSMMAIGGTYLLEAGY---AIGYSISAGG--NW 489
 DB 1168 STGTAGYNSLTITGTGSTQTAQESSSLTAGYGST--STAGYDSTLLTAGYGSTQTAAGKST 1225
 QY 490 IIKGTASGNSRGH-----FGASASVGYQ 512
 DB 1226 LTAGYGSNSTAGHSSSLIAGYGSTQIAGYE 1255

RESULT 11
 ID BIGA_SALTY STANDARD; PRT: 1953 AA.
 AC P25927; P25928; Q9XK03;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Putative surface-exposed virulence protein biga precursor.
 GN BIGA OR STM3478.
 OS *Salmonella typhimurium*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Salmonella*.
 OX NCBI_Taxid=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 14028;
 RA Stojiljkovic I., Valentine P., Heffron F.;
 RT "Salmonella typhimurium rhs homolog.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., All J., Dante M., Du P., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 RT LT2.";
 RL Nature 413:852-856(2001).
 RN [3]
 RP SEQUENCE OF 1-765 FROM N.A.
 RC STRAIN=LT2;
 RX MEDLINE=91100301; PubMed=1987123;
 RA Wu J.Y., Siegel L.M., Kredich N.M.;
 RT "High-level expression of *Escherichia coli* NADPH-sulfite reductase:
 RT Requirement for a cloned cyste plasmid to overcome limiting *str*heme
 RT cofactor.";
 RL J. Bacteriol. 173:325-333(1991).
 CC -1- CAUTION: Ref.3 sequence differs from that shown due to frameshifts
 CC in positions 414 and 732.
 CC -----
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 CC -----
 DR EMBL; AF133696; AAD39458.1; -;
 DR EMBL; AE008859; AAL22340.1; -;
 DR EMBL; M64606; AAA27042.1; ALT_FRAME.
 DR EMBL; M64606; AAA27043.1; ALT_FRAME.
 DR StyGene; SG10437; Diga.
 KW Virulence; Repeat; Signal; Complete proteome.
 KM Virulence; Repeat; Signal; Complete proteome.
 FT SIGNAL 1 27
 FT CHAIN 28 1953
 FT DOMAIN 101 252
 FT REPEAT 101 103
 FT REPEAT 104 113
 FT REPEAT 114 122
 FT REPEAT 123 133
 FT REPEAT 134 144
 FT REPEAT 145 155
 FT REPEAT 156 166
 FT REPEAT 167 177
 FT REPEAT 178 188
 FT REPEAT 189 199
 FT PUTATIVE SURFACE-EXPOSED VIRULENCE
 FT POTENTIAL.
 FT PROTEIN BIGA.
 FT 15 X 11 AA TANDEM REPEATS.
 FT 1 (INCOMPLETE).
 FT 2 (INCOMPLETE).
 FT 3 (INCOMPLETE).
 FT 4.
 FT 5.
 FT 6.
 FT 7.
 FT 8.
 FT 9.
 FT 10.


```
FT CONFLICT 126 126 V -> I (IN REF. 1).
FT CONFLICT 137 137 T -> N (IN REF. 1).
FT CONFLICT 157 157 G -> D (IN REF. 1).
FT CONFLICT 368 369 IS -> VN (IN REF. 1).
FT CONFLICT 374 388 KATLGAIKATTTK -> LQVGGVKKANTIN (IN
REF. 1).
FT CONFLICT 640 640 N -> D (IN REF. 1).
FT CONFLICT 669 669 V -> I (IN REF. 1).
FT CONFLICT 793 793 N -> D (IN REF. 1).
FT CONFLICT 803 804 VN -> IS (IN REF. 1).
FT CONFLICT 809 823 LRVGGVKKSNITIN -> KATLGAIKATTTK (IN
REF. 1).
FT CONFLICT 898 898 D -> Y (IN REF. 1).
FT CONFLICT 908 908 P -> N (IN REF. 1).
FT CONFLICT 985 985 N -> K (IN REF. 1).
FT CONFLICT 1009 1009 L -> S (IN REF. 1).
FT CONFLICT 1013 1013 Y -> S (IN REF. 1).
FT CONFLICT 1182 1182 K -> Q (IN REF. 1).
FT CONFLICT 1314 1314 N -> Y (IN REF. 4).
FT CONFLICT 1451 1451 H -> N (IN REF. 1).
FT CONFLICT 1624 1624 G -> D (IN REF. 1).
FT CONFLICT 1628 1628 E -> G (IN REF. 1).
FT CONFLICT 1872 1872 A -> V (IN REF. 1).
FT CONFLICT 1875 1875 T -> P (IN REF. 1).
FT CONFLICT 1878 1879 MS -> LP (IN REF. 1).
FT CONFLICT 1936 1936 E -> A (IN REF. 1).
FT CONFLICT 1965 1970 MTAFLP -> ITPPLS (IN REF. 1).
FT CONFLICT 1997 1997 G -> R (IN REF. 1).
SQ SEQUENCE 2021 AA; 203328 MM; 327FC42D/CB24668 CRC64;
```

Query Match Best Local Similarity 6.8%; Score 177.5; DB 1; Length 2021;

Matches 131; Conservative 56; Mismatches 225; Indels 189; Gaps 27;

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QY 19 VSELTNRHTRKASRYVTAVLALLLPATVOANDETGLINVEFKLSFGANGKKNVVIS 78
DB 670 IKATTTKLTNAASVLTITNVNAVLTGAIDMTGDNVGNILN-----GALSQVNTNIG 723
QY 79 DFGKLNFAKETAG--TNGD-----TIVHL--NGISGLTLMNTGATTVTNTDN----- 124
DB 724 NTNAALATISVGAKKATIGAGVAKATTTKLTNDMSAVTFTNPVVTGAIDMTGNANNCIAT 783
QY 125 VTDEKKRA---ASVKDLNAGWNINIKVPGTTASDNVDFVRTYDVEFLSADTKTTTV 180
DB 784 FTGDSVTGNIGMTNALATVNVAGGLRVGGVYKSTINLTJDNASVFTFTNPVVTGAI 843
QY 181 -NYESKNG-----KTEVKIGAKTSVI 202
DB 844 DMTGNMANGIVTFTGDSVTGNIGNTNALATISVGAKKATLGAIKATTTKLTNDMSAV 903
QY 203 KEKDKRLVTG---KKGKENGSSPTDEGGLVTAKEVIDAVNKAGWRKKTITANGQGTQAD 258
DB 904 TETNPVVTGAIDMTGNANNCIATFTGDSVT-----GNIGNTN 942
QY 259 KFTFTVSGTFTVTPASGNGTATVSKDDGNITVKYDVNVGDALNVNQLONGWN-----LD 314
DB 943 ALATVNVAGAVTLQAGSL-----DANNI-----DEGARSTLEFNGLDGGNAIYYE 991
QY 315 SKAVAGSSGKVISGNV-----PSKGMDETVINANGNIEITRNCKNIDTATSMTPQF 368
DB 992 KGALANGNNAILLNVNLTLLAYHLLTGTVAE--INIGAGNLFADISAGVTTILMAODIHF 1050
QY 369 SSVS-----LCAGADAPTLTVD-----DEG-----ALNVGSKDANKPVATIN 405
DB 1051 RAIDSALVLSNLTGCVGNNTILLADVLAPGVDEGTVTFDGVGNLNGS-----N 1100
QY 406 VAPGVKE-GDV-----TNAQLKGVAQN--LNNRIDNVNGNARAGIAQA 446
DB 1101 VAGAAKNIGDVGNKFTLLIYNAVTTTDDVNLEGI-QNVLIINNADFTSSA----- 1152
QY 447 IATAGLVQAVLPGKSMMAIGGGTGLGAGATGSSISAGS-----NMIIKGTASGNS 499
DB 1153 -FNAGTIO-----INDATYTTIDANN--GNLNIIPAGNIKFAHADQOLIIONSSGND 1199
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QY 500 R 500
DB 1200 R 1200

RESULT 13
SLAP_CAME
ID SLAP_CAME STANDARD; PRF; 933 AA.
AC P35827;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE S-layer protein (Surface array protein) (SAP).
OS S-layer protein (Surface array protein) (SAP).
OC Campylobacter fetus.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_Taxid:196;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
RC STRAIN=84-32 / 23D;
RX MEDLINE=9035448; PubMed=2387868;
RA Blaser M.J., Gotschlich E.C.;
RT "Surface array protein of Campylobacter fetus. Cloning and gene
structure."
RL J. Biol. Chem. 265:14529-14535(1990).
RN [2]
RX ERRATUM.
RX MEDLINE=91035477; PubMed=2229082;
RA Blaser M.J., Gotschlich E.C.;
RL J. Biol. Chem. 265:19372-19372(1990).
CC -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS
CC CRITICAL FOR VIRULENCE.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; J05577; AAA23032.1; -.
CC DR Cell wall; S-layer.
CC KW SEQUENCE 933 AA; 96757 MW; F88C729B4BA5B1E9 CRC64;
SQ

Query Match Best Local Similarity 6.8%; Score 176.5; DB 1; Length 933;
Matches 128; Conservative 67; Mismatches 231; Indels 165; Gaps 24;
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QY 31 SATVKTAVL---ATLFEATVOANDETGLINVE-----EKLSPGANGKKNVVIS 78
DB 251 TAITRAALLNDQAEILLITKRRTVENINIIISDLETSGDFVNGEKGKGVNLDIVSFAT 310
QY 79 D-TKGLNFAKETAGT-----NGDTVHLNGISGLTMDMLN 113
DB 311 DASKSVNV--ETTGTITAFTAAGTGKVDVYAGKISALTADSRSVNLTAINDTITLTSAN 368
QY 114 TGAFTVNTDNVTD-----DEKRRAA-----SVKDLVNLGNINIGVK 150
DB 369 AATSVNKKQKQAKDATITSMQCKYNNRRNRRIATITSAITAVENLTVAHATNALNGCMDK 428
QY 151 PGTTASDNVDFVRTYDVEFLSADTKTTTVN-VEKSDNG-----KTEVKI 195
DB 429 LATVTLIDNALTLAIDL-----KASSTILNLINSSVNGPKHLYSSKRRYCKFRRAAKV 481
QY 196 GAKTSVYKEK-----DGKLVYTGKKEKENGSSPTDEGGS---LVTAKEVIDAVNKAAGW 243
DB 482 KLMTTATDOTVTVLKANATDNLSLEFDSATAKTTSVTPASGSKTLVIGAEVETLVN----- 537
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OY 244 RMKTTTAN-----GQTGQADKF--ETVTSCTKVTTFASGNGTATATVSK--DDQGNITVK 292
DB 538 -IDTTAFNALOSVSGKGTGGGKFSVKTGTGDDKTEFV---GTTLEGESVIDAPGNDRTA 593
OY 293 YVNVNGDALNVNQLONGSGMNLDSKAVAG---SSGKVISGNSPSKGMDETVNINAGNNI 349
DB 594 MKSAALTSTANFTMINNIENVAISDAVATADLSSAFKNSVITTTTKEAATFTLTINKDOYI 653
OY 350 EITRNGKNIDTATSMTPOPSSVSLGAGADAPLTSVDEDEGALNVGSKDANKPVRITNVAPG 409
DB 654 -----NFTADAGSVKILITYKLN---DVTALMIVYKIVLDAAKD-----TRIALG 696
OY 410 VKEGVTNYAQLKGYAQNINRIDVNGNARAGIAQATAGLVQAYVLPKSMMAIGC-- 467
DB 697 TAAADKALV-----IDTGIETLNTISLVKATSPETTANTVNAKLTDVTIILDCMQ 747
OY 468 -----GTYLG-----EAGYALIGYSSISAGSNMIIKTCASGNS 499
DB 748 ITLGHAGTAGTDYTSKVSMDASALKAGLTEDASAITLGANATIKGSGSGADS 798

RESULT 14
SLAP CAUCR
ID STAP CAUCR STANDARD: PRT: 1025 AA.
AC P35828; Q46015; Q9RF12;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE S-layer protein (Paracrystalline surface layer protein).
GN RSA OR CCI007.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21; 646-660 AND 1021-1025.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=93007489; PubMed=1393820;
RA Gilchrist A., Fisher J.A., Smit J.K.;
RT "Nucleotide sequence analysis of the gene encoding the Caulobacter
RT crescentus paracrystalline surface layer protein."
RL Can. J. Microbiol. 38:193-202(1992).
RN [2]
RP REVISIONS TO 376; 636 AND 842-843.
RA Awram P.;
RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J53001;
RA Bingle W.H., Awram P.A., Nommellini J.F., Smit J.K.;
RT "The secretion signal of C. crescentus S-layer protein is located in
RT the C-terminal 82 amino acids of the molecule."
RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nieman W.C., Feldblyum T.V., Laub M.R., Ohba N., Maddock J.R.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Phade N.D., Ely B.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phade N.D., Ely B.,
RA Deboy R.J., Dodson R.J., Durkin A.S., Gwin M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouli H., Shetty J., Berry K.,
RA Ultebeck T., Tran K., Wolf A., Yamatchevan J., Ermolaeva M., White O.,
RA Salbeck S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
RN [5]
RP SEQUENCE OF 1-313 FROM N.A., AND SEQUENCE OF 1-20.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=89008089; PubMed=3049545;
RA Fisher J.A., Smit J.K., Agabian N.;
RT "Transcriptional analysis of the major surface array gene of

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RT Caulobacter crescentus."
RL J. Bacteriol. 170:4706-4713(1988).
RN [6]
RP CHARACTERIZATION.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=98292737; PubMed=9620954;
RA Awram P., Smit J.K.;
RT "The Caulobacter crescentus paracrystalline S-layer protein is
RT secreted by an ABC transporter (type I) secretion apparatus."
RL J. Bacteriol. 180:3062-3069(1998).
CC -I- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. PROBABLY ACTS AS A
CC PHYSICAL BARRIER TO PARASITES AND LYtic ENZYMES.
CC LAYER WITH HEXAGONAL SYMMETRY. SECRETED BY AN ABC TRANSPORTER
CC (TYPE I) SECRETION APPARATUS.
CC -I- MISCELLANEOUS: THE CALCIUM BINDING OF THIS PROTEIN MAY MEDIATE
CC SURFACE ATTACHMENT BY IONIC BRIDGING BETWEEN THE S-LAYER AND A
CC SPECIFIC MEMBRANE-ASSOCIATED OLIGOSACCHARIDE.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF062345; AAC38665.2; -.
DR EMBL: AF193063; AAF19365.1; -.
DR EMBL: AE005779; AAK22991.1; ALT_INIT.
DR PIR: A48995; A48995.
DR HSSP: P22629; 1SMC.
DR TIGR: CC1007; -.
DR Interpro: IPR001343; Hemlyan_Ca_bind.
DR Pfam: PF00353; hemolysinCbind; 3.
DR PRINTS: PR00313; CABDNCRPT.
RT Cell wall; S-layer; Calcium-binding; Complete proteome.
FT INIT_MEN 0
SQ SEQUENCE 1025 AA; 98001 MW; AD7A326E1363D8AC CRC64;

Query Match 6.7%; Score 175; DB 1; Length 1025;
Best Local Similarity 22.1%; Pred. No. 0.093;
Matches 135; Conservative 66; Mismatches 224; Indels 186; Gaps 29;

OY 34 VETAVLATL-----FATVOAN-----ATDETGLINVEKLSFGANGK 73
DB 191 VKAALIGTILNAAVTSYGIGVATATTAAMINDSLDGLSTDNAGVNLTTAPSSGVSST 250
OY 74 VNIISDTKGLNFAKETAGNGDTTV--HLNG-----IGSTL-----TMDL----- 111
DB 251 LSLTGTGDTL-----TGTANNNDTFVAGEVAGATLVGDTLSGAGCTVLLMNVQAAAVTA 305
OY 112 LNTGAT-INVNTNDVTDDEKKRAASVKDYLVNAGNMIIKVKPPTASDNDVFRVDTVEF 170
DB 306 LPTGVTSIGIETMANVTS-----GAAT--TLNVTSSGVGTITLALNVTSGAAGTQTATAGACON 358
OY 171 LSADRTTIVNESKDNCKTEVKIGAKTSVYKERDGLVYKKGKENG-----SS 221
DB 359 LRTATTAADAAANVAADGGANVIV---ASTGV---ISGTTVYGANNAAGTYSVSVANSST 412
OY 222 TDESGGLVTAKEVIDAVKAKGRMKT-----TANGQT----- 254
DB 413 TTTGAIATVGTGAAVVAQTAGNAVVTTLQADVTVTGNSSTAVVTOATAATAGATVAG 472
OY 255 -----GQADRFETYSG-----KRYVTASGNGTATATVSKDDQ 286
DB 473 RVNGAVTTTDSAAASATAGKATATVTLGSPGATIDSSALTTVNL--SGTGSLSLIGR--- 528
OY 287 GNITVYVNVGDALNVNQLONGSGMNLDSKAVAGS-----SGKVISGNSPSKGMKDE 339
DB 529 GALTATPTTANT-LTILNVGLTTTGAIITDSEAAADGFTTINAGSTASTIASLVAADAT 587

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:10 : Search time 37.678 Seconds
(without alignments)
3513.485 Million cell updates/sec

Title: US-09-771-382-24
Perfect score: 2602
Sequence: 1 MNKIRIIMNSALNMAVAVS.....TASGNSRGHFGASASGYQW 513

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_23:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.prodent:*
12: sp.virus:*
13: sp.vertibrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriaph:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2552.5	98.1	592	2	0930Y2
2	2514.5	96.6	592	2	09JPS9
3	2476.5	95.2	594	2	09JPI3
4	2472.5	95.0	594	2	09JPS2
5	2472	95.0	599	2	09JPR8
6	2468.5	94.9	590	2	09JPS3
7	2460.5	94.6	598	2	09JPS0
8	2460.5	94.6	598	2	09JPT0
9	2451.5	94.2	598	2	09JPS5
10	2448.5	94.1	594	2	09JPH7
11	2446.5	94.0	598	2	09JPH7
12	2419.5	93.0	600	2	09JPS6
13	2409.5	92.6	594	2	0930Y4
14	2407	92.5	591	16	09JRI8
15	2403	92.4	591	2	09JPS7
16	2402.5	92.3	592	2	09AQF0

17	2395	92.0	591	2	0930Y3	0930Y3 neisseria m
18	2351.5	90.4	592	16	09JQW4	09JQW4 neisseria m
19	2343.5	90.1	600	2	09JPS5	09JPS5 neisseria m
20	2314	88.9	589	2	0930Y1	0930Y1 neisseria m
21	2313.5	88.9	598	2	09JPR7	09JPR7 neisseria m
22	2304	88.5	595	2	09JPH0	09JPH0 neisseria m
23	2304	88.5	599	2	09JPS8	09JPS8 neisseria m
24	2303	88.5	589	2	09JPI0	09JPI0 neisseria m
25	2224.5	85.5	526	2	09JPS4	09JPS4 neisseria m
26	2224.5	85.5	530	2	09JPS1	09JPS1 neisseria m
27	966.5	37.1	1098	2	048152	048152 haemophilus
28	965.5	37.1	1096	2	08GM79	08GM79 haemophilus
29	939.5	36.1	2353	2	P71401	P71401 haemophilus
30	891.5	34.3	1204	2	08GM76	08GM76 haemophilus
31	873.5	33.6	1210	2	08GM74	08GM74 haemophilus
32	870.5	33.5	1210	2	08GM75	08GM75 haemophilus
33	705.5	27.1	1004	2	08GM77	08GM77 haemophilus
34	687.5	26.4	1002	2	08GM78	08GM78 haemophilus
35	403	15.5	1299	16	09F3X6	09F3X6 pasteurella
36	380	14.6	2314	2	08KOM8	08KOM8 moraxella c
37	371	14.3	1588	16	08XDG4	08XDG4 xyella fas
38	365	14.0	1190	16	09PC04	09PC04 xyella fas
39	363	14.0	1778	16	08RCB2	08RCB2 escherichia
40	361.5	13.9	1964	2	08KOM9	08KOM9 moraxella c
41	361	13.9	1107	16	09F2D8	09F2D8 salmoneilla
42	360	13.8	1461	16	08ZL64	08ZL64 salmoneilla
43	359.5	13.8	2059	16	09PD50	09PD50 xyella fas
44	333.5	12.8	641	16	08CKM1	08CKM1 yersinia pe
45	333.5	12.8	658	16	08ZHU0	08ZHU0 yersinia pe

ALIGNMENTS

RESULT 1
ID 0930Y2 PRELIMINARY; PRT; 592 AA.
AC 0930Y2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE NHA outer membrane protein.
GN NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN=H41;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF157609; AAK68870.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 592 AA: 61869 MW: F9403A0B4A18EAEV CRC64;

Query Match 98.1%; Score 2552.5; DB 2; Length 592;
Best Local Similarity 86.7%; Pred. No. 1.6e-101;
Matches 513; Conservative 0; Mismatches 0; Indels 79; Gaps 1;

QY	1	MNKIRIIMNSALNMAVAVSELTRNHTKRASATVKTAVLATLTFATVOANATDE-----	54
DB	1	MNKIRIIMNSALNMAVAVSELTRNHTKRASATVKTAVLATLTFATVOANATDEDEEEL	60
QY	55	-----TGLINWETKLSFGANGKRYNIISDTKGLNFAKETAGTNGDTTVHLN	101
DB	61	ESVQRSVGSIQASMEGSVELLETISMTNDSKEFVDPIYVTLKAGDNLIKIKONTNENT	120
QY	55	-----TGLINWETKLSFGANGKRYNIISDTKGLNFAKETAGTNGDTTVHLN	101

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Db 121 NASSTFYSLSKDLTGLINVEFEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVALN 180
Qy 102 GIGSTLTMLNTGATNTVNDNTDDEKKRAASYKVDVNLNMGNIKGVPFGTTASDNVDF 161
Db 181 GIGSTLTMLNTGATNTVNDNTDDEKKRAASYKVDVNLNMGNIKGVPFGTTASDNVDF 240
Qy 162 VRTYDVEFLSADTKTTTVNVESKDNKGKTEVKGAKTSVYKEKDKLVTGKGENSS 221
Db 241 VRTYDVEFLSADTKTTTVNVESKDNKGKTEVKGAKTSVYKEKDKLVTGKGENSS 300
Qy 222 TDEGGLVTAKEDVDAVNAKAGRMKTTTANGOTGADAFETVTSCTKTYTFASGNGTATV 281
Db 301 TDEGGLVTAKEDVDAVNAKAGRMKTTTANGOTGADAFETVTSCTKTYTFASGNGTATV 360
Qy 282 SKDDGNTTVKYDVNVGDLNVLNOLQNSGMNLSKAVAGSSGKVISGNVSPSKGMDETV 341
Db 361 SKDDGNTTVKYDVNVGDLNVLNOLQNSGMNLSKAVAGSSGKVISGNVSPSKGMDETV 420
Qy 342 NINAGNNIETFRNGKNIDIAISMTPOFSSVSLGAGADAPTLSVDEGALNVGSKDANKPV 401
Db 421 NINAGNNIETFRNGKNIDIAISMTPOFSSVSLGAGADAPTLSVDEGALNVGSKDANKPV 480
Qy 402 RTTNAPGVKEDDYNNVNAOLKGVNAONLNRRIDNVGNARAGIAQAIAATAGLVAATLPKGS 461
Db 481 RTTNAPGVKEDDYNNVNAOLKGVNAONLNRRIDNVGNARAGIAQAIAATAGLVAATLPKGS 540
Qy 462 MMAIGGTYLGEAGYAGYSSISAGNNIIGKTASGNSRGHFGASASVGYOM 513
Db 541 MMAIGGTYLGEAGYAGYSSISAGNNIIGKTASGNSRGHFGASASVGYOM 592

RESULT 2
ID 09JPS9 PRELIMINARY: PRT: 592 AA.
AC 09JPS9:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=860800;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappelli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226361; AAF42510.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada.
SQ SEQUENCE 592 AA: 61917 MW: 4A3471514FD3C879 CRC64;
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Query Match 96.6%; Score 2514.5; DB 2; Length 592;
Best Local Similarity 85.5%; Pred. No. 6.8e-100;
Matches 506; Conservative 2; Mismatches 5; Indels 79; Gaps 1;
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Qy 1 MNKIYRIIWSALNMAVAVSELTRNHTKRASATVTAVALTLLEFATVQANATDE----- 54
Db 1 MNKIYRIIWSALNMAVAVSELTRNHTKRASATVTAVALTLLEFATVQANATDEDEEDEL 60
Qy 55 ----- 54
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Db 61 ESVORSVVGSIQASMEGSELETTLSMTNDSKEFVDYIVVTLKAGDNLKIKONTNENT 120
Qy 55 -----TGLINVEFEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVALN 101
Db 121 NASSTFYSLSKDLTGLINVEFEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVALN 180
Qy 102 GIGSTLTMLNTGATNTVNDNTDDEKKRAASYKVDVNLNMGNIKGVPFGTTASDNVDF 161
Db 181 GIGSTLTMLNTGATNTVNDNTDDEKKRAASYKVDVNLNMGNIKGVPFGTTASDNVDF 240
Qy 162 VRTYDVEFLSADTKTTTVNVESKDNKGKTEVKGAKTSVYKEKDKLVTGKGENSS 221
Db 241 VRTYDVEFLSADTKTTTVNVESKDNKGKTEVKGAKTSVYKEKDKLVTGKGENSS 300
Qy 222 TDEGGLVTAKEDVDAVNAKAGRMKTTTANGOTGADAFETVTSCTKTYTFASGNGTATV 281
Db 301 TDEGGLVTAKEDVDAVNAKAGRMKTTTANGOTGADAFETVTSCTKTYTFASGNGTATV 360
Qy 282 SKDDGNTTVKYDVNVGDLNVLNOLQNSGMNLSKAVAGSSGKVISGNVSPSKGMDETV 341
Db 361 SKDDGNTTVKYDVNVGDLNVLNOLQNSGMNLSKAVAGSSGKVISGNVSPSKGMDETV 420
Qy 342 NINAGNNIETFRNGKNIDIAISMTPOFSSVSLGAGADAPTLSVDEGALNVGSKDANKPV 401
Db 421 NINAGNNIETFRNGKNIDIAISMTPOFSSVSLGAGADAPTLSVDEGALNVGSKDANKPV 480
Qy 402 RTTNAPGVKEDDYNNVNAOLKGVNAONLNRRIDNVGNARAGIAQAIAATAGLVAATLPKGS 461
Db 481 RTTNAPGVKEDDYNNVNAOLKGVNAONLNRRIDNVGNARAGIAQAIAATAGLVAATLPKGS 540
Qy 462 MMAIGGTYLGEAGYAGYSSISAGNNIIGKTASGNSRGHFGASASVGYOM 513
Db 541 MMAIGGTYLGEAGYAGYSSISAGNNIIGKTASGNSRGHFGASASVGYOM 592

RESULT 3
ID 09JPI3 PRELIMINARY: PRT: 594 AA.
AC 09JPI3:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88; and B232;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappelli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226376; AAF42525.1; -.
DR EMBL: AF226369; AAF42518.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada.
SQ SEQUENCE 594 AA: 62086 MW: 1B25E03B90D04B46 CRC64;
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Query Match 95.2%; Score 2476.5; DB 2; Length 594;
Best Local Similarity 84.0%; Pred. No. 2.8e-98;
Matches 499; Conservative 4; Mismatches 10; Indels 81; Gaps 1;
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Qy 1 MNKIYRIIWSALNMAVAVSELTRNHTKRASATVTAVALTLLEFATVQANATDE----- 54
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Db 1 MNKYRIIMNSALNMAWVSELFRNHTKRASATVATVATLTLFATVQASTDDDLYLE 60
QY 55 -----
Db 61 PVQRTAPVLSFHADSECTGEKEVTEEDSNMGVYFDKRGVLTAGTTTLKAGDNLIKQNTDE 120
QY 55 -----TGLINVEETEKLSPFANGKRVNITSDPKGLNFAKTAGTNGDTPVH 99
Db 121 NTNASSFTYSLKNDLTDLTSVEFEKLSFGANGKKVNTISDPTKGLNFAKTAGTNGDTPVH 180
QY 100 LINGSTLTDLMLNTGATVNTVNDVTDDEKKRAASVYKVDVLMAGWNIKGVKPGTTASDNV 159
Db 181 LINGSTLTDLTLNTGATVNTVNDVTDDEKKRAASVYKVDVLMAGWNIKGVKPGTTASDNV 240
QY 160 DPAVTYDVEFLSADPTTTTVNVESSKNGKRTTEVKIGAKTSVKEKDKLVTGKKGENG 219
Db 241 DPAVTYDVEFLSADPTTTTVNVESSKNGKRTTEVKIGAKTSVKEKDKLVTGKKGENG 300
QY 220 SSTDEGGLYTAKEVIDAVNKAQRMKTTPANGOTGADKFEVTSCTKYTFASGNGTTA 279
Db 301 SSTDEGGLYTAKEVIDAVNKAQRMKTTPANGOTGADKFEVTSCTKYTFASGNGTTA 360
QY 280 TVSKDDGNTTVKYDVNVDGALNVNOLQNSGMNLSKAVAGSSGKVISGVNPSPKGKME 339
Db 361 TVSKDDGNTTVKYDVNVDGALNVNOLQNSGMNLSKAVAGSSGKVISGVNPSPKGKME 420
QY 340 TVNINAGNNIEITRNGKNIDIAISMTPOFSSVSGAGADAPTLVSDEGALNVGSKDANK 399
Db 421 TVNINAGNNIEITRNGKNIDIAISMTPOFSSVSGAGADAPTLVSDEGALNVGSKDANK 480
QY 400 PVRTTNVAPGVEKEDVTNVAOLKGVAAQNLNRRIDNVNAGNRAGIAQAIATAGLVQAVLP 459
Db 481 PVRTTNVAPGVEKEDVTNVAOLKGVAAQNLNRRIDNVNAGNRAGIAQAIATAGLVQAVLP 540
QY 460 KSMMAIGGTYLGEAGYAIGYSSISAGNMIIKGTASGNSRGHGASASVGYOW 513
Db 541 KSMMAIGGTYLGEAGYAIGYSSISAGNMIIKGTASGNSRGHGASASVGYOW 594

RESULT 4
QY 09JPS2 PRELIMINARY; PRT; 594 AA.
AC 09JPS2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA92.
GN GNA92.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE31;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Masiagnani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Stormi E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226379; AAF42528.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada. 1
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;
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Best Local Similarity 83.8%; Pred. No. 4,2e-98;
Matches 498; Conservative 4; Mismatches 11; Indels 81; Gaps 1;

QY 1 MNKYRIIMNSALNMAWVSELFRNHTKRASATVATVATLTLFATVQAAATDE----- 54
Db 1 MNKYRIIMNSALNMAWVSELFRNHTKRASATVATVATLTLFATVQASTDDDLYLE 60
QY 55 -----
Db 61 PVQRTAPVLSFHADSECTGEKEVTEEDSNMGVYFDKRGVLTAGTTTLKAGDNLIKQNTDE 120
QY 55 -----TGLINVEETEKLSPFANGKRVNITSDPKGLNFAKTAGTNGDTPVH 99
Db 121 NTNASSFTYSLKNDLTDLTSVEFEKLSFGANGKKVNTISDPTKGLNFAKTAGTNGDTPVH 180
QY 100 LINGSTLTDLMLNTGATVNTVNDVTDDEKKRAASVYKVDVLMAGWNIKGVKPGTTASDNV 159
Db 181 LINGSTLTDLTLNTGATVNTVNDVTDDEKKRAASVYKVDVLMAGWNIKGVKPGTTASDNV 240
QY 160 DPAVTYDVEFLSADPTTTTVNVESSKNGKRTTEVKIGAKTSVKEKDKLVTGKKGENG 219
Db 241 DPAVTYDVEFLSADPTTTTVNVESSKNGKRTTEVKIGAKTSVKEKDKLVTGKKGENG 300
QY 220 SSTDEGGLYTAKEVIDAVNKAQRMKTTPANGOTGADKFEVTSCTKYTFASGNGTTA 279
Db 301 SSTDEGGLYTAKEVIDAVNKAQRMKTTPANGOTGADKFEVTSCTKYTFASGNGTTA 360
QY 280 TVSKDDGNTTVKYDVNVDGALNVNOLQNSGMNLSKAVAGSSGKVISGVNPSPKGKME 339
Db 361 TVSKDDGNTTVKYDVNVDGALNVNOLQNSGMNLSKAVAGSSGKVISGVNPSPKGKME 420
QY 340 TVNINAGNNIEITRNGKNIDIAISMTPOFSSVSGAGADAPTLVSDEGALNVGSKDANK 399
Db 421 TVNINAGNNIEITRNGKNIDIAISMTPOFSSVSGAGADAPTLVSDEGALNVGSKDANK 480
QY 400 PVRTTNVAPGVEKEDVTNVAOLKGVAAQNLNRRIDNVNAGNRAGIAQAIATAGLVQAVLP 459
Db 481 PVRTTNVAPGVEKEDVTNVAOLKGVAAQNLNRRIDNVNAGNRAGIAQAIATAGLVQAVLP 540
QY 460 KSMMAIGGTYLGEAGYAIGYSSISAGNMIIKGTASGNSRGHGASASVGYOW 513
Db 541 KSMMAIGGTYLGEAGYAIGYSSISAGNMIIKGTASGNSRGHGASASVGYOW 594

RESULT 5
QY 09JPS8 PRELIMINARY; PRT; 599 AA.
AC 09JPS8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA92 (Nhaa outer membrane protein).
GN GNA92 OR NHAa.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH38;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Masiagnani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Stormi E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226379; AAF42528.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada. 1
SQ SEQUENCE 599 AA; 62114 MW; 1E2A63A78F53D256 CRC64;
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RC STRAIN-H38.
 RA Peak 1.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
 RT "Identification and characterization of a gene encoding a novel outer
 RT membrane protein of *Neisseria meningitidis*.";
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF226383; AAF42532.1; -;
 DR EMBL: AF157608; AAK68869.1; -;
 DR InterPro: IPR005594; Yada.
 DR Pfam: PF03895; Yada; 1.
 SQ SEQUENCE 599 AA; 62844 MW; BBA16EBF53C1970C CRC64;

Query Match 95.0%; Score 2472; DB 2; Length 599;
 Best Local Similarity 83.1%; Pred. No. 4,5e-98;
 Matches 498; Conservative 5; Mismatches 10; Indels 86; Gaps 1;

QY 1 MNKIRIITWSALNMAVAVSELTRNHTKRASATVTAVALTLFFATVOANATDE----- 54
 DB 1 MNKIRIITWSALNMAVAVSELTRNHTKRASATVTAVALTLFFATVOANATDEDEEDL 60
 QY 55 ----- 54
 DB 61 EPVVSALVLQFMIDKEGENESTGNGMSIYYDNHNTLHGATVTLKAGDNLKIKONTN 120
 QY 55 -----TGLINVEFEKLSFGANGKKVNIISDTKGLNFAKETAAGTNG 94
 DB 121 KNTNENTNDSFTYSLKADLDLTISVETEKLSFGANGKVNITSDTKGLNFAKETAAGTNG 180
 QY 95 DTTVHLANGISTLTMDLNTGATVNTNDNTDDKKRAASVDYLNAGMNIKGVPGTT 154
 DB 181 DTTVHLANGISTLTMDLNTGATVNTNDNTDDKKRAASVDYLNAGMNIKGVPGTT 240
 QY 155 ASDNVDVRYTDFEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIEKDKLVTKGK 214
 DB 241 ASDNVDVRYTDFEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIEKDKLVTKGK 300
 QY 215 KGENSSPDEGEIYTAKEVIDAVNKGARMKTTTANGQTGOADFEYVTSCTXTTFASG 274
 DB 301 KGENSSPDEGEIYTAKEVIDAVNKGARMKTTTANGQTGOADFEYVTSCTXTTFASG 360
 QY 275 NGTTAVESKDDGNTTVKVDVNVGDALNVNOLONGSMNLDKRAVASSGKVTSGNVSPSK 334
 DB 361 KGTATVSKDDGNTTVKVDVNVGDALNVNOLONGSMNLDKRAVASSGKVTSGNVSPSK 420
 QY 335 GKMDFTVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLISVDEGALNVGS 394
 DB 421 GKMDFTVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLISVDEGALNVGS 480
 QY 395 KDANKPVRTTNVAPGVKGGDTVNVQOLKGVQONLNRRIDNVGNARAGIAQAIAATAGLVQ 454
 DB 481 KDANKPVRTTNVAPGVKGGDTVNVQOLKGVQONLNRRIDNVGNARAGIAQAIAATAGLVQ 540
 QY 455 AYLPGKSMALIGGTYLGEAGYALGYSSISAGNMNLIKGTASGNSRGHFGASASVGYOW 513
 DB 541 AYLPGKSMALIGGTYLGEAGYALGYSSISAGNMNLIKGTASGNSRGHFGASASVGYOW 599

RESULT 6
 Q9JPS3 PRELIMINARY; PRT: 590 AA.

AC Q9JPS3: 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE Outer membrane protein GNA92. 22, Last annotation update)
 DE Outer membrane protein GNA92.
 GN GNA92.
 OS *Neisseria meningitidis*.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NGE28;
 RX MEDLINE=20175756; PubMed=10710308;

RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
 RA Brocker M., Hundt E., Knapp B., Blair E., Mason T., Pettelin H.,
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
 RA Moxon E.R., Grandi G., Rappelli R.;
 RT "Identification of Vaccine Candidates Against Serogroup B
 RT Meningococcus by Whole-Genome Sequencing.";
 RL Science 287:1816-1820(2000).
 DR EMBL: AF226378; AAF42527.1; -;
 DR InterPro: IPR005594; Yada.
 DR Pfam: PF03895; Yada; 1.
 SQ SEQUENCE 590 AA; 61661 MW; BAA476AC300D80C8 CRC64;

Query Match 94.9%; Score 2468.5; DB 2; Length 590;
 Best Local Similarity 84.4%; Pred. No. 6,2e-98;
 Matches 498; Conservative 3; Mismatches 12; Indels 77; Gaps 1;

QY 1 MNKIRIITWSALNMAVAVSELTRNHTKRASATVTAVALTLFFATVOANATDE----- 54
 DB 1 MNKIRIITWSALNMAVAVSELTRNHTKRASATVTAVALTLFFATVOANATDEDEEDL 60
 QY 55 ----- 54
 DB 61 DPVQRTAVLVNSDEKTEGEKVENSDMAVYENEGVLTAGTITLKAGDNLKIKONG 120
 QY 55 -----TGLINVEFEKLSFGANGKKVNIISDTKGLNFAKETAAGTNG 103
 DB 121 TMTYSLKADLDLTISVETEKLSFGANGKVNITSDTKGLNFAKETAAGTNG 180
 QY 104 GSTLTMDLNTGATVNTNDNTDDKKRAASVDYLNAGMNIKGVPGTTASDNDVFR 163
 DB 181 GSTLTMDLNTGATVNTNDNTDDKKRAASVDYLNAGMNIKGVPGTTASDNDVFR 240
 QY 164 TYDVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIEKDKLVTKGKGENGSSTD 223
 DB 241 TYDVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIEKDKLVTKGKGENGSSTD 300
 QY 224 EGEGLVTAKEVIDAVNKGARMKTTTANGQTGOADFEYVTSCTXTTFASG 283
 DB 301 EGEGLVTAKEVIDAVNKGARMKTTTANGQTGOADFEYVTSCTXTTFASG 360
 QY 284 DDGNTTVKVDVNVGDALNVNOLONGSMNLDKRAVASSGKVTSGNVSPSKMDFTVNI 343
 DB 361 DDGNTTVKVDVNVGDALNVNOLONGSMNLDKRAVASSGKVTSGNVSPSKMDFTVNI 420
 QY 344 NAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLISVDEGALNVGS 403
 DB 421 NAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLISVDEGALNVGS 480
 QY 404 TNVAGVVEGDTVNVQOLKGVQONLNRRIDNVGNARAGIAQAIAATAGLVQ 463
 DB 481 TNVAGVVEGDTVNVQOLKGVQONLNRRIDNVGNARAGIAQAIAATAGLVQ 540
 QY 464 AIGGCTYLGAGYALGYSSISAGNMNLIKGTASGNSRGHFGASASVGYOW 513
 DB 541 AIGGCTYLGAGYALGYSSISAGNMNLIKGTASGNSRGHFGASASVGYOW 590

RESULT 7
 Q9JPS0 PRELIMINARY; PRT: 598 AA.

AC Q9JPS0: 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE Outer membrane protein GNA92. 22, Last annotation update)
 DE Outer membrane protein GNA92 (Nhda outer membrane protein).
 GN GNA92 OR NHNA.
 OS *Neisseria meningitidis*.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;

[1]
RN SEQUENCE FROM N.A.
RP STRAIN=NGH15;
RC MEDLINE=20175756; PubMed=10710308;
RA Plazza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H15;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of *Neisseria meningitidis*.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF226381; AAF42530.1; -;
DR EMBL: AF157607; AAK68868.1; -;
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 598 AA; 62763 MW; E6C7AEF0BB8A63CB CRC64;

Query Match 94.6%; Score 2460.5; DB 2; Length 598;
Best Local Similarity 82.9%; Pred. No. 1,4e-97;
Matches 496; Conservative 4; Mismatches 13; Indels 85; Gaps 1;

QY 1 MNKIYRIIIMNSALNAMA VAVSELTRNHRKRSATVATVATLTLFATVQANATDE----- 54
DB 1 MNKIYRIIIMNSALNAMA VAVSELTRNHRKRSATVATVATLTLFATVQANATDDDDLYLE 60
QY 55 ----- 54
DB 61 PVORTAVVLSFRSDKEGTGEKTEDSNMAVYDEKREVLKAGATTLKAGDNLIKONTNE 120
QY 55 -----TGLINVERTEKLSFGANGKKVNIISPTKGLNFAKETAGTNGD 95
DB 121 NTNENTNDSSFTYSLKKDLDTLSVETEKLSFGANGKKVNIISPTKGLNFAKETAGTNGD 180
QY 96 TTVHLNIGISTLTDLMLNTGATTNVTNDVNTDEKKRAASVKDYLNAGWNIKGVKPGTTA 155
DB 181 PTVHLNIGISTLTDLTLNTGATTNVTNDVNTDEKKRAASVKDYLNAGWNIKGVKPGTTA 240
QY 156 SDNVDFRITDYVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDKLVYTGK 215
DB 241 SDNVDFRITDYVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDKLVYTGK 300
QY 216 GENGSSTDEBEGGLTAKVEIDAVNKAAGRKTITTAANGOTGADKFEVTSGTKYTFASGN 275
DB 301 DENGSSTDEBEGGLTAKVEIDAVNKAAGRKTITTAANGOTGADKFEVTSGTKYTFASGN 360
QY 276 GTTATVSKDQGNITVYKDVNVGDALNVNOLNSGWNLDKRAVAGSSGKYISGNVSPSKG 335
DB 361 GTTATVSKDQGNITVYKDVNVGDALNVNOLNSGWNLDKRAVAGSSGKYISGNVSPSKG 420
QY 336 KMETVYINAGNNIEITRNKNKIDIASMTPOESSVSLGAGADAPTLVSDEGALNVGSK 395
DB 421 KMETVYINAGNNIEITRNKNKIDIASMTPOESSVSLGAGADAPTLVSDEGALNVGSK 480
QY 396 DANKPVRITNVAPGVKGDVTNVAQLKGVAONLNRIIDVNGNARAGIAAIAIATAGLYOA 455
DB 481 DANKPVRITNVAPGVKGDVTNVAQLKGVAONLNRIIDVNGNARAGIAAIAIATAGLYOA 540
QY 456 YLPGRSMMAIGGTYLGEAGYAGISISAGGMMIIGTASGNSRGHFGASASVGYOM 513
DB 541 YLPGRSMMAIGGTYLGEAGYAGISISISIDTGMNVIKGTASGNSRGHFGASASVGYOM 598

Q9JPT0
ID Q9JPT0 PRELIMINARY; PRT; 598 AA.
AC Q9JPT0;
DT 01-OCT-2000 (TReMBLrel. 15 Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS *Neisseria meningitidis*.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; *Neisseria*.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2996;
RA MEDLINE=20175756; PubMed=10710308;
RA Plazza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226381; AAF42508.1; -;
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 598 AA; 62763 MW; 63A6A3BD7F0F2EB3 CRC64;

Query Match 94.6%; Score 2460.5; DB 2; Length 598;
Best Local Similarity 82.8%; Pred. No. 1,4e-97;
Matches 495; Conservative 5; Mismatches 13; Indels 85; Gaps 1;

QY 1 MNKIYRIIIMNSALNAMA VAVSELTRNHRKRSATVATVATLTLFATVQANATDE----- 54
DB 1 MNKIYRIIIMNSALNAMA VAVSELTRNHRKRSATVATVATLTLFATVQANATDDDDLYLE 60
QY 55 ----- 54
DB 61 PVORTAVVLSFRSDKEGTGEKTEDSNMAVYDEKREVLKAGATTLKAGDNLIKONTNE 120
QY 55 -----TGLINVERTEKLSFGANGKKVNIISPTKGLNFAKETAGTNGD 95
DB 121 NTNENTNDSSFTYSLKKDLDTLSVETEKLSFGANGKKVNIISPTKGLNFAKETAGTNGD 180
QY 96 TTVHLNIGISTLTDLMLNTGATTNVTNDVNTDEKKRAASVKDYLNAGWNIKGVKPGTTA 155
DB 181 PTVHLNIGISTLTDLTLNTGATTNVTNDVNTDEKKRAASVKDYLNAGWNIKGVKPGTTA 240
QY 156 SDNVDFRITDYVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDKLVYTGK 215
DB 241 SDNVDFRITDYVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDKLVYTGK 300
QY 216 GENGSSTDEBEGGLTAKVEIDAVNKAAGRKTITTAANGOTGADKFEVTSGTKYTFASGN 275
DB 301 DENGSSTDEBEGGLTAKVEIDAVNKAAGRKTITTAANGOTGADKFEVTSGTKYTFASGN 360
QY 276 GTTATVSKDQGNITVYKDVNVGDALNVNOLNSGWNLDKRAVAGSSGKYISGNVSPSKG 335
DB 361 GTTATVSKDQGNITVYKDVNVGDALNVNOLNSGWNLDKRAVAGSSGKYISGNVSPSKG 420
QY 336 KMETVYINAGNNIEITRNKNKIDIASMTPOESSVSLGAGADAPTLVSDEGALNVGSK 395
DB 421 KMETVYINAGNNIEITRNKNKIDIASMTPOESSVSLGAGADAPTLVSDEGALNVGSK 480
QY 396 DANKPVRITNVAPGVKGDVTNVAQLKGVAONLNRIIDVNGNARAGIAAIAIATAGLYOA 455
DB 481 DANKPVRITNVAPGVKGDVTNVAQLKGVAONLNRIIDVNGNARAGIAAIAIATAGLYOA 540
QY 456 YLPGRSMMAIGGTYLGEAGYAGISISAGGMMIIGTASGNSRGHFGASASVGYOM 513
DB 541 YLPGRSMMAIGGTYLGEAGYAGISISISIDTGMNVIKGTASGNSRGHFGASASVGYOM 598

RESULT 8

Db 541 YLPKSMALIGGCTYRGEAGYAIGYSSISDTGNVNIKKTASGNSRGHGTSA SVGYQW 598

RESULT 9

0930Y5 PRELIMINARY; PRT; 598 AA.

AC 0930Y5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Nhma outer membrane protein.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OC Neisseriaceae; Neisseria.

OX NCBI_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-B210;

RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;

RT "Identification and characterization of a gene encoding a novel outer

membrane protein of Neisseria meningitidis.";

RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF157603; AAK68864.1; -

DR InterPro; IPR005594; Yada.

DR Pfam; PF03895; Yada; 1.

SO SEQUENCE 598 AA; 62687 MW; 18CEFFE6410A15DF CRC64;

Query Match 94.2%; Score 2451.5; DB 2; Length 598;

Best Local Similarity 82.6%; Pred. No. 3.3e-97;

Matches 494; Conservative 5; Mismatches 14; Indels 85; Gaps 1;

1 MNKIIRIINSLNMAVAVSELTRNHTKRASATVAVATLTLFATVQANATDE----- 54

1 MNKIIRIINSLNMAVAVSELTRNHTKRASATVAVATLTLFATVQANATDDDDLYLE 60

55 ----- 54

61 PVQRTAVVLSFRSDKEGTEGTEGTEDSNMVAVFDEKRVLKAGATILKAGDNLKIKONTNE 120

55 ----- 95

121 NTNEUTNDSSFTYSLKDLTLDTLSVETKLSFGANGKNKNTISDTGLNFAKETAGTNGD 180

96 TTVHLNGIGSTLTDMLNTGATTNTVNDVTDDEKKRAASVADVLNAGNNIKGVKGTGA 155

181 PTVHLNGIGSTLTDMLNTGATTNTVNDVTDDEKKRAASVADVLNAGNNIKGVKGTGA 240

156 SNNDVPVRYTYVEFLSADTKTTTVNVEESKDKGKTEVKGAKTSYIKERDGLVYGK 215

241 SNNDVPVRYTYVEFLSADTKTTTVNVEESKDKGKTEVKGAKTSYIKERDGLVYGK 300

216 GENGSTDEGEGLVAKVEYIDAVNKRAGMKTTTANGCGOAKDFETVSGTKVTFASGN 275

301 GENGSTDEGEGLVAKVEYIDAVNKRAGMKTTTANGCGOAKDFETVSGTKVTFASGN 360

276 GTTATVSKDDQGNITVYDVNVGDALNVNOLONGNLDISKAVAGSSGKVISGNVSPSKG 335

361 GTTATVSKDDQGNITVYDVNVGDALNVNOLONGNLDISKAVAGSSGKVISGNVSPSKG 420

336 KXDEVTININAGNNIETIRNGKNIDTASMTPOFSSVSGAGADAPLTVSDDEGALNVGSK 395

421 KXDEVTININAGNNIETIRNGKNIDTASMTPOFSSVSGAGADAPLTVSDDEGALNVGSK 480

336 DANKVVRTINVPAGKREGDVNTVAOLKGAONLNRIDNVNNGNARAGTAAATATGIVYA 455

481 DANKVVRTINVPAGKREGDVNTVAOLKGAONLNRIDNVNNGNARAGTAAATATGIVYA 540

456 YLPKSMALIGGCTYRGEAGYAIGYSSISAGGNNITIKKTASGNSRGHGTSA SVGYQW 513

541 YLPKSMALIGGCTYRGEAGYAIGYSSISDTGNVNIKKTASGNSRGHGTSA SVGYQW 598

RESULT 10

09JPH7

AC 09JPH7; PRELIMINARY; PRT; 594 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DE Outer membrane protein GNA992 (Nhma outer membrane protein).

GN GNA992 OR Nhma.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OC Neisseriaceae; Neisseria.

OX NCBI_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-B2198, and 297-0;

RA MEDLINE=20175756; PubMed=10710308;

RA Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,

RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,

RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

RA Brooker M., Hündt E., Knapp B., Blair E., Mason T., Tettelin H.,

RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

RA Moxon E.R., Grandi G., Rappelli R.;

RT "Identification of Vaccine Candidates Against Serogroup B

Meningococcus by Whole-Genome Sequencing.";

RL Science 287:1816-1820(2000).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-B2198;

RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;

RT "Identification and characterization of a gene encoding a novel outer

membrane protein of Neisseria meningitidis.";

RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF226368; AAF42517.1; -

DR EMBL; AF226358; AAF42507.1; -

DR EMBL; AF157604; AAK68865.1; -

DR InterPro; IPR005594; Yada.

DR Pfam; PF03895; Yada; 1.

SO SEQUENCE 594 AA; 62361 MW; 436BDEDE68263C5C CRC64;

Query Match 94.1%; Score 2448.5; DB 2; Length 594;

Best Local Similarity 83.2%; Pred. No. 4.4e-97;

Matches 494; Conservative 3; Mismatches 16; Indels 81; Gaps 1;

1 MNKIIRIINSLNMAVAVSELTRNHTKRASATVAVATLTLFATVQANATDE----- 54

1 MNKIIRIINSLNMAVAVSELTRNHTKRASATVAVATLTLFATVQANATDDDDLYLE 60

55 ----- 54

61 PVQRTAVVLSFRSDKEGTEGTEGTEDSNMVAVFDEKRVLKAGATILKAGDNLKIKONTNE 120

55 ----- 99

121 NTNDSSFTYSLKDLTLDTLSVETKLSFGANGKNKNTISDTGLNFAKETAGTNGDPTVH 180

100 LNGIGSTLTDMLNTGATTNTVNDVTDDEKKRAASVADVLNAGNNIKGVKGTASDNV 159

181 LNGIGSTLTDMLNTGATTNTVNDVTDDEKKRAASVADVLNAGNNIKGVKGTASDNV 240

160 DEVRTYDVEFLSADTKTTTVNVEESKDKGKTEVKGAKTSYIKERDGLVYGKKGENG 219

241 DEVRTYDVEFLSADTKTTTVNVEESKDKGKTEVKGAKTSYIKERDGLVYGKKGENG 300

220 SSTDEGEGLVAKVEYIDAVNKRAGMKTTTANGCGOAKDFETVSGTKVTFASGNCTTA 279

301 SSTDEGEGLVAKVEYIDAVNKRAGMKTTTANGCGOAKDFETVSGTKVTFASGNCTTA 360

280 TVSKDDQGNITVYDVNVGDALNVNOLONGNLDISKAVAGSSGKVISGNVSPSKGKDE 339

361 TVSKDDQGNITVYDVNVGDALNVNOLONGNLDISKAVAGSSGKVISGNVSPSKGKDE 420

07 GENESSIDEGBVIANEYIDHAKWAGWKNTITANGQIGADKEFIVISGKVFASNN 2/5
ZLO
|||||
301 DENGSSBDEGECEI YTHAK EVDTA WIRACWABD TTTTTT NCCOTC A D K E F I V I S G K V F A S N 360
DB

09	170ASDNDVFRVYDVEFASADIKKIVNVEBKDNKRTKVKIGAKTSVKKKDGLVTG	212
153		
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441		
541		
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9441		
9541		
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9841		
9941		
10041		

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QY 213 KKGNGSSTDEGEGLVTAKEVIDAVNKAQWRRKTTTANGQTGOADKFEFTVSGTKVTEA 272
    |||||
DB 301 KKGNGSSTDEGEGLVTAKEVIDAVNKAQWRRKTTTANGQTGOADKFEFTVSGTNVTEA 360
QY 273 SGNGTATVSKDQGNITVTKYDVNVGDALNVNOLQSSGNLDSKAAVAGSSGKIVSGNVSP 332
    |||||
DB 361 SGNGTATVSKDQGNITVTKYDVNVGDALNVNOLQSSGNLDSKAAVAGSSGKIVSGNVSP 420
QY 333 SKGKMEFVNINAGNNIETTRNGKNIDITSMTPQFSSVSLGAGADAPLTSVDEGALNV 392
    |||||
DB 421 SKGKMEFVNINAGNNIETTRNGKNIDITSMTPQFSSVSLGAGADAPLTSVDEGALNV 479
QY 393 GSKDANKPVRTINVAPEKGDVTNVAOLKGYAQNLRIDNVNGNARAGIAQAIATAGL 452
    |||||
DB 480 GSKDANKPVRTINVAPEKGDVTNVAOLKGYAQNLRIDNVNGNARAGIAQAIATAGL 539
QY 453 VOAYLPKSMMAIGGTTYGEAGYALGYSSISAGGWIITKGTASGNSRHFPGASASVGYO 512
    |||||
DB 540 VOAYLPKSMMAIGGTTYGEAGYALGYSSISAGGWIITKGTASGNSRHFPGASASVGYO 599
QY 513 W 513
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DB 600 W 600

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RESULT 13

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QY 0930Y4 PRELIMINARY; PRT; 594 AA.
AC 0930Y4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Nhma outer membrane protein.
GN Nhma.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG327;
RA Peak I.R., Srihanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.*;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157605; AAK68866.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62297 MW; 9DD48B04B3A8EA2 CRC64;

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Query Match 92.6%; Score 2409.5; DB 2; Length 594;
 Best Local Similarity 82.0%; Pred. No. 2e-95;
 Matches 487; Conservative 7; Mismatches 19; Indels 81; Gaps 1;

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QY 1 MKRIYIINSALNMAVAVSELTRNTRKASATVTKAVATLTLFAVVOANDE----- 54
    |||||
DB 1 MKRIYIINSALNMAVAVSELTRNTRKASATVTKAVATLTLFAVVOASTDDDLYLE 60
QY 55 ----- 54
DB 61 PVQRTAVVLSFRSDKCEKTEVEEDSNMGYVFEDKKGVTLAGTITLKAGDNLKIRKONTNE 120
QY 55 -----TGLINVEETKLSFGANGCKVNIISDTKGLNFAKETAGTNGDTVHA 99
    |||||
DB 121 NTNASSFTYSLKLDLTLSVGTGKLSFGANSNKVNIISDTKGLNFAKETAGTNGDTVHA 180
QY 100 LNCIGSTLTDLMLNGATNTVNDNTDDEKRAASVRYVLNAGNMIKGVKPGTASDVN 159
    |||||
DB 181 LNCIGSTLTDLMLNGATNTVNDNTDDEKRAASVRYVLNAGNMIKGVKPGTASDVN 240
QY 160 DFVRTDYVEFLSADTKTTTVNVEKNGKTEVKIGARTSVYKKEGDKLVYKGGKENG 219
    |||||
DB 241 DFVRTDYVEFLSADTKTTTVNVEKNGKTEVKIGARTSVYKKEGDKLVYKGGKENG 300

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QY 220 SSTDEGEGLVTAKEVIDAVNKAQWRRKTTTANGQTGOADKFEFTVSGTKVTEA 279
    |||||
DB 301 SSTDEGEGLVTAKEVIDAVNKAQWRRKTTTANGQTGOADKFEFTVSGTNVTEA 360
QY 280 TVSKDQGNITVTKYDVNVGDALNVNOLQSSGNLDSKAAVAGSSGKIVSGNVSPSKGKME 339
    |||||
DB 361 TVSKDQGNITVTKYDVNVGDALNVNOLQSSGNLDSKAAVAGSSGKIVSGNVSPSKGKME 420
QY 340 TVNINAGNNIETTRNGKNIDITSMTPQFSSVSLGAGADAPLTSVDEGALNVGSKDANK 399
    |||||
DB 421 TVNINAGNNIETTRNGKNIDITSMTPQFSSVSLGAGADAPLTSVDEGALNVGSKDANK 480
QY 400 PVRTINVAPEKGDVTNVAOLKGYAQNLRIDNVNGNARAGIAQAIATAGLVOAYLPD 459
    |||||
DB 481 PVRTINVAPEKGDVTNVAOLKGYAQNLRIDNVNGNARAGIAQAIATAGLVOAYLPD 540
QY 460 KSMMAIGGTTYGEAGYALGYSSISAGGWIITKGTASGNSRHFPGASASVGYOW 513
    |||||
DB 541 KSMMAIGGTTYGEAGYALGYSSISAGGWIITKGTASGNSRHFPGASASVGYOW 594

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RESULT 14

QY 09JRI8 PRELIMINARY; PRT; 591 AA.

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AC 09JRI8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992 (Adhesin) (Nhma outer membrane
DE protein).
GN GNA992 OR NMB0992 OR Nhma.
OS Neisseria meningitidis, and
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487; 491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B, B2169, B283, and H44/76;
RX MEDLINE=20175756; PubMed-10710308;
RA Pizze M., Scarlato V., Mastignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolli E., Capechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Stoni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-genome Sequencing.*;
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed-10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Nelson J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwin M.L., Deboy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Clecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Mastignani V., Pizze M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=N.meningitidis; STRAIN=PMC21;
RA Peak I.R., Srihanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.*;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AF226375; AAF42524.1; -
 DR EMBL; AF002450; AAF41395.1; -
 DR EMBL; AF226367; AAF42516.1; -
 DR EMBL; AF226370; AAF42519.1; -
 DR EMBL; AF226374; AAF42523.1; -
 DR EMBL; AF157611; AAK6872.1; -
 DR TIGR; NMB0992; -
 DR InterPro; IPR005594; Yada.
 DR Pfam; PF03895; Yada; 1.
 KW Complete proteome.
 SQ SEQUENCE 591 AA; 62112 MW; 762293CAE7F73EE6 CRC64;

Query Match 92.5%; Score 2407; DB 16; Length 591;
 Best Local Similarity 82.6%; Pred. No. 2.6e-95;
 Matches 489; Conservative 5; Mismatches 18; Indels 80; Gaps 2;

QY 1 MNKIRIIMNSALNAWAVSELTRNHRKRASATYKTAVALTLFATVOANATDE----- 54
 DB 1 MNKIRIIMNSALNAWAVSELTRNHRKRASATYKTAVALTLFATVOANNEOEEDL 60
 QY 55 ----- 54
 DB 61 YLDPVQRTAVNLIYNSDKEGTEKEKVEENSDMAVFNREKGVLTARETTLAKGNLTKQ 120
 QY 55 -----TGLINVEETKLSFGANGKRVNIISDTKGLNFAKETAGTNGDTTVHLN 101
 DB 121 NGTFEYSLKKDLNLSVGTETKLSFGANGKRVNITSDTKGLNFAKETAGTNGDTTVHLN 180
 QY 102 GIGSTLMDLNTGATTNVTNDNTDDEKKRAASVKDVLNAGMNKGVKPGTTASDNDV 161
 DB 181 GIGSTLMDLNTGATTNVTNDNTDDEKKRAASVKDVLNAGMNKGVKPGTTASDNDV 240
 QY 162 VRTDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVTKERDGLVTKGKGENSS 221
 DB 241 VRTDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVTKERDGLVTKGKGENSS 300
 QY 222 TDEEGVLTAKEVIDAVNKAQWRMKTTPANGOTGOADKFEVTSCTKVTAFASGNGTATV 281
 DB 301 TDEEGVLTAKEVIDAVNKAQWRMKTTPANGOTGOADKFEVTSCTKVTAFASGNGTATV 360
 QY 282 SKDOGNITVYDVNVDGALVNOLONGMNLDSKAVAGSSGKVIISGVNPSKGMDETV 341
 DB 361 SKDOGNITVYDVNVDGALVNOLONGMNLDSKAVAGSSGKVIISGVNPSKGMDETV 420
 QY 342 NINAGNIEITRNKNIDIASMTPOFSSVSLGAGADPTLSVDEGALNYSKDKANKPV 401
 DB 421 NINAGNIEITRNKNIDIASMTPOFSSVSLGAGADPTLSVDEGALNYSKDKANKPV 479
 QY 402 RITNVAQVKEGDTVNAQLKGVAQNLRIDNVNGNARAGIAOAIATAGLVQAYLPKGS 461
 DB 480 RITNVAQVKEGDTVNAQLKGVAQNLRIDNVNGNARAGIAOAIATAGLVQAYLPKGS 539
 QY 462 MMAIGGTYLGEAGYAGYSSISAGNMIIIGTASGNSRGHFGASASVGYOW 513
 DB 540 MMAIGGTYLGEAGYAGYSSISAGNMIIIGTASGNSRGHFGASASVGYOW 591

RESULT 15

Q9JPS7 PRELIMINARY; PRT; 591 AA.
 AC Q9JPS7;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE Outer membrane protein GNA92.
 GN GNA92.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STRAIN=B2147;

RX MEDLINE=20175756; PubMed=10710308;
 RA Piza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
 RA Comanducci M., Jennings G.T., Baldi L., Bartoloini E., Capecechi B.,
 RA Galeotti C.L., Iuzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
 RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
 RA Moxon E.R., Grandi G., Rappuoli R.;
 RT "Identification of Vaccine Candidates Against Serogroup B
 Meningococcus by Whole-Genome Sequencing";
 RL Science 287:1816-1820(2000).
 DR EMBL; AF226366; AAF42515.1; -
 DR InterPro; IPR005594; Yada.
 DR Pfam; PF03895; Yada; 1.
 SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;

Query Match 92.4%; Score 2403; DB 2; Length 591;
 Best Local Similarity 82.4%; Pred. No. 3.8e-95;
 Matches 488; Conservative 6; Mismatches 18; Indels 80; Gaps 2;

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 DB 1 MNKIRIIMNSALNAWAVSELTRNHRKRASATYKTAVALTLFATVOANNEOEEDL 60
 QY 55 ----- 54
 DB 61 YLDPVQRTAVNLIYNSDKEGTEKEKVEENSDMAVFNREKGVLTARETTLAKGNLTKQ 120
 QY 55 -----TGLINVEETKLSFGANGKRVNIISDTKGLNFAKETAGTNGDTTVHLN 101
 DB 121 NGTFEYSLKKDLNLSVGTETKLSFGANGKRVNITSDTKGLNFAKETAGTNGDTTVHLN 180
 QY 102 GIGSTLMDLNTGATTNVTNDNTDDEKKRAASVKDVLNAGMNKGVKPGTTASDNDV 161
 DB 181 GIGSTLMDLNTGATTNVTNDNTDDEKKRAASVKDVLNAGMNKGVKPGTTASDNDV 240
 QY 162 VRTDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVTKERDGLVTKGKGENSS 221
 DB 241 VRTDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVTKERDGLVTKGKGENSS 300
 QY 222 TDEEGVLTAKEVIDAVNKAQWRMKTTPANGOTGOADKFEVTSCTKVTAFASGNGTATV 281
 DB 301 TDEEGVLTAKEVIDAVNKAQWRMKTTPANGOTGOADKFEVTSCTKVTAFASGNGTATV 360
 QY 282 SKDOGNITVYDVNVDGALVNOLONGMNLDSKAVAGSSGKVIISGVNPSKGMDETV 341
 DB 361 SKDOGNITVYDVNVDGALVNOLONGMNLDSKAVAGSSGKVIISGVNPSKGMDETV 420
 QY 342 NINAGNIEITRNKNIDIASMTPOFSSVSLGAGADPTLSVDEGALNYSKDKANKPV 401
 DB 421 NINAGNIEITRNKNIDIASMTPOFSSVSLGAGADPTLSVDEGALNYSKDKANKPV 479
 QY 402 RITNVAQVKEGDTVNAQLKGVAQNLRIDNVNGNARAGIAOAIATAGLVQAYLPKGS 461
 DB 480 RITNVAQVKEGDTVNAQLKGVAQNLRIDNVNGNARAGIAOAIATAGLVQAYLPKGS 539
 QY 462 MMAIGGTYLGEAGYAGYSSISAGNMIIIGTASGNSRGHFGASASVGYOW 513
 DB 540 MMAIGGTYLGEAGYAGYSSISAGNMIIIGTASGNSRGHFGASASVGYOW 591

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 Job time : 40.678 secs

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:05:45 : Search time 34.9514 Seconds
(without alignments)
1848.325 Million cell updates/sec

Title: US-09-771-382-25
Perfect score: 2063
Sequence: 1 MNKTYRIIMNSALNANWVVS.....TASGNGRHFGASASVGYQM 407

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SIDSI/gcgdata/geneseq/emb1/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/emb1/AA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/emb1/AA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/emb1/AA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/emb1/AA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/emb1/AA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/emb1/AA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/emb1/AA1988.DAT:*
10: /SIDSI/gcgdata/geneseq/emb1/AA1989.DAT:*
11: /SIDSI/gcgdata/geneseq/emb1/AA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/emb1/AA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/emb1/AA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/emb1/AA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/emb1/AA1994.DAT:*
16: /SIDSI/gcgdata/geneseq/emb1/AA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/emb1/AA1996.DAT:*
18: /SIDSI/gcgdata/geneseq/emb1/AA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/emb1/AA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/emb1/AA2000.DAT:*
21: /SIDSI/gcgdata/geneseq/emb1/AA2001.DAT:*
22: /SIDSI/gcgdata/geneseq/emb1/AA2002.DAT:*
23: /SIDSI/gcgdata/geneseq/emb1/AA2003.DAT:*
24: /SIDSI/gcgdata/geneseq/emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2063	100.0	407	22	AAU06184
2	2040	98.9	433	22	AAU06185
3	2005.5	97.2	502	22	AAU06186
4	2000.5	97.0	512	22	AAU06182
5	1961	95.1	591	20	AAV27202
6	1961	95.1	591	20	AAV23746
7	1961	95.1	591	22	AAU06171
8	1956.5	94.8	592	20	AAV23737
9	1954	94.7	591	21	AAV57045

10	1949	94.5	591	20	AAV23741	A surface protein
11	1949	94.5	591	22	AAU06175	N. meningitidis Bg
12	1909	92.5	513	22	AAU06183	N. meningitidis H4
13	1893.5	91.8	592	22	AAU06180	N. meningitidis 22
14	1887.5	91.5	594	20	AAV23740	A surface protein
15	1887.5	91.5	594	21	AAV57044	BASB029 amino acid
16	1887.5	91.5	594	22	AAU06174	N. meningitidis Bg
17	1886	91.4	599	20	AAV23743	A surface protein
18	1886	91.4	599	22	AAU06176	N. meningitidis H3
19	1879.5	91.1	594	20	AAV23739	A surface protein
20	1879.5	91.1	594	22	AAU06179	N. meningitidis B2
21	1869.5	90.6	592	20	AAV23744	A surface protein
22	1869.5	90.6	592	22	AAU06172	N. meningitidis H4
23	1864.5	90.4	592	20	AAV27203	Amino acid sequence
24	1864.5	90.4	598	20	AAV23742	A surface protein
25	1864.5	90.4	598	22	AAU06177	N. meningitidis H1
26	1855.5	89.9	598	20	AAV23738	A surface protein
27	1855.5	89.9	598	22	AAU06178	N. meningitidis B2
28	1848	89.6	589	20	AAV23745	A surface protein
29	1848	89.6	589	22	AAU06173	N. meningitidis P2
30	1749.5	84.8	604	22	AAU06181	N. meningitidis su
31	660.5	32.0	1098	17	AAV93382	Haemophilus adhe
32	640	31.0	2411	17	AAV23860	Haemophilus influe
33	638	30.9	2353	17	AAV93383	Haemophilus adhe
34	625.5	30.3	1094	21	AAV23858	Haemophilus influe
35	600	29.1	116	21	AAV37832	Neisserial conserv
36	494	23.9	679	17	AAV93394	Haemophilus adhe
37	494	23.9	679	21	AAV23855	Haemophilus influe
38	402.5	19.5	1004	21	AAV23857	Haemophilus influe
39	391.5	19.0	1002	21	AAV23854	Haemophilus influe
40	366	17.7	72	21	AAV37830	Neisserial conserv
41	341.5	16.6	1104	21	AAV23856	Haemophilus influe
42	341.5	16.6	1104	21	AAV23859	Haemophilus influe
43	331	16.0	42	21	ABV52677	Escherichia coli p
44	319	15.5	2139	24	ABP1294	M. catarrhalis sur
45	317.5	15.4	2314	22	AAV69136	M. catarrhalis les

ALIGNMENTS

RESULT 1	
AAU06184	
ID	AAU06184 standard; Protein: 407 AA.
AC	AAU06184;
XX	
XX	24-OCT-2001 (first entry)
DT	
XX	
DE	N. meningitidis PMC21 Nhma deletion mutant #2.
XX	
KW	Surface antigen Nhma; meningococcal disease; meningitis vaccine;
KW	mutant; muteln.
XX	
OS	Neisseria meningitidis strain PMC21.
XX	
XX	Synthetic.
FT	
FT	Key
FT	Peptide
FT	/label=
FT	Protein
FT	/label=
FT	/note=
FT	claimed in claim 12
XX	
XX	WO200155182-A1.
XX	
XX	02-AUG-2001.
PD	
XX	
XX	25-JAN-2001; 2001WO-AU00069.
PF	
XX	
XX	25-JAN-2000; 2000US-0177917.
PR	
XX	

PA (UQOU) UNIV QUEENSLAND.
XX
PI Peak IRA, Jennings MP;
XX
DR WPI: 2001-488774/53.
DR N-PSDB: AAS09174.
XX
PT New Nnha surface antigen polypeptides and polynucleotides from
PT *Neisseria meningitidis*, useful in producing vaccines for treating or
PT preventing broad spectrum of *Neisseria meningitidis* -
XX
PS
XX Claim 12; Fig 7; 91pp; English.

SQ Sequence 407 AA;

Query Match	100.0%	Score 2063	DB 22	Length 407
Best Local Similarity	100.0%	Pred. NO. 5e-132		
Matches 407; Conservative	0	Mismatches	0	Indels 0
				Gaps 0

QY	1	MNKYIRIIMNSALNAAVVVSELTNRHHTKRASTVYTAVALTILFPTVOASANNVDFVRY	60
Db	1	MNKYIRIIMNSALNAAVVVSELTNRHHTKRASTVYTAVALTILFPTVOASANNVDFVRY	60
QY	61	DVEFELSADTKTTTVNVESEKONGKKEVEYIGAKTSVIEKDGKLVTKDGKGENGSTDEG	120
Db	61	DVEFELSADTKTTTVNVESEKONGKKEVEYIGAKTSVIEKDGKLVTKDGKGENGSTDEG	120
QY	121	EGLVTAKEVYIDAVNKKAGHRMKTTPPANGOTGQADKEEYTSGGINVPFASCKGTTATVSKD	180
Db	121	EGLVTAKEVYIDAVNKKAGHRMKTTPPANGOTGQADKEEYTSGGINVPFASCKGTTATVSKD	180
QY	181	QGNITVMDVNVGALANYNOLONGSMNLDSKRVAVSSGKVIISGNVSPSKGKMDENYNIA	240
Db	181	QGNITVMDVNVGALANYNOLONGSMNLDSKRVAVSSGKVIISGNVSPSKGKMDENYNIA	240
QY	241	GNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDGALVWGSKKDKPARIYV	300
Db	241	GNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDGALVWGSKKDKPARIYV	300
QY	301	APGVKEGDVTNVAOLKGYAQNMLNNEIDVNDGNARAGIAQALATPAGLVAQYILFGKSMATG	360
Db	301	APGVKEGDVTNVAOLKGYAQNMLNNEIDVNDGNARAGIAQALATPAGLVAQYILFGKSMATG	360
QY	361	GGYTRGARGAVALGYSSISDGGNWIITKTPASGSRHFGASASVGYQW	407
Db	361	GGYTRGARGAVALGYSSISDGGNWIITKTPASGSRHFGASASVGYQW	407

	RESULT 2
	AAU06185
ID	AAU06185 standard; Protein; 433 AA.
XX	
AC	AAU06185;
XX	
DT	24-OCT-2001 (first entry)
XX	
DE	N. meningitidis PMC21 Nhma deletion mutant #3.
XX	
KW	Surface antigen Nhma; meningococcal disease; meningitis vaccine; mutant; mutin.

XX	Neisseria meningitidis strain PMW21.	
OS	Synthetic.	
XX		
EH	Key	Location/Qualifiers
EH	Peptide	1..51
FT		/label= Signal-peptide
FT	Protein	52..433
FT		/label= Mature_Nbha_deletion_mutant_#3
FT		/note= "Predicted mature protein, specifically
FT		claimed in claim 12"
XX		
PN	WO200155182-A1.	
XX		
PD	02-AUG-2001.	
XX		
PF	25-JAN-2001; 2001WO-AU00069.	
XX		
PR	25-JAN-2000; 2000US-0177917.	
XX		
PA	(UYQU) UNIV QUEENSLAND.	
XX		
PI	Peak IRA, Jennings MP;	
XX		
XX	WPI; 2001-488774/53.	
DR	N-PSDB; AAS09175.	
XX		
PT	New Nbha surface antigen polypeptides and polynucleotides from	
PT	Neisseria meningitidis, useful in producing vaccines for treating or	
PT	preventing broad spectrum of Neisseria meningitidis -	
XX	Claim 12; Fig 8; 91pp; English.	

CC The present invention relates to the isolation of novel *Neisseria*
CC meningitidis mutant polypeptides of the surface antigen Nhba
CC (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of *N. meningitidis*, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of *N. meningitidis* strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence represents *N. meningitidis* strain PMC21 surface
CC antigen Nhba deletion mutant #3.
XX
XX Sequence 433 AA;
XQ

Query Match	98.9%	Score 2040	DB 22	Length 433
Best Local Similarity	94.0%	Pred. No. 2e-130		
Matches 407; Conservative	0	Mismatches	0	Indels 26; Gaps 1;

QY	1	MNKYYRILNMSALNAVYVSELNENHNRKRSATYKTVLTLLEATYQASNN-----	52
Db	1	MNKYYRILNMSALNAVYVSELNENHNRKRSATYKTVLTLLEATYQASNNRRAASYKDV	60
QY	53	-----NDYFATYDTVEPLSADIKTTTYVNESKONGKTEYKICAKT	94
Db	61	LNAGWNIRKGVKPGTTASDNDVFPATYDTVEFLSADIKTTTYVNESKONGKTEYKICAKT	120
QY	95	SVIKERKGLVYTGDKDGENGSSPDEGEGLYTAKFVIDAVNKAQRMTTTTANGOTGADK	154
Db	121	SVIKERKGLVYTGDKDGENGSSPDEGEGLYTAKFVIDAVNKAQRMTTTTANGOTGADK	180
QY	155	FETVTSCTNVTFASGKGTATVSKDQGNITVTVDVNVGALNVLNQLNSGMNLDKSAVA	214
Db	181	FETVTSCTNVTFASGKGTATVSKDQGNITVTVDVNVGALNVLNQLNSGMNLDKSAVA	240
QY	215	GSSGKTVISGVNVPBKGMDETVMNNAQNNIEIIPNGKNIDIAITSMTPQFSSVLSGARADA	274
Db	241	GSSGKTVISGVNVPBKGMDETVMNNAQNNIEIIPNGKNIDIAITSMTPQFSSVLSGARADA	300
QY	275	PTLSVDDDALNVGSKKDNKPVRITITNAPGVKEGQDVTVAQLKGAQNMNNRRIDVDGDNAR	334

|||||
Db PTLSDVDDALNVGSKDKPKVRLTNVAPGYKEGDTVNAOLKGVANLNNRIDVDCNAR 360
QY 335 AGTGAATATAGTGVAYLPKGSMAIGGTRGEGYAIIGYSSISDGNWIIKGTASGNSR 394
Db 361 AGTGAATATAGTGVAYLPKGSMAIGGTRGEGYAIIGYSSISDGNWIIKGTASGNSR 420
QY 395 GHFGASASVGYQW 407
Db 421 GHFGASASVGYQW 433

RESULT 3
AAU06186
ID AAU06186 standard; Protein: 502 AA.

XX AC AAU06186;
XX DT 24-OCT-2001 (first entry)
XX DE N. meningitidis PMC21 Nhma deletion mutant #4.
XX KM Surface antigen Nhma; meningococcal disease; meningitis vaccine;
XX mutant; muteln.
XX OS Neisseria meningitidis strain PMC21.
XX Synthetic.

FT Key Location/Qualifiers
FT Peptide 1..49
FT Protein /label= Signal_peptide
50..502
/note= "Mature_Nhma_deletion_mutant_#4
/note= "Predicted mature protein, specifically
claimed in claim 12"

XX WO200155182-A1.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-AU00069.

XX PR 25-JAN-2000; 2000US-0177917.
XX PA (UYOU) UNIV QUEENSLAND.
XX PI Peak IRA, Jennings MP;
XX DR WPI: 2001-48874/53.
XX DR N-PSDB; AAS09176.

XX PT New Nhma surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX PS
XX Claim 12; Fig 9; 91pp; English.

XX CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhma
CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC immunisations. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence represents N. meningitidis strain PMC21 surface
CC antigen Nhma deletion mutant #4.
XX
XX

SO Sequence 502 AA;

Query Match 97.2%; Score 2005.5; DB 22; Length 502;

Best Local Similarity 81.1%; Pred. No. 5.2e-128;
Matches 407; Conservative 0; Mismatches 0; Indels 95; Gaps 1;

QY 1 MNKIRIIMNSALNAMYVSELTNRNHRKRSATYKTAVALTLLEFATYQASNN----- 52
Db 1 MNKIRIIMNSALNAMYVSELTNRNHRKRSATYKTAVALTLLEFATYQASANTLKAGDNL 60
QY 53 ----- 52
Db 61 KIKQFTYSLKKDLTDLTSVTEKLSFSANGKNVITSDTKGLNFAKETAGNGDTYVHLN 120
QY 53 -----NDVEFRTYDVEEFLSADTKTTTVNESKDKKK 85
Db 121 GIGSTLFDRAASVQDVLNAGWNKGVKNVDFPRTYDVEEFLSADTKTTTVNESKDKKK 180
QY 86 TEVKIGAKTSYIKKDKGLYTKRKGENGSTDEGEGLYRAKEYIDAVNKRAGRMKTTTA 145
Db 181 TEVKIGAKTSYIKKDKGLYTKRKGENGSTDEGEGLYRAKEYIDAVNKRAGRMKTTTA 240
QY 146 NGQFGADKFEFTVSGTNVTFASGKGTATVSKDQGNITVYVNVGDALNVQLONSG 205
Db 241 NGQFGADKFEFTVSGTNVTFASGKGTATVSKDQGNITVYVNVGDALNVQLONSG 300
QY 206 WNLDSKAVAGSSGKVISGNVSPSKMDETVNINAGNNIETTRGNKIDATSMTPQFSS 265
Db 301 WNLDSKAVAGSSGKVISGNVSPSKMDETVNINAGNNIETTRGNKIDATSMTPQFSS 360
QY 266 VSLGAGADAPLTVSDGALNVGSKDKPKVRLTNVAPGVKEGDTVNAOLKGVANLNNR 325
Db 361 VSLGAGADAPLTVSDGALNVGSKDKPKVRLTNVAPGVKEGDTVNAOLKGVANLNNR 420
QY 326 IDNVGNAARAGIAQIATPAGIYQAYLPKGSMAIGGTRGEGYAIIGYSSISDGNWII 385
Db 421 IDNVGNAARAGIAQIATPAGIYQAYLPKGSMAIGGTRGEGYAIIGYSSISDGNWII 480
QY 386 KGTASGNSRGHFGASASVGYQW 407
Db 481 KGTASGNSRGHFGASASVGYQW 502

RESULT 4
AAU06182
ID AAU06182 standard; Protein: 512 AA.

XX AC AAU06182;
XX DT 24-OCT-2001 (first entry)
XX DE N. meningitidis PMC21 Nhma deletion mutant #1.
XX KM Surface antigen Nhma; meningococcal disease; meningitis vaccine;
XX mutant; muteln.
XX OS Neisseria meningitidis strain PMC21.
XX Synthetic.

FT Key Location/Qualifiers
FT Peptide 1..51
FT Protein /label= Signal_peptide
52..512
/label= "Mature_Nhma_deletion_mutant_#1
/note= "Predicted mature protein, specifically
claimed in claim 12"

XX WO200155182-A1.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-AU00069.

XX PR 25-JAN-2000; 2000US-0177917.
XX PA (UYOU) UNIV QUEENSLAND.
XX

```
XX Peak IRA, Jennings MP;
PI
XX
DR WPI: 2001-48774/53.
DR N-PSDB: AAS09172.
XX
PT New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis.
XX
PS Claim 12; Fig 5; 91pp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence represents N. meningitidis strain PMC21 surface
CC antigen Nhha deletion mutant #1.
XX
SQ Sequence 512 AA;
Query Match 97.0%; Score 2000.5; DB 22; Length 512;
Best Local Similarity 79.5%; Pred. No. 1.2e-127;
Matches 407; Conservative 0; Mismatches 0; Indels 105; Gaps 1;
QY 1 MKKIRIITWNSALNMAVYVSELTNRHTRKASATVKTAVLATLLEFATVQASAN----- 52
DB 1 MKKIRIITWNSALNMAVYVSELTNRHTRKASATVKTAVLATLLEFATVQASANNEDLTISV 60
QY 53 ----- 52
DB 61 GTEKLSFSANGKVKVITSDTKGLNFAKETAGTNGDTVHLNGIGSTLDTLNTGATTNV 120
QY 53 -----NDFPVRTYDIVEFLSADTKTTTV 75
DB 121 TNDNTVDEKKRAASVKDVLNMGWNIKGVKPGTTASDNDVFRITDYTFELSDRKTITV 180
QY 76 NWESKDNCKTEVKIGAKTSVKEKDGKLVTKDKGENSSSTDEGEGLTAKEDVAVNK 135
DB 181 NWESKDNCKTEVKIGAKTSVKEKDGKLVTKDKGENSSSTDEGEGLTAKEDVAVNK 240
QY 136 AGMRKTTTANGOTGADKFEFVTSCTNTVFASGKGTATVSKDDGNTTMTDVAVGDA 195
DB 241 AGMRKTTTANGOTGADKFEFVTSCTNTVFASGKGTATVSKDDGNTTMTDVAVGDA 300
QY 196 LNVNOLONGWNLDSKAVAGSSGKVLSCNVSPSKGMDETVINAGNNIEITRNGKNDI 255
DB 301 LNVNOLONGWNLDSKAVAGSSGKVLSCNVSPSKGMDETVINAGNNIEITRNGKNDI 360
QY 256 AFSMTPPOSSSVSLGAGADAPLTSLVDGALNVGSKDKNKFVRTTNVAPGVKEEDVTNVAL 315
DB 361 AFSMTPPOSSSVSLGAGADAPLTSLVDGALNVGSKDKNKFVRTTNVAPGVKEEDVTNVAL 420
QY 316 KGVANLNNRIDNVGNGNARAGIAQALATPAGLVQAVLPKSSMAIGGTYRGAGYAGIS 375
DB 421 KGVANLNNRIDNVGNGNARAGIAQALATPAGLVQAVLPKSSMAIGGTYRGAGYAGIS 480
QY 376 SISDGNMILIKGTASGNSRGHFGASASVGYQW 407
DB 481 SISDGNMILIKGTASGNSRGHFGASASVGYQW 512
RESULT 5
AAV27202
ID AAV27202 standard; Protein; 591 AA.
XX
AC AAV27202;
```

```
XX 24-SEP-1999 (first entry)
DT
XX Amino acid sequence of N. meningitidis protein ORF40-1.
DE
XX
KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;
KW bacterial infection; treatment.
XX
OS Neisseria meningitidis.
XX
PN W0936544-A2.
XX
PD 22-JUL-1999.
XX
PF 14-JAN-1999; .99WO-IB00103.
XX
PR 09-OCT-1998; 98GB-0022143.
PR 14-JAN-1998; 98GB-0000760.
PR 01-SEP-1998; 98GB-0019015.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Grandi G, Masignani V, Pizsa M, Rappuoli R, Scarlato V;
XX
DR WPI: 1999-444400/37.
DR N-PSDB: AAX99124.
XX
PT New protein and its nucleotide sequence, useful in vaccines or
PT diagnostic compositions for treating and/or preventing Neisseria
PT meningitidis infections
XX
PS Claim 1; Page 62; 123pp; English.
XX
CC The invention provides proteins (AAV27201-245) from Neisseria
CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)
CC encoding the proteins. Compositions comprising the proteins, nucleic acid
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a
CC vaccine composition or a diagnostic composition. The composition is also
CC useful for treating or preventing an infection due to Neisseria
CC bacteria, especially Neisseria meningitidis.
XX
SQ Sequence 591 AA;
Query Match 95.1%; Score 1961; DB 20; Length 591;
Best Local Similarity 68.9%; Pred. No. 6.6e-125;
Matches 407; Conservative 0; Mismatches 0; Indels 184; Gaps 1;
QY 1 MKKIRIITWNSALNMAVYVSELTNRHTRKASATVKTAVLATLLEFATVQASAN----- 52
DB 1 MKKIRIITWNSALNMAVYVSELTNRHTRKASATVKTAVLATLLEFATVQASANNEQEDL 60
QY 53 ----- 52
DB 61 YLDPQRTVAVLIVNSDKRGTEKGEKVEENSDMAVFNKGVLTAREITLAKGNLTKIQ 120
QY 53 ----- 52
DB 121 NGTNPYSLKDLTDLTSVTEKLSFSANGKNVITSDTKGLNFAKETAGTNGDTVHLN 180
QY 53 -----NDF 56
DB 181 GIGSTLTDLTGATTNVTNDNTVDEKKRAASVKDVLNMGWNIKGVKPGTTASDNDV 240
QY 57 VRTYDVEFLSADTKTTTVNWSKDNCKTEVKIGAKTSVKEKDGKLVTKDKGENSS 116
DB 241 VRTYDVEFLSADTKTTTVNWSKDNCKTEVKIGAKTSVKEKDGKLVTKDKGENSS 300
QY 117 TDEGEGLTAKEDVAVNKAGMRKTTTANGOTGADKFEFVTSCTNTVFASGKGTATV 176
DB 301 TDEGEGLTAKEDVAVNKAGMRKTTTANGOTGADKFEFVTSCTNTVFASGKGTATV 360
QY 177 SKDDGNTTMTDVAVGALNVLNOLONGWNLDSKAVAGSSGKVLSCNVSPSKGMDETV 236
DB 361 SKDDGNTTMTDVAVGALNVLNOLONGWNLDSKAVAGSSGKVLSCNVSPSKGMDETV 420
```

Db 361 SKDOGNITVWYDVNVGDALNVNOLNSGWNLDKKAVALGSSGKVIISGNVSPSKGMDETV 420
 QY 237 NINAGNNIEITRNCKNIDIASMTPOFSSVSLGAGADAPTLSDGDALNVGSKKDNKPYR 296
 Db 421 NINAGNNIEITRNCKNIDIASMTPOFSSVSLGAGADAPTLSDGDALNVGSKKDNKPYR 480
 QY 297 ITNVAPEGKEDVTNVAOLKQVAAONLNRRIDNVGNARAGIAQAIAATAGLVQAYLPCKSM 356
 Db 481 ITNVAPEGKEDVTNVAOLKQVAAONLNRRIDNVGNARAGIAQAIAATAGLVQAYLPCKSM 540-
 QY 357 MAIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 407
 Db 541 MAIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 591

RESULT 6
 AAY23746
 ID AAY23746 standard; Protein: 591 AA.

XX AAY23746;
 AC 08-SEP-1999 (first entry)
 DT
 XX
 DE A surface protein of Neisseria meningitidis.
 XX
 KW Surface protein; surface glycoprotein; infection; vaccine;
 KM immunoreactive peptide.
 XX
 OS Neisseria meningitidis.
 XX
 PN MO9931132-A1.
 PD 24-JUN-1999.
 PE 14-DEC-1998; 98WO-AU01031.
 PR 12-DEC-1997; 97GB-0026398.
 PA (ISIS-) ISIS INNOVATION LTD.
 PA (UYOU) UNIV QUEENSLAND.
 XX
 PI Jennings MP, Moxon ER, Peak IRA;
 DR WPI: 1999-418754/35.
 DR N-PSDB: AAX85798.

XX
 PT Neisseria meningitidis surface proteins useful for treating N.
 PT meningitidis infections
 XX
 PS Claim 1; Page 127-128; 132pp; English.
 XX
 CC The present sequence represents a surface protein of Neisseria
 CC meningitidis which is approximately 62 kDa. The N. meningitidis
 CC surface glycoproteins, nucleic acids, the primers and optionally
 CC a thermostable polymerase, or antibodies are useful in a kit for
 CC the detection or diagnosis of N. meningitidis infection in humans.
 CC The N. meningitidis surface glycoproteins can also be used to
 CC prevent or treat N. meningitidis infection in humans, especially
 CC in the form of vaccines. The proteins and antibodies can also
 CC be used to identify immunoreactive peptides.
 XX
 SO Sequence 591 AA;

Query Match 95.1%; Score 1961; DB 20; Length 591;
 Best Local Similarity 68.9%; Pred. No. 6.6e-125;
 Matches 407; Conservative 0; Mismatches 0; Indels 184; Gaps 1;

QY 1 MNKIYRIIWSALNAAWVVSSELPNRHTRKASATVKTAVLATLFLFATVQASAN----- 52
 Db 1 MNKIYRIIWSALNAAWVVSSELPNRHTRKASATVKTAVLATLFLFATVQASANNEQEDL 60
 QY 53 ----- 52

Db 61 YLDPVORTVAVLIVNSDKEGTGEKEKEVENSMAVYFNEKGVLTAETITLAKGDNLIKQ 120
 QY 53 ----- 52
 Db 121 NGTFYTSLKADLIDLISVTEKLSFSAKNGKVNITSDTKLNAKETAGTNGOTYVHLN 180
 QY 53 -----NVDF 56
 Db 181 GIGSTLIDTLTNGATTNVTNDNTDDEKRRASVQDVLANGMNKGKPKPTTASDNVDF 240
 QY 57 VRTYDVEEFLSADTKTTTVNVEKDNCKTEVKTGAFTSVIKERDGLVTKDKGENSS 116
 Db 241 VRTYDVEEFLSADTKTTTVNVEKDNCKTEVKTGAFTSVIKERDGLVTKDKGENSS 300
 QY 117 TDEEGLYTAKEDVDANKKAGMRKTTTANQOTGQADKFEVTVSGTNTVTFASGCTATV 176
 Db 301 TDEEGLYTAKEDVDANKKAGMRKTTTANQOTGQADKFEVTVSGTNTVTFASGCTATV 360
 QY 177 SKDOGNITVWYDVNVGDALNVNOLNSGWNLDKKAVALGSSGKVIISGNVSPSKGMDETV 236
 Db 361 SKDOGNITVWYDVNVGDALNVNOLNSGWNLDKKAVALGSSGKVIISGNVSPSKGMDETV 420
 QY 237 NINAGNNIEITRNCKNIDIASMTPOFSSVSLGAGADAPTLSDGDALNVGSKKDNKPYR 296
 Db 421 NINAGNNIEITRNCKNIDIASMTPOFSSVSLGAGADAPTLSDGDALNVGSKKDNKPYR 480
 QY 297 ITNVAPEGKEDVTNVAOLKQVAAONLNRRIDNVGNARAGIAQAIAATAGLVQAYLPCKSM 356
 Db 481 ITNVAPEGKEDVTNVAOLKQVAAONLNRRIDNVGNARAGIAQAIAATAGLVQAYLPCKSM 540
 QY 357 MAIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 407
 Db 541 MAIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 591

RESULT 7
 AAU06171
 ID AAU06171 standard; Protein: 591 AA.
 XX
 AC AAU06171;
 DT 24-OCT-2001 (first entry)
 XX
 DE N. meningitidis PMC21 surface antigen NhhA polypeptide sequence.
 XX
 KW Surface antigen NhhA; meningococcal disease; meningitis vaccine.
 XX
 OS Neisseria meningitidis strain PMC21.
 XX
 FH Key
 FT Peptide
 FT 1.51
 FT /label= Signal_peptide
 FT 1..50
 FT /label= C1
 FT /note= "Conserved region 1"
 FT 51..108
 FT /label= V1
 FT /note= "Variable region 1"
 FT 52..591
 FT /label= Mature_NhhA
 FT /note= "Predicted mature protein, specifically
 FT claimed in claim 12"
 FT 109..120
 FT /label= C2
 FT /note= "Conserved region 2"
 FT 121..124
 FT /label= V2
 FT /note= "Variable region 2"
 FT 125..188
 FT /label= C3
 FT /note= "Conserved region 3"
 FT 189..210
 FT /label= V3

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FT      /note= "Variable region 3"
FT      Region
FT      211...229
FT      /label= C4
FT      /note= "Conserved region 4"
FT      Region
FT      230...236
FT      /label= V4
FT      /note= "Variable region 4"
FT      237...591
FT      /label= C5
FT      /note= "Conserved region 5"
XX
XX      WO200155182-A1.
XX
XX      02-AUG-2001.
XX
XX      25-JAN-2001; 2001WO-AU00069.
XX
XX      25-JAN-2000; 2000US-0177917.
XX
XX      (UYOU ) UNIV QUEENSLAND.
XX
XX      Peak IRA, Jennings MP;
XX
XX      WPI: 2001-488774/53.
XX      N-PSDB: AAS09161.
XX
XX      New Nhma surface antigen polypeptides and polynucleotides from
XX      Neisseria meningitidis, useful in producing vaccines for treating or
XX      preventing broad spectrum of Neisseria meningitidis -
XX
XX      Claim 9; Fig 1; 91pp; English.
XX
XX      The present invention relates to the isolation of novel Neisseria
XX      meningitidis mutant polypeptides of the surface antigen Nhma
XX      (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are
XX      characterised by deletions of non-conserved amino acids, particularly
XX      the deletion of variable regions. The deletion mutants are useful in
XX      diagnostics, therapeutic and prophylactic vaccines against a broader
XX      spectrum of N. meningitidis, and in designing and/or screening of
XX      medicaments. The mutant proteins when used as a vaccine can effectively
XX      immunise against a broader spectrum of N. meningitidis strains than
XX      would be expected from a corresponding wild-type surface antigen.
XX      The present sequence representing the wild type surface antigen Nhma
XX      from N. meningitidis strain PMC21 is 1 of 10 Nhma polypeptide sequences
XX      (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX      the present invention.
XX
XX      Sequence 591 AA:
SQ      Query Match      95.1%; Score 1961; DB 22; Length 591;
      Best Local Similarity 68.9%; Pred. No. 6,6e-125;
      Matches 407; Conservative 0; Mismatches 0; Indels 184; Gaps 1;
OY      1 MKKTRITWNSALNMAVVVSELTNRHTRKASATVTAVALTLLEFATYQASAN----- 52
      1 MKKTRITWNSALNMAVVVSELTNRHTRKASATVTAVALTLLEFATYQASANNEQEDDL 60
DB
OY      53 ----- 52
DB
OY      61 YLDPVQRTAVAVLIIVNSDKGTEGKEKEVEENSDMAYFNEKGVLTAREITLKAGDNLIKIKO 120
OY      53 ----- 52
DB      121 NGTNFTYSLKDLFDLTSVTEKLSFSAANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN 180
OY      53 -----NDF 56
DB      181 GIGSLTJDTLLTNGATTNTVNDNTDEKRAASVKVDVINAQMNIGKVPRTTASDNDF 240
OY      57 VRTYDVEFLSADTFTTNNVESKDKGKTEVKIGAKTSVIREKDGKLTVTGDKGNGSS 116
      241 VRTYDVEFLSADTFTTNNVESKDKGKTEVKIGAKTSVIREKDGKLTVTGDKGNGSS 300

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OY      117 TDEGEGLYTAKEVIDAVNKAQGRMKTTTANGOTGQADKFERYTSGTNTVFASGKTTATV 176
DB      301 TDEGEGLYTAKEVIDAVNKAQGRMKTTTANGOTGQADKFERYTSGTNTVFASGKTTATV 360
OY      177 SKDDGNGITVMYDVVAGLALNVLONSGMNLDSKAVAGSSGKVTSGNVSPSKGMDETV 236
DB      361 SKDDGNGITVMYDVVAGLALNVLONSGMNLDSKAVAGSSGKVTSGNVSPSKGMDETV 420
OY      237 NINAGNNIETFRNGKNIDIAITSMPTQFSSVSLGAGADAPTLISVDDALNVGSKDKNKPVR 296
DB      421 NINAGNNIETFRNGKNIDIAITSMPTQFSSVSLGAGADAPTLISVDDALNVGSKDKNKPVR 480
OY      297 ITNVAPEGKEDVTVAQLKGYAQNLLNRRIDNVGNAARAGTAQAATATAGLYQATIPGSM 356
DB      481 ITNVAPEGKEDVTVAQLKGYAQNLLNRRIDNVGNAARAGTAQAATATAGLYQATIPGSM 540
OY      357 MAIGGCTYRGEGYAGYAGYSISDGNWIIKGTASNGRFGASASVGYOW 407
DB      541 MAIGGCTYRGEGYAGYAGYSISDGNWIIKGTASNGRFGASASVGYOW 591

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RESULT 8
AAV23737
ID      AAV23737 standard; Protein; 592 AA.
XX
XX      AAV23737;
AC      08-SEP-1999 (first entry)
XX
XX      A surface protein of Neisseria meningitidis.
DE
XX      Surface protein; surface glycoprotein; infection; vaccine;
KW      immunoreactive peptide.
XX
XX      Neisseria meningitidis.
OS      WO931132-A1.
XX
XX      24-JUN-1999.
PD
XX      14-DEC-1998; 98WO-AU01031.
PF
XX      12-DEC-1997; 97GB-0026398.
PR
XX      (ISIS-) ISIS INNOVATION LTD.
PA      (UYOU ) UNIV QUEENSLAND.
XX
XX      Jennings MP, Moxon ER, Peak IRA;
PI
XX      WPI: 1999-418754/35.
DR      N-PSDB: AAX85788.
XX
XX      Neisseria meningitidis surface proteins useful for treating N.
XX      meningitidis infections
XX
XX      Claim 1; Page 86-87; 132pp; English.
XX
XX      The present sequence represents a surface protein of Neisseria
XX      meningitidis which is approximately 62 kDa. The N. meningitidis
XX      surface glycoproteins, nucleic acids, the primers and optionally
XX      a thermostable polymerase, or antibodies are useful in a kit for
XX      the detection of N. meningitidis infection in humans.
XX      The N. meningitidis surface glycoproteins can also be used to
XX      prevent or treat N. meningitidis infection in humans, especially
XX      in the form of vaccines. The proteins and antibodies can also
XX      be used to identify immunoreactive peptides.
XX
XX      Sequence 592 AA:
SQ

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Query Match      94.8%; Score 1956.5; DB 20; Length 592;
Best Local Similarity 68.6%; Pred. No. 1.3e-124;
Matches 406; Conservative 0; Mismatches 1; Indels 185; Gaps 1;

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QY 1 MNKIYRIIWSALNANWVSELTFRNHTKRASATVKTAVLATLLFATVOASAN----- 52
Db 1 MNKIYRIIWSALNANWVSELTFRNHTKRASATVKTAVLATLLFATVOASANNEPRK 60
QY 53 ----- 52
Db 61 LYLDPVQRTVAVLVNSDEKTEGEKEVEENSDMAVYFNEKGVLTAREITLKAGDNLKIK 120
QY 53 ----- 52
Db 121 QNGTNFTYSLKKDLTDLTSVTEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDPTVHL 180
QY 53 -----NVD 55
Db 181 NGIGSTLTDLTLNMGATNTVNDNVTDDEKKRAASVVDVLAAGWNIKGVKPGTTASDNVD 240
QY 56 FVRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTIVYKEKDKLVTGDKDGENGS 115
Db 241 FVRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTIVYKEKDKLVTGDKDGENGS 300
QY 116 STDEGEGLVTAKEVIDAVNKGWBMKTTTANGOTGOADKPEFTVSGTNVTFASGKGTAT 175
Db 301 STDEGEGLVTAKEVIDAVNKGWBMKTTTANGOTGOADKPEFTVSGTNVTFASGKGTAT 360
QY 176 VSKDDGNTVMTDVNVGDALNVNQLONGSMNLSKAVAGSSGKVIISGNVSPSKKMDET 235
Db 361 VSKDDGNTVMTDVNVGDALNVNQLONGSMNLSKAVAGSSGKVIISGNVSPSKKMDET 420
QY 236 VTNAGNNITITNGRKIDATSMTPPFSSVSLGACADAPTLTLYVDGALNVGSKKDKPV 295
Db 421 VTNAGNNITITNGRKIDATSMTPPFSSVSLGACADAPTLTLYVDGALNVGSKKDKPV 480
QY 296 RITNVAPGVEGDVTNVAQIKGVAONLNRRIDNVGDGNARAGIAQAITAGIYQAYLPFGS 355
Db 481 RITNVAPGVEGDVTNVAQIKGVAONLNRRIDNVGDGNARAGIAQAITAGIYQAYLPFGS 540
QY 356 MMAIGGTYRGAGYALGYSSISDGGWIIKGTASGNSRGHFGASASVGYOW 407
Db 541 MMAIGGTYRGAGYALGYSSISDGGWIIKGTASGNSRGHFGASASVGYOW 592

RESULT 9
AAV57045
ID AAV57045 standard; Protein: 591 AA.
XX
XX AAV57045:
XX
D1 21-FEB-2000 (first entry)
XX
XX BASB029 amino acid sequence from N. meningitidis strain H44/76.
DE
XX
XX BASB029: Nisseria meningitidis; surface fibril protein; HSF; diagnosis;
KM infection; treatment; prevent; antibacterial drug.
XX
XX Neisseria meningitidis.
OS
XX
XX Key Location/Qualifiers
FH MISC-difference 90
FT MISC-difference 92 /note= "Encoded by AAT"
FT MISC-difference 98 /note= "Encoded by GAT"
FT MISC-difference 98 /note= "Encoded by AAC"
FT MISC-difference 108 /note= "Encoded by AAC"
FT MISC-difference 123 /note= "Encoded by AATC"
FT MISC-difference 123 /note= "Encoded by ACA"
FT MISC-difference 269 /note= "Encoded by AAA"
FT MISC-difference 389 /note= "Encoded by CGT"
XX
XX W09558683-A2.

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XX 18-NOV-1999.
PD
XX
XX 07-MAY-1999; 99MO-EP03255.
PF
XX
XX 13-MAY-1998; 98GB-0010276.
PR
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
PA
XX
XX Ruelle J;
PI
XX
XX WPI: 2000-053103/04.
DR
XX N-PSDB: AA239865.
PT
XX New polypeptide from neisseria meningitidis useful for diagnosis,
XX treatment or prevention of bacterial infections in mammal
XX
XX Claim 4; Fig 2; 74pp; English.
XX
XX This is the Neisseria meningitidis BASB029 amino acid sequence from
XX serogroup B strain H44/76. The BASB029 protein is homologous to the
XX Hemophilus influenzae surface fibril (HSF) protein. The invention
XX relates to BASB029 polynucleotide sequences (AA239864-239865) and
XX polypeptide sequences (AAV57044-Y57045) and their immunogenic fragments.
XX BASB029 polypeptides are useful in a method of diagnosing a Neisseria
XX meningitidis infection in a mammal. Compositions containing BASB029
XX polynucleotides and polypeptides are useful for generating an immune
XX response in an animal. A therapeutic composition comprising an antibody
XX directed against BASB029 is useful in treating humans with Neisseria
XX meningitidis disease. The polynucleotide is useful in the diagnosis of
XX the stage of infection, type of infection, susceptibility to an
XX infection which results from increased or decreased expression of the
XX polynucleotide, and for therapeutic or prophylactic purposes,
XX particularly genetic immunisation. Antibodies against BASB029
XX polynucleotides and polypeptides are also useful for treating infections
XX particularly bacterial infections. The protein is useful in the
XX screening and development of antibacterial drugs. Fused recombinant
XX protein is useful for the stimulation of the immune system of an organism
XX receiving the protein.
XX
XX Sequence 591 AA:
SQ
Query Match 94.7%; Score 1954; DB 21; Length 591;
Best Local Similarity 68.5%; Pred. No. 2e-124;
Matches 405; Conservative 1; Mismatches 1; Indels 184; Gaps 1;
QY 1 MNKIYRIIWSALNANWVSELTFRNHTKRASATVKTAVLATLLFATVOASAN----- 52
Db 1 MNKIYRIIWSALNANWVSELTFRNHTKRASATVKTAVLATLLFATVOASANNEDEEDL 60
QY 53 ----- 52
Db 61 YLDPVQRTVAVLVNSDEKTEGEKEVEENSDMAVYFNEKGVLTAREITLKAGDNLKIKO 120
QY 53 ----- 52
Db 121 NGSNFTYSLKKDLTDLTSVTEKLSFSAANGKVNITSDTKGLNFAKETAGTNGDPTVHLN 180
QY 53 -----NVD 56
Db 181 GIGSTLTDLTLNMGATNTVNDNVTDDEKKRAASVVDVLAAGWNIKGVKPGTTASDNVD 240
QY 57 VRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTIVYKEKDKLVTGDKDGENGS 116
Db 241 VRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTIVYKEKDKLVTGDKDGENGS 300
QY 117 TDEGEGLVTAKEVIDAVNKGWBMKTTTANGOTGOADKPEFTVSGTNVTFASGKGTATV 176
Db 301 TDEGEGLVTAKEVIDAVNKGWBMKTTTANGOTGOADKPEFTVSGTNVTFASGKGTATV 360
QY 177 SKDDGNTVMTDVNVGDALNVNQLONGSMNLSKAVAGSSGKVIISGNVSPSKKMDETV 236
Db 361 SKDDGNTVMTDVNVGDALNVNQLONGSMNLSKAVAGSSGKVIISGNVSPSKKMDETV 420

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OY 237 NINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKDKNKEVR 296
DB 421 NINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKDKNKEVR 480
OY 297 ITNVAPEGKEDVTNVAOLKGYAQNLLNNRIDVGNARAGIAQAIAATAGLVQAYLPKSKM 356
DB 481 ITNVAPEGKEDVTNVAOLKGYAQNLLNNRIDVGNARAGIAQAIAATAGLVQAYLPKSKM 540
OY 357 MAIGGGTYRGEAGYAIIGYSSISDGGNWLTKGTASGNSGHHFGASASVGYOW 407
DB 541 MAIGGGTYRGEAGYAIIGYSSISDGGNWLTKGTASGNSGHHFGASASVGYOW 591

RESULT 10
AA023741
ID AA023741 standard; Protein: 591 AA.
AC AA023741;
XX
XX 08-SEP-1999 (first entry)
DE A surface protein of Neisseria meningitidis.
KM Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
XX Neisseria meningitidis.
OS
XX
XX WO991132-A1.
PN
XX 24-JUN-1999.
PD
XX
XX 14-DEC-1998; 98WO-AU01031.
PF
XX
XX 12-DEC-1997; 97GB-0026398.
PR
XX
XX (ISIS-) ISIS INNOVATION LTD.
PA (UYOU) UNITV QUEENSLAND.
XX
XX Jennings MP, Moxon ER, Peak IRA;
PI
XX
XX WPI: 1999-418754/35.
DR N-PSDB: AAX85793.
XX
XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
XX Claim 1; Page 104-106; 132pp; English.
PS
XX
XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
CC
XX
SQ Sequence 591 AA:

Query Match 94.5%; Score 1949; DB 20; Length 591;
Best Local Similarity 68.5%; Pred. No. 4.3e-124;
Matches 405; Conservative 1; Mismatches 1; Indels 184; Gaps 1;
OY 1 MNKITYRIIWSALNMAVVVSELTNRNHTKRASATVKTAVIATLLFATVQASAN----- 52
DB 1 MNEIRIITWSALNMAVVVSELTNRNHTKRASATVKTAVIATLLFATVQASANNEQEDL 60
OY 53 ----- 52
DB 61 YLDPVLRVAVLIVNSKEGTEKEKVEBNSDMAVYFNEKGVLTARETTLKAGDNLIKQ 120

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OY 53 ----- 52
DB 121 NGTNFTYSLKAKDLIDLTVSTGEKLSFSANGKVNITSDTKGLNFAKETAGTNGPTVHLN 180
OY 53 ----- -NDF 56
DB 181 GIGSLIDLTLTNGATTNTNDNVTDDKKRAASVKDYLANAGMNIKGVPPTTASDNVDF 240
OY 57 VRTDYVEFLSADRTKTTVNVEESKDNKTEVKIGAKTSVYKEKDGKLVYTGKDGKNGCSS 116
DB 241 VRTDYVEFLSADRTKTTVNVEESKDNKTEVKIGAKTSVYKEKDGKLVYTGKDGKNGCSS 300
OY 117 TDEGEGLVTAKVEIDAVNKAQMRKTTTANGQFGQADKFETVTSGTNTVFAAGKGTATV 176
DB 301 TDEGEGLVTAKVEIDAVNKAQMRKTTTANGQFGQADKFETVTSGTNTVFAAGKGTATV 360
OY 177 SKDDOGNTTVMYDVVVGALNVNQLONGGWNLDKFAVAGSSGKYSYSGNVSPSKGMDFTV 236
DB 361 SKDDOGNTTVMYDVVVGALNVNQLONGGWNLDKFAVAGSSGKYSYSGNVSPSKGMDFTV 420
OY 237 NINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKDKNKEVR 296
DB 421 NINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKDKNKEVR 480
OY 297 ITNVAPEGKEDVTNVAOLKGYAQNLLNNRIDVGNARAGIAQAIAATAGLVQAYLPKSKM 356
DB 481 ITNVAPEGKEDVTNVAOLKGYAQNLLNNRIDVGNARAGIAQAIAATAGLVQAYLPKSKM 540
OY 357 MAIGGGTYRGEAGYAIIGYSSISDGGNWLTKGTASGNSGHHFGASASVGYOW 407
DB 541 MAIGGGTYRGEAGYAIIGYSSISDGGNWLTKGTASGNSGHHFGASASVGYOW 591

RESULT 11
AA006175
ID AA006175 standard; Protein: 591 AA.
AC AA006175;
XX
XX 24-OCT-2001 (first entry)
DE N. meningitidis EG329 surface antigen NnhA polypeptide sequence.
KM Surface antigen NnhA; meningococcal disease; meningitis vaccine.
XX
XX Neisseria meningitidis strain EG329.
OS
XX
XX Location/Qualifiers
FH 1..50
FT Region
FT /label= C1
FT /note= "Conserved region 1"
FT 51..108
FT Region
FT /label= V1
FT /note= "Variable region 1"
FT 109..120
FT Region
FT /label= C2
FT /note= "Conserved region 2"
FT 121..124
FT Region
FT /label= V2
FT /note= "Variable region 2"
FT 125..188
FT Region
FT /label= C3
FT /note= "Conserved region 3"
FT 189..210
FT Region
FT /label= V3
FT /note= "Variable region 3"
FT 211..229
FT Region
FT /label= C4
FT /note= "Conserved region 4"
FT 230..236
FT Region
FT /label= V4
FT /note= "Variable region 4"

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Ft	Region		237..591
Ft	/label= C5		
Ft	/note= "Conserved region 5"		
Pn			
Xx	WO200155182-A1.		
Pd			
Pf	02 -AUG- 2001.		
Xx			
Xx	25-JAN- 2001; 2001W0-AU00069.		
Xr			
Pr	25-JAN-2000; 2000US-0177917.		
Pa	(UYOU) UNIV QUEENSLAND.		
Xx			
F1	Peak IRA, Jennings MP;		
Xx			
Dk	WP1: 2001-488774/53.		
Nr	N-PSDB; AAS09165.		
Pt	New Nhha surface antigen polypeptides and polymucleotides from		
Pt	Neisseria meningitidis , useful in producing vaccines for treating or		
Pt	preventing broad spectrum of Neisseria meningitidis .		
Ps			
Cc	Claim 9; Fig 1; 91pp: English.		
Cc	The present invention relates to the isolation of novel Neisseria		
Cc	meningitidis mutant polypeptides of the surface antigen Nhba		
Cc	(AAU06182-AAU06186). The modified or mutant Nhba polypeptides are		
Cc	characterised by deletions of non-conserved amino acids, particularly		
Cc	the deletion of variable regions. The deletion mutants are useful in		
Cc	diagnostics, therapeutic and prophylactic vaccines against a broader		
Cc	spectrum of N. meningitidis, and in designing and/or screening of		
Cc	medicaments. The mutant proteins when used as a vaccine can effectively		
Cc	immunise against a broader spectrum of N. meningitidis strains than		
Cc	would be expected from a corresponding wild-type surface antigen.		
Cc	The present sequence representing the wild type surface antigen Nhba		
Cc	from N. meningitidis strain EG329 is 1 of 10 Nhba polypeptide sequences		
Cc	(AAU06171-AAU06180) from 10 different N. meningitidis strains given in		
Cc	the present invention.		
SQ	Sequence 591 AA:		
Oy	Query Match 94.5%; Score 1949; DB 22; Length 591; Best Local Similarity 68.5%; Pred. No. 4,3e+124; Matches 405; Conservative 1; Mismatches 1; Indels 184; Gaps 1;		
Oy	1 MNKIYRIITWSALNAVVSSELTNRHTRRASATVTAVALTILFTVQAASAN----- 52 		
Db	1 MNEIIRIIITSALNAVVSVSELTRNHRKRASATVKAVLATILLFATVOASANNBQEEDL 60		
Oy	53 ----- 52		
Db	61 YLDPLRTVAVLIVNSDEKGEKEKYVEENDSMAYPFMEKVLRRETIKAGDWLIKIQ 120		
Oy	53 ----- 52		
Db	121 NGTFETSIKKDIDLTISVTGTEKLFSANGKNVNITSDTKGLNFPAKETAGTGDTTVHLN 180		
Oy	53 -----NDP 56		
Db	181 GIGSTLTDTLNTGATTNVTDNDNYTDDCKRAASVRYDLINAGWNIKGYRPGTTASDNDF 240 		
Oy	57 VRTVDYEVELSADPTTTTNVESRKNGKTTEVIKAFTSVIERKGKLVYGDKDGKSGSS 116		
Db	241 VRITYDYEFELSAIDPTTTTNVESRKNGKTTEVIKAFTSVIERKGKLVYTGDCKEENGSS 300		
Oy	117 TDEEGYLTAKEVIDAVNKAGRMTKTTANGOTGOADRFEYTSCTNYPFGSKGTATAV 176 		
Db	301 TDEGGYLTAKEVIDAVNKAGRMTKTTANGOTGOADRFEYTSCTNYPFGSKGTATAV 360		
Oy	177 SKDOGNITWTADVVGALANVNOQLONGSWINDASAAGSSGVYSIGNVPSPKGMKDDEV 236 		
Db	361 SKDDOGNITWTADVVGALANVNOQLONGSWINDASAAGSSGVYSIGNVPSPKGMKDDEV 420		

Oy		237	NINAGNNIETTRNGKNDIATSWTPEFSSVSIGACADAPTLSVDDDALNVGSKDKNRPVR	296
Dd		421	NINAGNNIETTRNGKNDIATSWTPEFSSVSIGACADAPTLSVDGDALNVGSKDKNRPVR	480
Oy		297	ITTVAPGVCKBDVTNVAOLKGVAQNINRDNWDVNCNARAGIAQAIAATAGLVQAVLPGKSM	356
Dd		481	ITTVAPGVCKBDVTNVAOLKGVAQNINRDNWDVNCNARAGIAQAIAATAGLVQAVLPGKSM	540
Oy		357	MATGGGYREAGYATGYSSISDGCWIIITKTGAASGNRSRGHFGAASVGYOW	407
Dd		541	MATGGGYREAGYATGYSSISDGCWIIITKTGAASGNRSRGHFGAASVGYOW	591
<hr/>				
RESULT 12				
	AAU06183	ID	AAU06183 standard; Protein: 513 AA.	
	XX	AC	AAU06183:	
	XX	DT	24-OCT-2001 (first entry)	
	XX	DE	N. meningitidis H41 Nhma deletion mutant.	
	XX	KW	Surface antigen Nhma; meningococcal disease; meningitis vaccine;	
	XX	KW	mutant; muteln.	
	OS		Neisseria meningitidis strain H41.	
	OS		Synthetic.	
	FH	Key	Location/Qualifiers	
	FT	Peptide	1..51	
	FT		/label= Signal_peptide	
	FT	Protein	52..513	
	FT		/label= Mature_Nhma_deletion_mutant	
	FT		/note= "Predicted mature protein, specifically claimed in claim 12"	
	PN		WO200155182-A1.	
	PD		02-AUG-2001.	
	PF		25-JAN-2001; 2001WO-AU00069.	
	PR		25-JAN-2000; 2000US-017917.	
	PA	(UYQU) UNIV QUEENSLAND.		
	PI	Peak IRA, Jennings MP;		
	DR	WPI: 2001-488774/53.		
	DR	N-PSTD; AAS09173.		
	PT	New Nhma surface antigen polypeptides and polynucleotides from		
	PT	Neisseria meningitidis, useful in producing vaccines for treating or		
	PS	preventing broad spectrum of Neisseria meningitidis -		
	PS	Claim 12; Fig 6; 9ipp; English.		
	CC	The present invention relates to the isolation of novel Neisseria		
	CC	meningitidis mutant polypeptides of the surface antigen Nhma		
	CC	(AAU06182-AAU06186). The modified or mutant Nhma polypeptides are		
	CC	characterised by deletions of non-conserved amino acids, particularly		
	CC	the deletion of variable regions. The deletion mutants are useful in		
	CC	diagnostics, therapeutic and prophylactic vaccines against a broader		
	CC	spectrum of N. meningitidis, and in designing and/or screening of		
	CC	micromements. The mutant proteins when used as a vaccine can effectively		
	CC	immunise against a broader spectrum of N. meningitidis strains than		
	CC	would be expected from a corresponding wild-type surface antigen.		
	CC	The present sequence represents N. meningitidis strain H41 surface		
	CC	antigen Nhma deletion mutant.		
	XX	Sequence 513 AA;		
	XX			

Query Match	92.5%	Score 1909;	DB 22;	Length 513;
Best Local Similarity	76.6%;	Pred. No. 1_9e-121;		
Matches 393;	Conservative 4;	Mismatches 10;	Indels 106;	Gaps 2

OY	1	MNKIRRIIMNSALNMVVVSELTNRHMKTKASATVKTAVLATLTLFATVQASA-----	51
Dd	1	:	
		1 MNKIRRIIMNSALNMVAVSELTRNHMKTSATVTAKVALATLTLFAIVQANMDETGLIN	60
OY	52	-----	51
Dd	61	ETEKLSPGANGKKVNIISDTKGLNFAKETAGTNGDITVHLNGIGSTLTMDLINLTGATTNV	120
OY	52	-----NNVDVFRTDYTFEFLSADFKTTTY	75
Dd	121	TNDNYTDDEKKRAASVKDYLNAGMNIKGVKPGETTASIDNVDFVKTDTVEFLSADTKTTY	180
OY	76	NVESKDNGKTEVKGIGAKTSVIKEKDGKLVYTGDKDGENSSDDEGEGLVTAKEVIDAVNK	135
Dd	181		
		1 NVESKDNGKTEVKGIGAKTSVIKEKDGKLVYTGDKDGENSSDDEGEGLVTAKEVIDAVNK	240
OY	136	AGWRKKTITTAGNQTCOADKFETVYSGTNVTPASGCGTATVYSKDDGNITVMYDVNGDA	195
Dd	241	AGWRKKTITTAGNQTCOADKFETVYSGTKVTFPASGCGTATVYSKDDGNITVYKDVAVGDA	300
OY	196	LNVNQLONGNMJDSKAVAAGSGKYISGVNSPSKGMDETVNINNGNNIETPRNGKNIDI	255
Dd	301	LNVNQLONGNMJDSKAIVAAGSGKYISGVNSPSKGMDETVNINAGNNIETPRNGKNIDI	360
OY	256	ATSMTPPOFSVSLGAGAAPTLSVDGD-ALNYGSKKDNKPVRITTNAPGVKEGDVNVAAQ	314
Dd	361	ATSMTPPOFSVSLGAGADAPLTSDVEDGALNGSKDANKPVRLITNVAPEGKEDVTNVAAQ	420
OY	315	LKGYAQNINNNRIDNDVNGARAGIAQAIALTAGLYQAYLPBKSMAIIGGGTYRGEAGTAIG	374
Dd	421		
		421 LKGYAQNINNNRIDNDVNGARAGIAQAIALTAGLYQAYLPBKSMAIIGGGTYRGEAGTAIG	480
OY	375	SSISDGNMIITKGFTASGNSRGHFHGASASVGYYQM 407	
Dd	481	SSISAGGWIIITKGFTASGNSRGHFHGASASVGYYQM 513	

RESULT 13

AU06180	ID	AAU06180 standard; Protein; 592 AA.
xx	xx	
AC	AAU06180;	
XX	XX	
DT	DT	24-OCT-2001 (first entry)
DE	DE	N. meningitidis Z2491 surface antigen NhhA polypeptide sequence.
xx	xx	
KW	KW	Surface antigen NhhA; meningococcal disease; meningitis vaccine.
XX	XX	
xx	xx	
Neisseria meningitidis strain Z2491.		
Key	Location/Qualifiers	
FT	FT	1..50
FT	/label= C1	
FT	/note= "Conserved region 1"	
FT	51..102	
FT	/label= V1	
FT	/note= "Variable region 1"	
FT	103..114	
FT	/label= C2	
FT	/note= "Conserved region 2"	
FT	115..124	
FT	/label= V2	
FT	/note= "Variable region 2"	
FT	125..188	
FT	/label= C3	
FT	/note= "Conserved region 3"	
FT	189..208	
Region	Region	

FT	/label= V3
FT	/note= "Variable region 3"
FT	209..227
FT	/label= C4
FT	/note= "Conserved region 4"
FT	228..236
FT	/label= V4
FT	/note= "Variable region 4"
FT	237..592
FT	/label= C5
FT	/note= "Conserved region 5"
PN	
PD	WO200155182-A1.
PP	02-AUG-2001.
PR	25-JAN-2001; 2001WO-AU000069.
PS	25-JAN-2000; 2000US-O177917.
PT	(UYOU) UNIV QUEENSLAND.
XX	
XX	Peak IRA, Jennings MP;
DR	WPI; 2001-488774/53.
DR	N-PSDB; AAS09170.
PT	New Nhba surface antigen polypeptides and polynucleotides from
PT	Neisseria meningitidis, useful in producing vaccines for treating or
PT	preventing broad spectrum of Neisseria meningitidis -
XX	
PS	Claim 9; Fig 1; 91pp; English.
XX	
CC	The present invention relates to the isolation of novel Neisseria
CC	meningitidis mutant polypeptides of the surface antigen Nhba
CC	(AAU06182-AAU06186). The modified or mutant Nhba polypeptides are
CC	characterised by deletions of non-conserved amino acids, particularly
CC	the deletion of variable regions. The deletion mutants are useful in
CC	diagnostics, therapeutic and prophylactic vaccines against a broader
CC	spectrum of N. meningitidis, and in designing and/or screening of
CC	medicaments. The mutant proteins when used as a vaccine can effectively
CC	immunise against a broader spectrum of N. meningitidis strains than
CC	would be expected from a corresponding wild-type surface antigen.
CC	The present sequence representing the wild type surface antigen Nhba
CC	from N. meningitidis strain Z2491 is 1 of 10 Nhba polypeptide sequences
CC	(AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC	the present invention.
XX	
SQ	Sequence 592 AA:
	Query Match 91.8%; Score 1893.5; DB 22; Length 592;
	Best Local Similarity 66.9%; Pred. No. 2.5e-120;
	Matches 396; Conservative 4; Mismatches 7; Indels 185; Gaps 2
OY	1 MNKIYRIIMNSALNAVVSSELTNRHTRKASATVTAVALATLFFPYVOASA----- 51 : Db 1 MNKIYRIIMNSALNAVVSSELTNRHTRKASATVTAVALATLFFPYVOANAIDEDDEBEL 60
OY	52 ----- 51
Db	61 ESVORSVGSIQASMESGSELETISLSMTINDSKFEVDYIYVTLKAGDNLIKONTNENT 120
OY	52 ----- 51
Db	121 NASSFYSLLKDLTGLINVTETKLSEFANGKKVNIIISPTKGLNFPAKETAGTCGTTHLIN 180
OY	52 -----NNYDF 56 Db 181 GIGSTINDTLTGSSASHVDAONOSTHYTRRASIKRYVLNAGMNIKEVKTKGSTTGGSENDF 240
OY	57 VRITYDVEEFLSADTKRTTVNVESKDNGKKEITEVGAKTSVIKEDGKLYTGDKCENSGS 116 241 VRITDYVEEFLSADTKRTTVNVESKNGRKRETEVGAKTSVIKEDGKLYTGDKCENSGS 300

QY 117 TDEGELVTAKEVIDAVNKAQMRKTTTANGQTGAADKEFTVSGTNTVFASGKGTATV 176
 DB 301 TDEGELVTAKEVIDAVNKAQMRKTTTANGQTGAADKEFTVSGTNTVFASGKGTATV 360
 QY 177 SKDDOGNITVMDVNVGDALNVNOLNSGWNLDKSAVAGSSGKVIISGNVSPSKGKMDFTV 236
 DB 361 SKDDOGNITVMDVNVGDALNVNOLNSGWNLDKSAVAGSSGKVIISGNVSPSKGKMDFTV 420
 QY 237 NINAGNNEITRNKKNIDATSMTPPFSSVSLGAGADAPTLSDVGD-ALNVSKKNKRPV 295
 DB 421 NINAGNNEITRNKKNIDATSMTPPFSSVSLGAGADAPTLSDVGDALNVSKKNKRPV 480
 QY 296 RITNVAPGVKESDVTNVNOLKGVNQLNNRINDVNDGNARAGIAQAIAATAGLVQAYLPGKS 355
 DB 481 RITNVAPGVKESDVTNVNOLKGVNQLNNRINDVNDGNARAGIAQAIAATAGLVQAYLPGKS 540
 QY 356 MMAIGGTYRGEGAGTAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 407
 DB 541 MMAIGGTYRGEGAGTAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 592

RESULT 14

ID AAY23740 standard; Protein: 594 AA.

AC AAY23740;

DT 08-SEP-1999 (first entry)

DE A surface protein of Neisseria meningitidis.

KM Surface protein; surface glycoprotein; infection; vaccine;

XX immunoreactive peptide.

OS Neisseria meningitidis.

PN WO9931132-A1.

PD 24-JUN-1999.

PF 14-DEC-1998: 98WO-AU01031.

PR 12-DEC-1997: 97GB-0026398.

PA (ISIS-) ISIS INNOVATION LTD.

XX (UYOU) UNIV QUEBENS LAND.

PI Jennings MP, Moxon ER, Peak IRA;

XX WPI: 1999-418754/35.

DR N-PSDB: AAX85792.

PT Neisseria meningitidis surface proteins useful for treating N.

XX meningitidis infections

PS Claim 1; Page 100-101; 132pp; English.

CC The present sequence represents a surface protein of Neisseria

CC meningitidis which is approximately 62 kDa. The N. meningitidis

CC surface glycoproteins, nucleic acids, the primers and optionally

CC a thermostable polymerase, or antibodies are useful in a kit for

CC the detection or diagnosis of N. meningitidis infection in humans.

CC The N. meningitidis surface glycoproteins can also be used to

CC prevent or treat N. meningitidis infection in humans, especially

CC in the form of vaccines. The proteins and antibodies can also

CC be used to identify immunoreactive peptides.

CC Sequence 594 AA;

CC Query Match 91.5%; Score 1887.5; DB 20; Length 594;

CC Best Local Similarity 66.5%; Pred. No. 6.4e-120;

CC Matches 395; Conservative 5; Mismatches 7; Indels 187; Gaps 2;

QY 1 MKKTRIIWNSALNAVVSSELRNHTKRASATVKTAVALTLFLFATVQAS----- 50
 DB 1 MKKTRIIWNSALNAVVSSELRNHTKRASATVKTAVALTLFLFATVQASSTDDDDLYLE 60
 QY 51 ----- 50
 DB 61 PVQRTAVVLSFRSDKEGTEKEVEYEDSNMGVYFDDKGVLTAGTITLKAGDNLIKONTNE 120
 QY 51 ----- 50
 DB 121 NTNASSFTYSLKDLTDLTSVGT EKLFSANSKNVNTSDTGLNFAKRTAETNGDTTVH 180
 QY 51 ----- ANNV 54
 DB 181 LMGISLTLDTLNLTGATTNTNDVNTDDEKRAASVRYLNAQWNIKGVKPGTTASDNY 240
 QY 55 DEVRVYDIVEFLSADTKRTTVNVEESKDNCKTEVKIGAKTSYIKEDGKLVTKDKGNG 114
 DB 241 DEVRVYDIVEFLSADTKRTTVNVEESKDNCKTEVKIGAKTSYIKEDGKLVTKDKGNG 300
 QY 115 SSTDEGELVTAKEVIDAVNKAQMRKTTTANGQTGAADKEFTVSGTNTVFASGKGTATV 174
 DB 301 SSTDEGELVTAKEVIDAVNKAQMRKTTTANGQTGAADKEFTVSGTNTVFASGKGTATV 360
 QY 175 TVSKDDOGNITVMDVNVGDALNVNOLNSGWNLDKSAVAGSSGKVIISGNVSPSKGKMD 234
 DB 361 TVSKDDOGNITVMDVNVGDALNVNOLNSGWNLDKSAVAGSSGKVIISGNVSPSKGKMD 420
 QY 235 TVNINAGNNEITRNKKNIDATSMTPPFSSVSLGAGADAPTLSDVGD-ALNVSKKNK 293
 DB 421 TVNINAGNNEITRNKKNIDATSMTPPFSSVSLGAGADAPTLSDVGDALNVSKKNK 480
 QY 294 PVRTNVAPGVKESDVTNVNOLKGVNQLNNRINDVNDGNARAGIAQAIAATAGLVQAYLPG 353
 DB 481 PVRTNVAPGVKESDVTNVNOLKGVNQLNNRINDVNDGNARAGIAQAIAATAGLVQAYLPG 540
 QY 354 KSMMAIGGTYRGEGAGTAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 407
 DB 541 KSMMAIGGTYRGEGAGTAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 594

RESULT 15

ID AAY57044 standard; Protein: 594 AA.

AC AAY57044;

DT 21-FEB-2000 (first entry)

DE BASB029 amino acid sequence from N. meningitidis strain ATCC13090.

KW BASB029; Neisseria meningitidis; surface fibril protein; HSF; diagnosis;

XX infection; treatment; prevent; antibacterial drug.

OS Neisseria meningitidis.

XX Key Location/Qualifiers

FT Misc-difference 104 /note="Encoded by AATC"

PN WO9958683-A2.

XX 18-NOV-1999.

PF 07-MAY-1999: 99WO-EP03255.

PR 13-MAY-1998: 98GB-0010276.

PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.

PI Ruelle J;

XX

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:14:45 ; Search time 10.884 Seconds
(without alignments)
1582.188 Million cell updates/sec

Title: US-09-771-382-25

Perfect score: 2063

Sequence: 1 MNKIRIIMNSALNMAWVVS.....TASGNSRGHFGASASGYQW 407

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

328717

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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6: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1961	95.1	591	3	US-09-377-155-21
2	1961	95.1	591	4	US-09-669-974-21
3	1956.5	94.8	592	3	US-09-377-155-2
4	1956.5	94.8	592	4	US-09-669-974-2
5	1949	94.5	591	3	US-09-377-155-11
6	1949	94.5	591	4	US-09-669-974-11
7	1887.5	91.5	594	4	US-09-377-155-9
8	1887.5	91.5	594	4	US-09-669-974-9
9	1886	91.4	599	4	US-09-377-155-15
10	1886	91.4	599	4	US-09-669-974-15
11	1879.5	91.1	594	3	US-09-377-155-7
12	1879.5	91.1	594	4	US-09-669-974-7
13	1869.5	90.6	592	3	US-09-377-155-17
14	1869.5	90.6	592	4	US-09-669-974-17
15	1864.5	90.4	598	3	US-09-377-155-13
16	1864.5	90.4	598	4	US-09-669-974-13
17	1855.5	89.9	588	3	US-09-377-155-5
18	1855.5	89.9	588	4	US-09-669-974-5
19	1848	89.6	589	4	US-09-377-155-19
20	1848	89.6	589	4	US-09-669-974-19
21	660.5	32.0	1098	1	US-08-409-995-2
22	660.5	32.0	1098	3	US-08-685-467-2
23	660.5	32.0	1098	3	US-09-377-155-32
24	660.5	32.0	1098	3	US-08-913-942-2
25	660.5	32.0	1098	4	US-09-669-974-32
26	660.5	32.0	1098	4	US-09-268-347-44
27	642.5	31.1	658	1	US-08-409-995-5

28	642.5	31.1	658	3	US-08-685-467-5	Sequence 5, Appl1
29	642.5	31.1	658	3	US-08-913-942-5	Sequence 5, Appl1
30	640	31.0	2411	4	US-09-268-347-36	Sequence 36, Appl1
31	638	30.9	2353	3	US-09-377-155-33	Sequence 33, Appl1
32	638	30.9	2353	3	US-08-913-942-4	Sequence 4, Appl1
33	638	30.9	2353	4	US-09-669-974-33	Sequence 33, Appl1
34	638	30.9	2354	4	US-09-268-347-47	Sequence 47, Appl1
35	625.5	30.3	1094	4	US-09-268-347-32	Sequence 32, Appl1
36	580.5	28.1	607	1	US-08-409-995-6	Sequence 6, Appl1
37	580.5	28.1	607	3	US-08-685-467-6	Sequence 6, Appl1
38	580.5	28.1	607	3	US-08-913-942-6	Sequence 6, Appl1
39	580.5	28.1	1912	1	US-08-409-995-4	Sequence 4, Appl1
40	580.5	28.1	1912	3	US-08-685-467-4	Sequence 4, Appl1
41	494	23.9	679	3	US-08-913-942-15	Sequence 15, Appl1
42	494	23.9	679	4	US-09-268-347-26	Sequence 26, Appl1
43	402.5	19.5	1004	4	US-09-268-347-30	Sequence 30, Appl1
44	391.5	19.0	1002	4	US-09-268-347-24	Sequence 24, Appl1
45	341.5	16.6	1104	4	US-09-268-347-28	Sequence 28, Appl1

ALIGNMENTS

RESULT 1					
US-09-377-155-21					
; Sequence 21, Application US/09377155					
; Patent No. 6197312					
; GENERAL INFORMATION:					
; APPLICANT: PEAK, Ian Richard Anselm					
; APPLICANT: JENNINGS, Michael Paul					
; APPLICANT: MOXON, E. Richard					
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN					
; FILE REFERENCE: 065064/0128					
; CURRENT APPLICATION NUMBER: US/09/377, 155					
; PRIOR FILING DATE: 1999-08-19					
; PRIOR APPLICATION NUMBER: PCT/AU98/01031					
; PRIOR FILING DATE: 1998-12-14					
; PRIOR APPLICATION NUMBER: GB 9726398.2					
; NUMBER OF SEQ ID NOS: 33					
; SOFTWARE: Patent In Ver. 2.0					
; SEQ ID NO 21					
; LENGTH: 591					
; TYPE: PRT					
; ORGANISM: Neisseria meningitidis					
; US-09-377-155-21					
Query Match					
Best Local Similarity 95.1%; Score 1961; DB 3; Length 591;					
Matches 407; Conservative 0; Mismatches 0; Indels 184; Gaps 1;					
QY	1	MNKIRIIMNSALNMAWVVS	ELTRNHTKRASATVKTAVLTLLFATVQASAN	-----	52
DB	1	MNKIRIIMNSALNMAWVVS	ELTRNHTKRASATVKTAVLTLLFATVQASANNEDEBDL		60
QY	53	-----	-----	-----	52
DB	61	YLDPVQRTAVLIVNSDKEGTGEKEVENSMAVFNKGVLTAREITLKAGDNLIKQ			120
QY	53	-----	-----	-----	52
DB	121	NGNTFTYSLKKDLTDLTSGTEKLSFSAANGKNVITSDTGKLNPAKETAGTNGDTYVHLN			180
QY	53	-----	-----	-----	56
DB	181	GIGSTLDTLNTGATGTTVNDVTDDEKKRAASVKKDVLNAGNMIKGVKPGTTASDVDF			240
QY	57	VRTYDVEEFLSADTKTTTVVESKDNKKEVIGKATSVYIKKDGKLVYNGKKGESS			116
DB	241	VRTYDVEEFLSADTKTTTVVESKDNKKEVIGKATSVYIKKDGKLVYNGKKGESS			300
QY	117	TDEGEGLVTKKEVIDAVNKKAGWRKTTTANGQTCQADKFEFTVTSQTVNTPASGKGTATV			176

Db 301 TDEBEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTVSGTNTVTFASGKGTATV 360
Qy 177 SKDDOGNITVWYDVNVGDALNVNOLONGMNLDSKAVAGSSGKVTSGNVSPSKGMDTV 236
Db 361 SKDDOGNITVWYDVNVGDALNVNOLONGMNLDSKAVAGSSGKVTSGNVSPSKGMDTV 420
Qy 237 NINAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDDALNVSSKKDNKPR 296
Db 421 NINAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDDALNVSSKKDNKPR 480
Qy 297 ITNAPGVKEGDVTVNAOLKGAQNLNRRINDVGNARAGIAQAIATAGLVAQAYLPGRSM 356
Db 481 ITNAPGVKEGDVTVNAOLKGAQNLNRRINDVGNARAGIAQAIATAGLVAQAYLPGRSM 540
Qy 357 MAIGGTYRGEAGYAGYSSISDGGNMIKGTASGNSRHFASASVGYOW 407
Db 541 MAIGGTYRGEAGYAGYSSISDGGNMIKGTASGNSRHFASASVGYOW 591

RESULT 2
US-09-669-974-21

; Sequence 21, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-21

Query Match 95.1%; Score 1961; DB 4; Length 591;
Best Local Similarity 68.9%; Pred. No. 1e-155;
Matches 407; Conservative 0; Mismatches 0; Indels 184; Gaps 1;

Qy 1 MNKIYRIIWSALNANVYVSELTNRNHTKRASATVKTAVLATLLEFATVOASAN----- 52
Db 1 MNKIYRIIWSALNANVYVSELTNRNHTKRASATVKTAVLATLLEFATVOASANNEBERDL 60
Qy 53 ----- 52
Db 61 YLDPVQRTAVAVLIYNSDEKTEGKEKVEENSDMAVYFNEKGVLTAREITLAKGDNLIKQ 120
Qy 53 ----- 52
Db 121 NGTNFTYSLKKDLTDLTSVTEKLSFSANGKNVITSDTKGLNPAKETAGTNGDTYHLN 180
Qy 53 ----- 52
Db 181 GIGSTLTDLTLLNTGATTNVTNDNVTDDEKKRAASVYKVDLNAQWNIKGVKPGTTASDNDV 240
Qy 57 VRTDVTVEFLSADTKTTTVNVESKDNKKTVEKIGAKTSVYKEKDKGLVYTGDKDGENSS 116
Db 241 VRTDVTVEFLSADTKTTTVNVESKDNKKTVEKIGAKTSVYKEKDKGLVYTGDKDGENSS 300
Qy 117 TDEBEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTVSGTNTVTFASGKGTATV 176
Db 301 TDEBEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTVSGTNTVTFASGKGTATV 360

Qy 177 SKDDOGNITVWYDVNVGDALNVNOLONGMNLDSKAVAGSSGKVTSGNVSPSKGMDTV 236
Db 361 SKDDOGNITVWYDVNVGDALNVNOLONGMNLDSKAVAGSSGKVTSGNVSPSKGMDTV 420
Qy 237 NINAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDDALNVSSKKDNKPR 296
Db 421 NINAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDDALNVSSKKDNKPR 480
Qy 297 ITNAPGVKEGDVTVNAOLKGAQNLNRRINDVGNARAGIAQAIATAGLVAQAYLPGRSM 356
Db 481 ITNAPGVKEGDVTVNAOLKGAQNLNRRINDVGNARAGIAQAIATAGLVAQAYLPGRSM 540
Qy 357 MAIGGTYRGEAGYAGYSSISDGGNMIKGTASGNSRHFASASVGYOW 407
Db 541 MAIGGTYRGEAGYAGYSSISDGGNMIKGTASGNSRHFASASVGYOW 591

RESULT 3
US-09-377-155-2

; Sequence 2, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-2

Query Match 94.8%; Score 1956.5; DB 3; Length 592;
Best Local Similarity 68.6%; Pred. No. 2.4e-155;
Matches 406; Conservative 0; Mismatches 1; Indels 185; Gaps 1;

Qy 1 MNKIYRIIWSALNANVYVSELTNRNHTKRASATVKTAVLATLLEFATVOASAN----- 52
Db 1 MNKIYRIIWSALNANVYVSELTNRNHTKRASATVKTAVLATLLEFATVOASANNEPRKKD 60
Qy 53 ----- 52
Db 61 YLDPVQRTAVAVLIYNSDEKTEGKEKVEENSDMAVYFNEKGVLTAREITLAKGDNLIK 120
Qy 53 ----- 52
Db 121 QNGTNFTYSLKKDLTDLTSVTEKLSFSANGKNVITSDTKGLNPAKETAGTNGDTYHL 180
Qy 53 ----- 52
Db 181 NGISLTLDLTLLNTGATTNVTNDNVTDDEKKRAASVYKVDLNAQWNIKGVKPGTTASDNDV 240
Qy 56 FVRTYDVTVEFLSADTKTTTVNVESKDNKKTVEKIGAKTSVYKEKDKGLVYTGDKDGENS 115
Db 241 FVRTYDVTVEFLSADTKTTTVNVESKDNKKTVEKIGAKTSVYKEKDKGLVYTGDKDGENS 300
Qy 116 STDEBEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTVSGTNTVTFASGKGTAT 175
Db 301 STDEBEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTVSGTNTVTFASGKGTAT 360
Qy 176 VSKDDOGNITVWYDVNVGDALNVNOLONGMNLDSKAVAGSSGKVTSGNVSPSKGMDTV 235
Db 361 VSKDDOGNITVWYDVNVGDALNVNOLONGMNLDSKAVAGSSGKVTSGNVSPSKGMDTV 420

Db 481 ITNVAPEGEDVTNVAOLKGVNQLNLRINDVGNAGIAQAIATATGLVOAYIPGKSM 540
QY 357 MAIGGTYRGEAGYAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 407
Db 541 MAIGGTYRGEAGYAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 591

RESULT 6
US-09-669-974-11
; Sequence 11, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-11

Query Match 94.5%; Score 1949; DB 4; Length 591;
Best Local Similarity 68.5%; Pred. No. 1e-154;
Matches 405; Conservative 1; Mismatches 1; Indels 184; Gaps 1;
QY 1 MNKIYRIIWSALNMAVVSSELTNRNHTKRASATVAVLATLLEFATVOASAN----- 52
Db 1 MNKIYRIIWSALNMAVVSSELTNRNHTKRASATVAVLATLLEFATVOASANNEOEEDL 60
QY 53 ----- 52
Db 61 YLDPLVLTAVLIVNSDKEGTEKEKEVENSMDAVYFNEKGVLAAREITLAKAGDMLIKIQ 120
QY 53 ----- 52
Db 121 NGTNTFYSLKKDLDLTLSVTEKLSFSANGKNVNTSDTKGLNFAKETAINGDTTVLNLN 180
QY 53 -----NVDF 56
Db 181 GIGSTLDTLLNTGATVNTNDNVTDDEKKRAASVADVNLNAGWNLIKGVKPGTTASDNDF 240
QY 57 VRTDVTVEFLSADPTTTVNVESKONGKKEVKGAKTSVKEKKGKLVTKDKGENSS 116
Db 241 VRTDVTVEFLSADPTTTVNVESKONGKKEVKGAKTSVKEKKGKLVTKDKGENSS 300
QY 117 TDEGGLVTAKVIDAVNKAAGRMKTTTANGOTGADAFETVTSNTVTFASGKGTATV 176
Db 301 TDEGGLVTAKVIDAVNKAAGRMKTTTANGOTGADAFETVTSNTVTFASGKGTATV 360
QY 177 SKDDOGNITVMYDVNVGDLNVLNOLNSGWNLSKAVAGSSGKVISGNAVSPSKGMDET 236
Db 361 SKDDOGNITVMYDVNVGDLNVLNOLNSGWNLSKAVAGSSGKVISGNAVSPSKGMDET 420
QY 237 NINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDGALNVGSKKNKPYR 296
Db 421 NINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDGALNVGSKKNKPYR 480
QY 297 ITNVAPEGEDVTNVAOLKGVNQLNLRINDVGNAGIAQAIATATGLVOAYIPGKSM 356
Db 481 ITNVAPEGEDVTNVAOLKGVNQLNLRINDVGNAGIAQAIATATGLVOAYIPGKSM 540

QY 357 MAIGGTYRGEAGYAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 407
Db 541 MAIGGTYRGEAGYAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 591
RESULT 7
US-09-377-155-9
; Sequence 9, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-9

Query Match 91.5%; Score 1887.5; DB 3; Length 594;
Best Local Similarity 66.5%; Pred. No. 1.4e-149;
Matches 395; Conservative 5; Mismatches 7; Indels 187; Gaps 2;
QY 1 MNKIYRIIWSALNMAVVSSELTNRNHTKRASATVAVLATLLEFATVOAS----- 50
Db 1 MNKIYRIIWSALNMAVVSSELTNRNHTKRASATVAVLATLLEFATVOASTDDDDLYLE 60
QY 51 ----- 50
Db 61 PVQRTAVVLSRDSKEGTEKEVTEEDSNMGVYFDKGVLTAGTTLAKAGDMLIKIQNTNE 120
QY 51 ----- 50
Db 121 NTMASTFYSLKKDLDLTLSVTEKLSFSANSKNVNTSDTKGLNFAKETAETNGDTTVH 180
QY 51 -----ANV 54
Db 181 LNGISTLTDLTLNTGATVNTNDNVTDDEKKRAASVADVNLNAGWNLIKGVKPGTTASDNV 240
QY 55 DVRTYDVTVEFLSADPTTTVNVESKONGKKEVKGAKTSVKEKKGKLVTKDKGENG 114
Db 241 DVRTYDVTVEFLSADPTTTVNVESKONGKKEVKGAKTSVKEKKGKLVTKDKGENG 300
QY 115 SSTDGEGLVTAKVIDAVNKAAGRMKTTTANGOTGADAFETVTSNTVTFASGKGT 174
Db 301 SSTDGEGLVTAKVIDAVNKAAGRMKTTTANGOTGADAFETVTSNTVTFASGKGT 360
QY 175 TVSKDDOGNITVMYDVNVGDLNVLNOLNSGWNLSKAVAGSSGKVISGNAVSPSKGMDE 234
Db 361 TVSKDDOGNITVMYDVNVGDLNVLNOLNSGWNLSKAVAGSSGKVISGNAVSPSKGMDE 420
QY 235 TVNINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDGALNVGSKKNK 293
Db 421 TVNINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDGALNVGSKKNK 480
QY 294 FVRTNVAPEGEDVTNVAOLKGVNQLNLRINDVGNAGIAQAIATATGLVOAYIPG 353
Db 481 FVRTNVAPEGEDVTNVAOLKGVNQLNLRINDVGNAGIAQAIATATGLVOAYIPG 540
QY 354 KSMMAIGGTYRGEAGYAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 407
Db 541 KSMMAIGGTYRGEAGYAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 594

RESULT 8
US-09-669-974-9
; Sequence 9, Application US/09669974
; Patent No. 6331173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669, 974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-9

Query Match 91.5%; Score 1887.5; DB 4; Length 594;
Best Local Similarity 66.5%; Pred. No. 1.4e-149;
Matches 395; Conservative 5; Mismatches 17; Indels 187; Gaps 2;
QY 1 MNKRIIIMNSALNANVAVSELTRNHTKRASATVATVATLTLFATVQAAS----- 50
DB 1 MNKRIIIMNSALNANVAVSELTRNHTKRASATVATVATLTLFATVQAASSTDDDLXLE 60
QY 51 ----- 50
DB 61 PVORTAVVLSFRSDKEGTEGEVTEDESNMGVYFDKKGVLTAQTITLKAGDNLKIKONTNE 120
QY 51 ----- 50
DB 121 NTNASSFTYSLKLDLTLTSVTEKLSFSANSKNVITSDTKGLNFAKKTAEINGDTTVH 180
QY 51 -----ANNV 54
DB 181 LNCIGSTLDTLLNTGATTNVTNDNTDDEKRAASVYKDVNLNAGWNIKGVKPGTTASDNV 240
QY 55 DFRVRYDYVEFLSADTKTTTVNVEESKDNKRTVEKIGAKTSVIREKDGKLVTKGKENG 114
DB 241 DFRVRYDYVEFLSADTKTTTVNVEESKDNKRTVEKIGAKTSVIREKDGKLVTKGKENG 300
QY 115 SSTDEGEGLVTAKEVIDAVNKAQWMMKTTTANGOTGADKFEVTVSGTNTVTFASGKTGA 174
DB 301 SSTDEGEGLVTAKEVIDAVNKAQWMMKTTTANGOTGADKFEVTVSGTNTVTFASGKTGA 360
QY 175 TVSKDOGNITVYDVNVDALNVNQLNSGNMLDSKAVAGSSGKVISGNVSPSKGKMD 234
DB 361 TVSKDOGNITVYDVNVDALNVNQLNSGNMLDSKAVAGSSGKVISGNVSPSKGKMD 420
QY 235 TVVINAGNNIETTRNGKNIDIAFSMTPOESSVSLGAGADAPTLISVDGD-ALNVGSKDKNK 293
DB 421 TVVINAGNNIETTRNGKNIDIAFSMTPOESSVSLGAGADAPTLISVDDEGALNVGSKDKNK 480
QY 294 PVKITVAVPGVEKGDVTNVAQLKGVAONLNRIIDNVGDNARAGIAQAIAATAGIYQAVLP 353
DB 481 PVKITVAVPGVEKGDVTNVAQLKGVAONLNRIIDNVGDNARAGIAQAIAATAGIYQAVLP 540
QY 354 KSMMAIGGTYRGEAGYALGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 407
DB 541 KSMMAIGGTYRGEAGYALGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 594

RESULT 9

US-09-377-155-15
; Sequence 15, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-15

Query Match 91.4%; Score 1886; DB 3; Length 599;
Best Local Similarity 66.1%; Pred. No. 2e-149;
Matches 396; Conservative 3; Mismatches 8; Indels 192; Gaps 2;

QY 1 MNKRIIIMNSALNANVAVSELTRNHTKRASATVATVATLTLFATVQAAS----- 51
DB 1 MNKRIIIMNSALNANVAVSELTRNHTKRASATVATVATLTLFATVQAASSTDEDEEEL 60
QY 52 ----- 51
DB 61 EPVYRSALVYQFMIDKEGNGENESTGNIGSIYDNNHTLHGATVTLKAGDNLKIKONTN 120
QY 52 ----- 51
DB 121 KNTNENTNDSFTYSLKLDLTLTSVTEKLSFGANGKNVITSDTKGLNFAKKTACTING 180
QY 52 ----- 51
DB 181 DTVVHLNGISTLDTLLNTGATTNVTNDNTDDEKRAASVYKDVNLNAGWNIKGVKPGTT 240
QY 52 --NNVDFVRYDYVEFLSADTKTTTVNVEESKDNKRTVEKIGAKTSVIREKDGKLVTKG 109
DB 241 ASDNVDFVRYDYVEFLSADTKTTTVNVEESKDNKRTVEKIGAKTSVIREKDGKLVTKG 300
QY 110 KGENSSTDEGEGLVTAKEVIDAVNKAQWMMKTTTANGOTGADKFEVTVSGTNTVTFASG 169
DB 301 KGENSSTDEGEGLVTAKEVIDAVNKAQWMMKTTTANGOTGADKFEVTVSGTNTVTFASG 360
QY 170 KGTATVYSKDOGNITVYDVNVDALNVNQLNSGNMLDSKAVAGSSGKVISGNVSPSK 229
DB 361 KGTATVYSKDOGNITVYDVNVDALNVNQLNSGNMLDSKAVAGSSGKVISGNVSPSK 420
QY 230 GKMDETVINAGNNIETTRNGKNIDIAFSMTPOESSVSLGAGADAPTLISVDGD-DALVGS 288
DB 421 GKMDETVINAGNNIETTRNGKNIDIAFSMTPOESSVSLGAGADAPTLISVDKCALVGS 480
QY 289 KDKNKPVKITVAVPGVEKGDVTNVAQLKGVAONLNRIIDNVGDNARAGIAQAIAATAGIYQ 348
DB 481 KDKNKPVKITVAVPGVEKGDVTNVAQLKGVAONLNRIIDNVGDNARAGIAQAIAATAGIYQ 540
QY 349 AYLPGRKSMMAIGGTYRGEAGYALGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 407
DB 541 AYLPGRKSMMAIGGTYRGEAGYALGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 599

RESULT 10
US-09-669-974-15
; Sequence 15, Application US/09669974
; Patent No. 6331173
; GENERAL INFORMATION:

```

; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentl Ver. 2.0
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; US-09-669-974-15

```

```

Query Match      91.4%; Score 1886; DB 4; Length 599;
Best Local Similarity 66.1%; Pred. No. 2e-149;
Matches 396; Conservative 3; Mismatches 8; Indels 192; Gaps 2;

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QY 1 MNKIRIIMNSALNMAVVVSELTNRNHTKRASATVAVLATLFFATVOASA----- 51
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DB 1 MNKIRIIMNSALNMAVVVSELTNRNHTKRASATVAVLATLFFATVOANATDEDEDEEEL 60
   |||||||
QY 52 ----- 51
DB 61 EPVVSALVLOFMIDKEGNGENESTGNIGWSIYYDNHNTLHGATVTLKAGDNLKIKONTN 120
QY 52 ----- 51
DB 121 KNTNENTDSSFTYSLKKDLDDLTJSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180
QY 52 ----- 51
DB 181 DTTVHLNGIGSTLTDTLLNTGATNTVNDNTDDEKKRAASVDVNLNAGWNIGVYKPGTT 240
QY 52 ----- 51
DB 52 ---NNVDFTYDTVEFLSADTKTTTVNVEESKDNKGKTEVKGAKTSVKEKDKLVTKGD 109
   |||||||
DB 241 ASDNDVFTYDTVEFLSADTKTTTVNVEESKDNKGKTEVKGAKTSVKEKDKLVTKGK 300
QY 110 KGENSSTDEGEGLVTAKEVIDAVNKAQWMTTANGOTGOADKFEFTVSGTNTVTFASG 169
   |||||||
DB 301 KGENSSSTDEGEGLVTAKEVIDAVNKAQWMTTANGOTGOADKFEFTVSGTNTVTFASG 360
QY 170 KGTATVSKDQGNITVMDVNVGDALNVNQLNSGWNLDKRAVAGSSGKVISGNVSPSK 229
   |||||||
DB 361 KGTATVSKDQGNITVMDVNVGDALNVNQLNSGWNLDKRAVAGSSGKVISGNVSPSK 420
QY 230 GKMDTVINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLSSVDKGLNNGS 288
   |||||||
DB 421 GKMDTVINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLSSVDKGLNNGS 480
QY 289 KKDKNPVRITNVAPGVKGGDVTNVAOLKGYAQNLLNRRIDNVGNNRAGIAQATAGLVQ 348
   |||||||
DB 481 KKDKNPVRITNVAPGVKGGDVTNVAOLKGYAQNLLNRRIDNVGNNRAGIAQATAGLVQ 540
QY 349 AYLPGKSMMAIGGTYRGEAGYALIGYSSISDGMNIIKGTASGNSRGHFGASASVGYQW 407
   |||||||
DB 541 AYLPGKSMMAIGGTYRGEAGYALIGYSSISDGMNIIKGTASGNSRGHFGASASVGYQW 599

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RESULT 11
US-09-377-155-7
; Sequence 7, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul

```

```

; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentl Ver. 2.0
; SEQ ID NO: 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; US-09-377-155-7

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Query Match      91.1%; Score 1879.5; DB 3; Length 594;
Best Local Similarity 66.5%; Pred. No. 6.7e-149;
Matches 395; Conservative 3; Mismatches 9; Indels 187; Gaps 2;

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QY 1 MNKIRIIMNSALNMAVVVSELTNRNHTKRASATVAVLATLFFATVOASA----- 51
   |||||||
DB 1 MNKIRIIMNSALNMAVVVSELTNRNHTKRASATVAVLATLFFATVOANATDDDDDDLYLE 60
   |||||||
QY 52 ----- 51
DB 61 PVQRTAVVLSFRSDEKGEKGEKGEDSNMAYVFDEKRVLKAGATTLKAGDNLKIKONTNE 120
QY 52 ----- 51
DB 121 NTNDSFTYSLKKDLDDLTJSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGDPTVH 180
QY 52 ----- 51
DB 181 LMGISTLTDTLLNTGATNTVNDNTDDEKKRAASVDVNLNAGWNIGVYKPGTTASDNV 240
QY 55 DFTYDTVEFLSADTKTTTVNVEESKDNKGKTEVKGAKTSVKEKDKLVTKGDENG 114
   |||||||
DB 241 DFTYDTVEFLSADTKTTTVNVEESKDNKGKTEVKGAKTSVKEKDKLVTKGDENG 300
QY 115 SSTDEGEGLVTAKEVIDAVNKAQWMTTANGOTGOADKFEFTVSGTNTVTFASGKTGA 174
   |||||||
DB 301 SSTDEGEGLVTAKEVIDAVNKAQWMTTANGOTGOADKFEFTVSGTNTVTFASGKTGA 360
QY 175 TVSKDQGNITVMDVNVGDALNVNQLNSGWNLDKRAVAGSSGKVISGNVSPSKKMD 234
   |||||||
DB 361 TVSKDQGNITVMDVNVGDALNVNQLNSGWNLDKRAVAGSSGKVISGNVSPSKKMD 420
QY 235 TVNINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLSSVDKGLNNGS 293
   |||||||
DB 421 TVNINAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLSSVDKGLNNGS 480
QY 294 PVRTITNVAPGVKGGDVTNVAOLKGYAQNLLNRRIDNVGNNRAGIAQATAGLVQATPG 353
   |||||||
DB 481 PVRTITNVAPGVKGGDVTNVAOLKGYAQNLLNRRIDNVGNNRAGIAQATAGLVQATPG 540
QY 354 KSMMAIGGTYRGEAGYALIGYSSISDGMNIIKGTASGNSRGHFGASASVGYQW 407
   |||||||
DB 541 KSMMAIGGTYRGEAGYALIGYSSISDGMNIIKGTASGNSRGHFGASASVGYQW 594

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RESULT 12
US-09-669-974-7
; Sequence 7, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974

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```

: CURRENT FILING DATE: 2000-09-26
: PRIOR APPLICATION NUMBER: US 09/377,155
: PRIOR FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 7
: LENGTH: 594
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-669-974-7

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; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-17

Query Match          90.6%;   Score 1869.5;   DB 3;   Length 592;
Best Local Similarity 66.4%;   Pred. No. 4.6e-146;
Matches 393; Conservative 4; Mismatches 10; Indels 185; Gaps 2

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[illegible]

OY		1	MNKIYRIWNSALNAAVVSLELTNRHMKRASATYKTAVALATLLEFPTVOASA-----	51
Dd		1	MNKIYRIWNSALNAAVVSLELTNRHMKRASATYKTAVALATLLEFPTVOANMTDEDEEBEL	60
OY		52	-----	51
Dd		61	ESVQRSVYGSIQASMESSVELETJISLSMTNDSKFEVDPYIYVTLKAGDNIAKIOMTNEFT	120
OY		52	-----	51
Dd		121	NASSFTYSLKDLINGLINVFTEKLSFGANGKKVNIISDTKGLNFAKETAGTGIDTYVHLN	180
OY		52	-----	56
Dd		181	GIGSTLADMNLNGATTNTNDNTDDEKKRAASYKDVLNAGWNIKGVKPCTTASDNDF	240
OY		57	VRFPTDVEFLSADTKTTVTVNYESKDKNGKKTTEYKIGAKTSVIKEKDGILVYGKDKGENSS	116
Dd		241	VRTDPTVBFSLADPKTTVTNVNESKDKNGKKTTEYKIGAKTSVIKEKDGILVYGKDKGENSS	300
OY		117	TDEBGBLVATAEVIDAVNAKACMRMKTTPANGOTGADKFETYVTSNTVPASGKTATV	176
Dd		301	TDEBGBLVATAEVIDAVNAKACMRMKTTPANGOTGADKFETYVTSNTVPASGKTATV	360
OY		177	SKDDOGNTTWADVNVGDALNVNOLONSGWNLDASKVAVSGSGXVISGNVSPSKGMDEFV	236
Dd		361	SKDDOGNTTWADVNVGDALNVNOLONSGWNLDASKVAVSGSGXVISGNVSPSKGMDEFV	420
OY		237	NINAGNNIEIRNGKNIDIASMTPOFSVSLGAGADAPTLSVDGD-ALNVSKKDKNPV	295
Dd		421	NINAGNNIEIRNGKNIDIASMTPOFSVSLGAGADAPTLSVDGDALNVSCKANRPV	480
OY		296	RITVNAVPCVKEGDYTNVAOLKGVAONLNRRIDNVGDNAPAGIAQAIAATAGLVOAYLPGRS	355
Dd		481	RITVNAVPCVKEGDYTNVAOLKGVAONLNRRIDNVGDNAPAGIAQAIAATAGLVOAYLPGRS	540
OY		356	MAAIGGGYRREAGYAIGYSSISDCGNIIKGTASGNSRGHFGASASGYOW	407
Dd		541	MAAIGGGYRREAGYAIGYSSISAGGNWIKGTASGNSRGHFGASASGYOW	592
US-0974-17				
US-0974-17				
Sequence 17, Application US/09669974				
Patent No. 6333173				
GENERAL INFORMATION:				
APPLICANT: PEAK, Ian Richard Anselm				
APPLICANT: JENNINGS, Michael Paul				
APPLICANT: MOXON, E. Richard				
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN				
FILE REFERENCE: 065064/0128				
CURRENT APPLICATION NUMBER: US/09/669, 974				
CURRENT FILING DATE: 2000-09-26				
PRIOR APPLICATION NUMBER: US 09/377,155				
PRIOR FILING DATE: 1999-08-19				
PRIOR APPLICATION NUMBER: PCT/AU98/01031				
PRIOR FILING DATE: 1998-12-14				
PRIOR APPLICATION NUMBER: GB 9726398 2				

;; PRIOR FILING DATE: 1997-12-12
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO 17
;; LENGTH: 592
;; TYPE: PRT
;; ORGANISM: Neisseria meningitidis
US-09-669-974-17

Query Match 90.6%; Score 1869.5; DB 4; Length 592;
Best Local Similarity 66.4%; Pred. No. 4.6e-148;
Matches 393; Conservative 4; Mismatches 10; Indels 185; Gaps 2;

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OY 1 MNKIYRIIWSALNAAVVVSELTNRNHTKRASATVAVLATLLEFATVOASA----- 51
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DB 1 MNKIYRIIWSALNAAVVSELTNRNHTKRASATVAVLATLLEFATVOANATDEDEBEL 60
OY 52 ----- 51
DB 61 ESVQSVVGSIQASMEGSVELETTLSMTNDSKEFVDPIYVYTLKAGDNLKIKONTNENT 120
OY 52 ----- 51
DB 121 NASSFTYSLKKDILGLINVTETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN 180
OY 52 -----NNVDF 56
DB 181 GIGSTLFDMLNTGATNTVNDNTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNDVF 240
OY 57 VRTDYVEFLSADTKTTTVNVEESKDNKKTEVKIGAKTSVIREKDKGLVTGKDGENGSS 116
DB 241 VRTDYVEFLSADTKTTTVNVEESKDNKKTEVKIGAKTSVIREKDKGLVTGKDGENGSS 300
OY 117 TDEGEGLVTAKEVIDAVNKAQWMTTANGOTGADAFETVTSNTVTFASGKGTATV 176
DB 301 TDEGEGLVTAKEVIDAVNKAQWMTTANGOTGADAFETVTSNTVTFASGKGTATV 360
OY 177 SKDDOGNITTVAVNVDGALNVNOLONGMNDKSAVAGSSGKVTISGVNPSKGMDET 236
DB 361 SKDDOGNITTVAVNVDGALNVNOLONGMNDKSAVAGSSGKVTISGVNPSKGMDET 420
OY 227 NINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLISVDGD-ALNVGSKDKNKP 295
DB 421 NINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLISVDGDALNVGSKDKNKP 480
OY 296 RITNVAPGVKEGDVTNVNQLKGVNQLNLRIDNVGNARAGIAQAIATAGLVOAYLPKGS 355
DB 481 RITNVAPGVKEGDVTNVNQLKGVNQLNLRIDNVGNARAGIAQAIATAGLVOAYLPKGS 540
OY 356 MMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 407
DB 541 MMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 592
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RESULT 15
US-09-377-155-13
; Sequence 13, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377, 155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13

;; LENGTH: 598
;; TYPE: PRT
;; ORGANISM: Neisseria meningitidis
US-09-377-155-13

Query Match 90.4%; Score 1864.5; DB 3; Length 598;
Best Local Similarity 65.6%; Pred. No. 1.2e-147;
Matches 392; Conservative 4; Mismatches 11; Indels 191; Gaps 2;

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OY 1 MNKIYRIIWSALNAAVVVSELTNRNHTKRASATVAVLATLLEFATVOASA----- 51
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DB 1 MNKIYRIIWSALNAAVVSELTNRNHTKRASATVAVLATLLEFATVOANATDDDDLYLE 60
OY 52 ----- 51
DB 61 PVQRTAVVLSFRSDEKTEGEKTEDSNMVAYFDEKRVLKAGALTLKAGDNLKIKONTNE 120
OY 52 ----- 51
DB 121 NTNENTDSFTYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180
OY 52 ----- 51
DB 181 PTVHLNGISTLTDTLTNTGATNTVNDNTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 240
OY 52 -NNVDFVRTDYVEFLSADTKTTTVNVEESKDNKKTEVKIGAKTSVIREKDKGLVTGDK 110
DB 241 SDNVDFVRTDYVEFLSADTKTTTVNVEESKDNKKTEVKIGAKTSVIREKDKGLVTGDK 300
OY 111 GENGSTDEGEGLVTAKEVIDAVNKAQWMTTANGOTGADAFETVTSNTVTFASGK 170
DB 301 DENGSTDEGEGLVTAKEVIDAVNKAQWMTTANGOTGADAFETVTSNTVTFASGK 360
OY 171 GTTATVSKDDOGNITTVAVNVDGALNVNOLONGMNDKSAVAGSSGKVTISGVNPSK 230
DB 361 GTTATVSKDDOGNITTVAVNVDGALNVNOLONGMNDKSAVAGSSGKVTISGVNPSK 420
OY 231 KMDFTVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLISVDGD-ALNVGSK 289
DB 421 KMDFTVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLISVDGDALNVGSK 480
OY 290 KDNKPVRTITNVAPGVKEGDVTNVNQLKGVNQLNLRIDNVGNARAGIAQAIATAGLVOA 349
DB 481 DANKPVRTITNVAPGVKEGDVTNVNQLKGVNQLNLRIDNVGNARAGIAQAIATAGLVOA 540
OY 350 YLPKSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 407
DB 541 YLPKSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 598
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Search completed: October 6, 2003, 09:35:45
Job time : 13.884 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:35 ; Search time 11.6505 Seconds
(without alignments)
3359.577 Million cell updates/sec

Title: US-09-771-382-25
Perfect score: 2063
Sequence: 1 MNKIYRIIINMSALNMAVYVS.....TASGNSRGHFQASASVGYQM 407

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_76:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1961	95.1	591	2	G81133
2	1893.5	91.6	592	2	A81888
3	341	16.5	1190	2	A82615
4	332.5	16.1	2059	2	D82671
5	331	16.0	1588	2	A86036
6	331	16.0	1588	2	H91188
7	330	15.5	1107	2	AC0976
8	307.5	14.9	658	2	AH0110
9	277.5	13.5	288	2	I64138
10	211	10.2	1004	2	C82672
11	188.5	9.1	3705	2	AD0123
12	185	9.0	1286	2	S28634
13	183.5	8.9	365	2	AB3486
14	175.5	8.5	1018	2	H83135
15	175	8.5	1325	2	A64905
16	172	8.3	364	2	A81019
17	172	8.3	585	2	F90961
18	172	8.3	585	2	F85809
19	171.5	8.3	1091	2	G64964
20	170	8.2	1335	2	T17508
21	165	8.0	4919	2	T31105
22	164.5	8.0	1910	2	AF0394
23	162	7.9	584	2	C48658
24	161.5	7.8	936	2	I40711
25	159	7.7	1343	2	E90893
26	159	7.7	1477	2	B43855
27	159	7.7	5188	2	B83547
28	159	7.7	5291	2	F90696
29	158.5	7.7	949	2	D90803

30	158.5	7.7	1005	2	H85611	probable adhesin z
31	156.5	7.6	933	2	S41539	fibritogen-binding
32	156	7.6	1035	2	AD3203	autotransporter pr
33	156	7.6	1343	2	D85724	hypothetical prote
34	156	7.6	4152	2	T31102	filamentous hemagg
35	155.5	7.5	989	2	D89852	ABC-type transport
36	155	7.5	2020	2	C48399	probable exported
37	154	7.5	364	2	AE0169	surface array prot
38	154	7.5	920	2	I40614	hypothetical prote
39	154	7.5	1461	2	E90696	adhesin/invasin-11
40	153.5	7.4	338	2	D90697	adhesin/invasin-11
41	153.5	7.4	338	2	G85547	adhesin/invasin-11
42	151.5	7.3	3013	2	AB0480	probable invasin y
43	151	7.3	595	2	A48658	flagellin - Escher
44	151	7.3	980	2	H90681	probable flagellin
45	151	7.3	980	2	D85532	probable structura

ALIGNMENTS

RESULT 1									
G81133									
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)									
C:Species: Neisseria meningitidis									
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001									
C:Accession: G81133									
R:Jettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathavan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizzo, M. Science 287, 1809-1815, 2000									
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappelli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: A81000; MIMD:2015755; PMID:10710307									
A:Accession: G81133									
A>Status: preliminary									
A:Molecule type: DNA									
A:Residues: 1-591 <TET>									
A:Cross-references: GB:AE002450; GB:AE002098; MID:g7226229; PIDN:AAF41395.1; PID:g722									
A:Experimental source: serogroup B, strain MC58									
C:Genetics:									
A:Gene: NMB0992									
Query Match 95.1%; Score 1961; DB 2; Length 591;									
Best Local Similarity 68.9%; Pred. NO.5-5e-102;									
Matches 407; Conservative 0; Mismatches 0; Indels 184; Gaps 1;									
QY	1	MNKIYRIIINMSALNMAVYVSELRNHTKRASATVKTAVLATLTFATVOASAN-----	52						
DB	1	MNKIYRIIINMSALNMAVYVSELRNHTKRASATVKTAVLATLTFATVOASANBEQEDL	60						
QY	53	-----	52						
DB	61	YLDPVORTAVLIVNSDKEGTGEKEVEENSDAVYFNEKGVLTAREITLKAGDNLIKIKO	120						
QY	53	-----	52						
DB	121	NGTNFTYSLKKDLTDLTSVCTEKLSPSANGKNVITSPTKGLNPAKETAGTNGDTTVHNLN	180						
QY	53	-----	52						
DB	181	GIGSTLDLTLNLTGATTNTNDVNTDEKKRAASVADVLNAGNNINGVKPGTTASDNVDF	240						
QY	57	VRRYDVEVERISADFTKTTTVNVEESKDKGKTEVIGAKTSYIKKDGKLVTKGKENGSS	116						
DB	241	VRRYDVEVERISADFTKTTTVNVEESKDKGKTEVIGAKTSYIKKDGKLVTKGKENGSS	300						
QY	117	TDEGEGLVAKVEYIDAVNKGAWRKTTTANGGTGQADKPEFTVSGTNVFPASGKGTATV	176						
DB	301	TDEGEGLVAKVEYIDAVNKGAWRKTTTANGGTGQADKPEFTVSGTNVFPASGKGTATV	360						
QY	177	SKDDQGNITVWYDVNVGDAALNVNOLONGNLDLSKAVAGSSGKVISGNNVSPSGKMDERV	236						

Db 361 SKDQGNITVAVDVAAGDALNVNOLQNSGMWLDKAVAGSGSKVTSIGNVSPSKGMDFTV 420
OY 237 NINAGNNIETIRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDGALNVGSKKNKPYR 296
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Db 421 NINAGNNIETIRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDGALNVGSKKNKPYR 480
OY 297 ITNVAPEKEDVTNVAOLKGVAAQNLNRRIDNVGNARAGIAQAIAATAGLVQAVLPGKSM 356
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Db 481 ITNVAPEKEDVTNVAOLKGVAAQNLNRRIDNVGNARAGIAQAIAATAGLVQAVLPGKSM 540
OY 357 MAIGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRGGHFGASASVGYOM 407
|||||
Db 541 MAIGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRGGHFGASASVGYOM 591

RESULT 2

Ab1888
probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain Z249
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: Ab1888
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: Ab1775; MUID:20222556; PMID:10761919
A:Accession: Ab1888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-592 <PAR>
A:Cross-references: GB:AL162755; GB:AL157959; NID:97379742; PIDN:CA884461.1; PID:9737989
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1200

Query Match 91.8%; Score 1893.5; DB 2; Length 592;
Best Local Similarity 66.9%; Pred. No. 3,1e-98;
Matches 396; Conservative 4; Mismatches 7; Indels 185; Gaps 2;
OY 1 MNKIYRIIWNALNVAWVSELTNRNHTKRASATVTAVALTLEATVOASA----- 51
|||||
Db 1 MNKIYRIIWNALNVAWVSELTNRNHTKRASATVTAVALTLEATVOANNTDEDEBEL 60
OY 52 ----- 51
Db 61 ESVOBSVSGSIQASMEGSELETISLMTNDSKEFVDPIYVTLKAGDNLIKONTNENT 120
OY 52 ----- 51
Db 121 NASSETYSLKQDLTGLINVEERKLSFGANGKKVNIISPTKGLNFAKETAGTNGDTTHLN 180
OY 52 -----NNYDF 56
Db 181 GIGSLDTDTLGLSSASHVDAGNOSTHYTRASIKDVLNAGNNIKVKTGSGTTCSENVDF 240
OY 57 VRTDYVEPLSADTKTTTVNVEESKDNKGAKTEYKIGAKTSVIEKDKGLVTGKDKGENSS 116
|||||
Db 241 VRTDYVEPLSADTKTTTVNVEESKDNKGAKTEYKIGAKTSVIEKDKGLVTGKDKGENSS 300
OY 117 TDEGGLVTAKEVIDAVKAKGMRKTTTANGOTGADKEFYVTSNTNTPASGKCTTATV 176
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Db 301 TDEGGLVTAKEVIDAVKAKGMRKTTTANGOTGADKEFYVTSNTNTPASGKCTTATV 360
OY 177 SKDQGNITVAVDVAAGDALNVNOLQNSGMWLDKAVAGSGSKVTSIGNVSPSKGMDFTV 236
Db 361 SKDQGNITVAVDVAAGDALNVNOLQNSGMWLDKAVAGSGSKVTSIGNVSPSKGMDFTV 420
OY 237 NINAGNNIETIRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDG-ALNVGSKKNKPY 295
Db 421 NINAGNNIETIRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDG-ALNVGSKKNKPY 480
OY 296 RITNVAPEKEDVTNVAOLKGVAAQNLNRRIDNVGNARAGIAQAIAATAGLVQAVLPGKS 355
|||||

Db 481 RITNVAPEKEDVTNVAOLKGVAAQNLNRRIDNVGNARAGIAQAIAATAGLVQAVLPGKS 540
OY 356 MAIGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRGGHFGASASVGYOM 407
|||||
Db 541 MAIGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRGGHFGASASVGYOM 592

RESULT 3

surface protein XF1981 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: Ab2615
R:anonymus, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: Ab2515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: Ab2615
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1190 <STM>
A:Cross-references: GB:AE004017; GB:AE003849; NID:99107083; PIDN:AFB84783.1; GSPDB:GN
A:Experimental source: Strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Bioness, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Klajim, J.P.; Krieger, J.E.; Kurimae, E.E.; La
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1981

Query Match 16.5%; Score 341; DB 2; Length 1190;
Best Local Similarity 27.4%; Pred. No. 1.9e-11;
Matches 121; Conservative 60; Mismatches 161; Indels 100; Gaps 17;
OY 8 IMNSALNVAWVSELTNRNHTKRASATVKT-AV-LATLFAVVOASANNVDFVRYDFEF 65
Db 807 VTSSGINAG-----SKRTNVAAGTADTDAVNLSQLTFMAAGSAGKSVHYTYD----- 856
OY 66 LSADTKTTTVNVEESKDNKGAKTEYKIGAKTSVIEKDKGLVTGKDKGENG-SSTDEGLV 124
|||||
Db 857 --GGTGGNNGDAGTGRSIAVGGLTASA-----EGATVAGSGLAASGKSFATGRNAV 910
OY 125 TAKEYIDAVNKAQRMRKTTTANGOTGADKEFYVTSNTNTPASGKCTTATVSDDCNI 184
Db 911 ASAGSVALGD-GAKDGAEGAESTYGRKSLQNTNVTGVSADSKGSTRVS-----NV 964
OY 185 TWNYDVNNGDALNVNOL-----QNSGMWLDKAVAGSGSKVTSIGNVSPSKGMDFTVINA 240
Db 965 ADAKEAT--DAVNLQDLRVDANRRYDNKIEISLSEQGT-----YKNS 1008
OY 241 GNNIETIRNGKNIDIAISMTPOFSSVSLGAGADAPTLISV-----DGDALNVGSK--KD 291
Db 1009 LNN-----SATP-----IAAGVDATATGCAVATAGSADSIAMGNKASASAD 1048
OY 292 NKPV-----RITNVAPEKEDVTNVAOLKGVAAQNLNRRIDNV 329
Db 1049 NAVAIGHNSVADRANTVSVSGASERQVTNVAAGTADTDAVNLSQLNLGLITAKOYTDTG 1108
OY 330 DGNAR-----AGIAQAIATAGLVQAVLPGKSMMAIGGTYRGEAGYAIIGYSSISDGNWII 385
Db 1109 VGLRDRDIDGVAALAIATANLPQATIPGRKMTSVGVSSYRQOSALAVGVSSVSGRNVF 1168

QY 386 KGTASNSRGHFGASASVGYOM 407
Db 1169 KFGSGANTRSOVGIGAGVGYOM 1190

RESULT 4

surface protein XFI529 [imported] - Xylella fastidiosa (strain 9a5c)
D82671
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: D82671
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A>Note: for a complete list of authors see reference number A59328 below
A:Accession: D82671
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2059 <SIM>
A:Cross-references: GB:AE003982; GB:AE003849; NID:9106554; PIDN:AAF84338.1; GSPDB:GN001
R:Stimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; B
Brites, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir, H
as-Neto, E.; Docena, C.; El-Doiry, H.; Facinani, A.P.; Ferreira, A.J.S.
A:Authors: Ferreira, V.C.A.; Perito, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kurame, E.E.; Laigt
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsushima, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savasak
M.; Tshabko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Genetics: annotation
A:Gene: XFI529

Query Match 16.1%; Score 332.5; DB 2; Length 2059;
Best Local Similarity 29.3%; Pred. No. 1.1e-10;
Matches 96; Conservative 53; Mismatches 112; Indels 71; Gaps 12;
QY 79 SKDNGKTEVKGATGKSVIEKDKLVTG--KDKGSGNSTDEGGLVTAKEVIDAVNKAAG 137
Db 1792 AKSGGRAEFTYGTGYSQVQNNYGTGVDAAKGETSIS--VADAKEMAVN--- 1844
QY 138 WRKTTTANGOTGADKFEFTVTSGTNVTFAAGKGTATVSKDDGNTTAVYDVNVDALN 197
Db 1845 LRQIDAVAAOKSNLQTDLM-----RHEINIEDVFKIKGD--S 1880
QY 198 VNOLONGMNLDSKAVAGSSGKVTSGNVSPSKGMDVTVMNNGNIEIRNCKNIDIAI 257
Db 1881 ASSYKMGVN---AMAIGTMAAASGTESVALGK---NTNVASNAVAI--GNG----- 1925
QY 258 SMTPOFSSVIGAGADAPTLSDVDALNVGSKKDKNPVRTTNVAPGKGVDTVAQDLG 317
Db 1926 SVADRAVSIVSGS-----GSEK-----QYTNVAAGTADDAVAVSGLNQ 1965
QY 318 VAONLNRRIDNVGNAR---AGIAQAIATAGLQVAVLPKGSMAIIGGTYRGEAGYAG 373
Db 1966 GLITAKQYTDGMVGNLRRRTSGVAAAIATANLQAVYQGRGMSVGSVSSYQGSALAVG 2025
QY 374 YSSISDGNMNLIGTASNSRGHFGASASVGYOM 407
Db 2026 VSAVSESGHWFKFGSGSANTRSHVGVAGVGYOM 2059

RESULT 5
A86036
probable adhesin 25029 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: A86036
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A86036
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1588 <STO>
A:Cross-references: GB:AE005174; NID:912518349; PIDN:AAG58749.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: z5029

Query Match 16.0%; Score 331; DB 2; Length 1588;
Best Local Similarity 26.8%; Pred. No. 9.7e-11;
Matches 117; Conservative 59; Mismatches 168; Indels 92; Gaps 15;
QY 46 TYOASANNVDFRTYDFEFLSADTKTNTVNESKDKGKTEVIGAKTSVYKEK----- 100
Db 1171 TVKQLQAIAGAVATTPPKRYHANSTEDSLAVGT-----DSLAMGAKTIYNGDKGIGIC 1224
QY 101 -----DGKLVYTKDKGE-----NGSFTDEGGLVTAKEVIDAVNKAAGWRMKT 142
Db 1225 YGAYVDANALNGIAIGSNAQVIHNSIAIGNSTTGAQNTYATVANNDAPONSVGEFSV 1284
QY 143 TTANGQ-----TGADKREFTVTSGTNVTFAAGKGTATVSKDDGNTTAVM----- 187
Db 1285 GSADGGQQTITNVAAGSAD-----TDAVNV--GOLKVTDAQVSQNTQ--STNLNDRVNTLD 1336
QY 188 -----YVNVGDAI-----NVNOLONGMNLDSKAVAGSSGKVTSGNVSPSKGKM 232
Db 1337 SRVNTENGIDIVTTGSGTKFYKNTTGTGVDASAGKRSVAIGSSISIAADNSVALGGSV 1396
QY 233 ---DETVINAGNNIEITRN---GKN---IDIAISMTPOFSSVIGAGADAPTLSDVDG 282
Db 1397 ATEENTISVGSSTNQRRITNVAAKNATDAVNVQALKSESGAGVRYTPDKDG---SIDYS 1453
QY 283 ALNVGSKKDKNPVITVNAAGVYKRGDVTNNAQLKQVQ-----NLNNRIDVNDG 331
Db 1454 NITLGG--GNGGTRTISVNSAGVNNNDVNVNAQLKQVETKQYTDORVENVENKLSKTES 1512
QY 332 NARAGIAQAIATAGLQVAVLPKGSMAIIGGTYRGEAGYAGYSSISDGNMIRKGTASG 391
Db 1513 KLSGCIASAMAATGLPQATYTPGASMASIGGTYNGESAVALGVMSANGRMVYKLOGST 1572
QY 392 NSRGHFGASASVGYOM 407
Db 1573 NSCGEYSALGAGIOW 1588

RESULT 6
H91188
probable adhesin ECs4480 [similarity] - Escherichia coli (strain O157:H7, substrain R
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001
C:Accession: H91188
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hatlori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: H91188
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1588 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA837903.1; PID:913363955; GSPDB:GN00154
C:Genetics: annotation
A:Gene: ECs4480

Query Match 16.0%; Score 331; DB 2; Length 1588;

QY	46	TVQASANNVDFVRYTDFVEFLSADTKTTYNVESKDNCKTEVKIGAKTSVIKER-----	100
Db	1171	TVROLONAGAVATTPKRYFHFANSTEDSLAVGT-----DSLAMGAKTIYNGDKIGIG	1224
QY	101	-----DGKLYTGKRGKE-----NGSSTDEGEGLVTAKEVIDAVNKGKGRMKT	142
Db	1225	YGAVYDANALNGAIGSNAQYIHVNSAIGSGSTTTRCAQNTYAYANNDAQNSGEFSV	1284
QY	143	TTANGQ-----TGQADKFETVTSQTNVTPASCKGTATVSKPDQGNITWM-----	187
Db	1285	GSAPGQGNQITVNAAGSAD-----TDAVNV--GQLKYIDAQVSOQTQ--STHLDNRVYTL	1336
QY	188	-----YDVNNGDAL-----NVNOLONGMNLDSKRAVAGSSGKVIISGVSPSKGM	232
Db	1337	SRVTNIENGIGDIYTGSTKRYKTNFTDGVDSAQGDVSALIGSGSIAMAADNSVALGTCVS	1396
QY	233	---DEVTYNINAGNNIEITRN---GKN---IDTATSMTPQPSVSLGAGADAPLLSDGD	282
Db	1397	ATEENTTISVGSSTINQRRITNYAAGKNATDAVNAQLQSSEAGVGRYDTRKADG---SIDYS	1453
QY	283	ALANYSKDKNCPVRIITNVAPGVEKEDVTYNAQLKGVAQ-----NLNNRLIDNVG	331
Db	1454	NITLIGG--GNGGTTIISNVSAGVNNNDVYNAQLQSQVETQYTDQRREVEDNKILSTES	1512
QY	332	NARAGIAQAITAGLVQAYLPGKSMALIGGTYRGEAGAYAGYSISIDGNNIITKGTAS	391
Db	1513	KLSGGISASAMAMTGLPQATYTPGASMASIGGTYNGESAVALGVMSVANSGRWYVKLGOST	1572
QY	392	NSRHFPGASASVGYOW	407
Db	1573	NSQGEYSALGAGIOW	1588

```

RESULT 7
AC0976
Probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serovar Typh
C:Species: Salmonella enterica subsp. enterica serovar Typhi
C:Note: This species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AC0976
R.Parikhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
th, T.; Comerston, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0302; MUID:21534947; PMID:11677608
A:Accession: AC0976
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1107 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD03303.1; PID:g16f504923; GSPDB:GN00176
C:Genetics:
A:Gene: sapB

Query March      15.5%   Score 320; DB 2; Length 1107;
Best Local Similarity 26.7%; Pred. No. 2.6e-10;
Matches 115; Conservative 59; Mismatches 176; Indels 80; Gaps 15;

OY    46 TVQASANNVDFVRTDVEFLSADTK--TTTVANESKDKNGKKEFEVK-----IGAKTSVI 97
||| : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : |
Db    690 TVRLQLAIGAIVTTTTPKRYHANSTEEDSLAVGIDSLAMGAKTIVNMDAGIGICILNTLVM 749

OY    98 KEKDGLVTGKNGE-----NGSSTDGC-EGLVTAKEVIDAYNKAGRMKRTTANG 147
||| : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : |
Db    750 ADAINGIAIGSNANFANHSIANGNSQTFRGAOTDTAYAMMDTPQSVMG-EFSVGSDG 808

OY    148 Q-----TGQAOKFEFTVYSTINTFPASGGKTATVSKDDOGNTTYADVA----- 191
||| : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : |
Db    809 QRQITNVAAAGSAD---TDVVNV--GQLKVTAQVSRMTQSITNLNLTQVSNLDRVTNI 861

```

192 ----VGDLALNVQNLQNSGWNLD-----SKAIVSGSSGKYSIGSVSPSKG---MBETVN 237

Db 862 ENGIGDLYVTGSGIKFYFTNTDGDADANAQAGASVIGSGSTAAENSVALGTNSVADBA NT 921

QY 238 INAGNNIEITR-----NGKNIDIATSMTPQFSSVSLGACADAPTLVSDGDALNVGS 288

Db 922 VSVGSSITQORRITNVAAGVNNNTDAVNVAAQLKASAGSVRETNADG---SVNYSVLNLD 978

QY 289 KKDKNKPVRIITNVAAGVEGDTVTNVAQLKVAQ-----NLNKRINDVGNARAGI 337

Db 979 GSGG-TRIGVNSAAVNDTDAVNVAAQLKRSVEANFTYTDKMGEMNKKIGIEKMSGCI 1037

QY 338 AQAATATGLOAVLYPCKSMMAIGGTYRGEGAGVIAIGSSISDGNMTIIRKCTAGSNGRHF 397

Db 1038 ASAAAMAGLPDAVAPGAMNTSINAGTNGESAVALGVISVSESGGWYKLGTSNSGQDY 1097

QY 398 GASASVGVQW 407

Db 1098 SAAIGAGFQW 1107

RESULT 8

AH0110

Probable surface protein (partial) YP00902 [Imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis

C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001

C:Accession: AH0110

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G

11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell

Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AH0110

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-658 <KUR>

A:Cross-references: GB:AL590842; PIDN:CA89747.1; PID:g15978974; GSPDB:GN00175

C:Genetics:

A:Gene: YP00902

Query Match 14.9%; Score 307.5; DB 2; Length 658;

Best Local Similarity 26.1%; Pred. No. 6.8e-10;

Matches 115; Conservative 65; Mismatches 176; Indels 85; Gaps 16;

QY 3 KITVIINNSALNMYVYSELTRNHTKASATVTAVL---ATLLFATVQASAN--NVDFV 57

Db 267 KITGVAAAGSSSDAVNVAOLTAAGDVOQONTANTISLGNVYTTIEGSMASIANGGGVKY 326

QY 58 RTYDT-VEPLSADTKTTTVNVESKDNCKT-----EVKIGAKTSVYKEKDGKLTGVKDK 110

Db 327 HANSTQPDVSAAGTNSVAIGPALSASNALASGAGVAIG--DGAASADSGSVALIGQS 384

QY 111 GENGSSYDEEGELTAAKEVIDAVNKAQMRMKTTTANGCOTGQADKFTVTSCTNVTPASGK 170

Db 385 GDNCRGVENYIG-----KYSNASNTSSG-----TVSGNTAT----- 416

QY 171 GTTATVSKDDQGNITTVAVDVNGDALNVNQLQNSGWNLDKAVAGSSGKYSISGVSPSKG 230

Db 417 GETRTVSVNADG-----LQARDVAVNLRLDGG-----IASIVVENNVNSGLQN 459

QY 231 KMETVAININGNNI-ETTRNGKNIDI--ATSMTPQFSSVSLGACADAP-----TL 277

Db 460 GTDGMFQVNNSSGLAKSATGANSATGCAASVSGNNSTAFSGGAKATTAANSALGANSV 519

QY 278 SYVDGALNVGSKKDNKEPRTTNVAPGVKEGDTVTNVAQLKVAQN---LNKRINDVGNARAGI 333

Db 520 ADRANSVSVGSGNER--QITNVAAPATQGTDAVNFQDLKTSISQNTAANYTNQRYSELKQDL 577

QY 334 R-----AGTAAIATAGLVQAVLPCKSMMAIGGTYRGEGAGVIAIGSSISDGNMTIIR 386

Db 578 RKONSVLSAATIASMAASLTOPYTGSSMTTIGAAISYROSALSLGSSVSSISDGRWVSK 637

C:Genetics:
A:Gene: Yaph

Query Match 9.1%; Score 188.5; DB 2; Length 3705;
Best Local Similarity 23.3%; Pred. No. 0.023;
Matches 113; Conservative 61; Mismatches 184; Indels 127; Gaps 20;

```
OY 1 MNKIRITWNSALNANVVSSELTNRNH--TKRASATVKTAVLATLTFATVQASANNVDFVR 58
DB 1 MNITFKVIMNANSLANVWVSELAQRIKTKSSRNLSISGVLPKPFQSVSKLFRKNLAL 60
OY 59 TYDVEFLSADTKTTTAVVESKDKGKTEVKIGAKTSVIREKDG---KLVNGKKGENG 115
DB 61 SLGSLVFLS-----TGFVPAADITVSTQAEISALS-----NGYDKIILIGADITLLGS 109
OY 116 STDEGEGLVTAKEVIDAVNKKAGWRKTTTANGQTQGAQKFEVTSCTVTFVSGSGTAT 175
DB 110 LT---VNMVTSNQVYIDGGKFGFLVNNNTTNGL-----VSSG-----SGLTLLQN 152
OY 176 VSKDDQGN-----ITWYD-----TVNGDALN-- 197
DB 153 MSKIDSNANYSMVYVLANGTAVNVIYNNIDFLGSSQLLYMGAYGATNSIMTFGLNDV 212
OY 198 -VNOLQNSGMNLDKRAVAG-----SSGKVISGNVSPSKGMDVYVINAANNIETTRNGK 251
DB 213 VVNDRADEIGEVNKLAFGRFHVHTGSSVTSFVSTGGANNSTMDPFSAGADVKIDRTGS 272
OY 252 NIDTATSWTPOF-----SSVSLGAGADAPTLSDGDALNVGSKKDKPVRITVAVGV 304
DB 273 TGDLTSTGVNAFATTFADGASFELIANONVSGTTTNGLEIGSNS-----IDGFGGV 327
OY 305 K-----EGDVTVAQLKVAQNLNRIIDVNDGNARAGI-AQALATAGLVQAVLPPKSM 356
DB 328 KIVLOSRSDDGSIIS-----GNGIDNATNTNA-GAINNNAAGDANVINYLNCTGSIL 375
OY 357 MAIGGGTY-----RGEAGYATGSSISDG-GNMWIK--GTASGNSRGHFG 398
DB 376 KATMTGILATKANNANASDIYIRAGDITTAATGATISATHNGTGVKIKNDGTTSTTAGIAI 435
OY 399 ASAGV 403
DB 436 SSASI 440
```

RESULT 12

S28634

adhesin AIDA-I precursor - Escherichia coli plasmid pIB6

C:Species: Escherichia coli

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 08-Oct-1999

C:Accession: S28634; S22680; S28881; S72657

R:Benz, I.

submitted to the EMBL Data Library, March 1992

A:Reference number: S28634

A:Molecule type: DNA

A:Residues: 11286 <BEN>

A:Cross-references: EMBL:X65022; NID:942254; PIDN:CAA6156.1; PID:942255

R:Benz, I.; Schmidt, M.A.

Mol. Microbiol. 6, 1539-1546, 1992

A:Title: AIDA-I, the adhesin involved in diffuse adherence of the diarrhoeagenic Escheri

A:Reference number: S22680; MUID:92326638; PMID:1625582

A:Accession: S22680

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 839-1286 <BE2>

A:Cross-references: EMBL:X65022

A:Experimental source: strain 2787

A:Accession: S28881

A:Molecule type: protein

A:Residues: 50-56 <BE3>

A:Experimental source: strain 2787

R:Suhr, M.; Benz, I.; Schmidt, M.A.

Mol. Microbiol. 22, 31-42, 1996

A:Title: Processing of the AIDA-I precursor: removal of AIDA and evidence for the out

A:Reference number: S72657; MUID:97053419; PMID:8899706

A:Accession: S72657

A:Molecule type: protein

A:Residues: 847-856 <SUH>

A:Experimental source: DABC strain 2787

C:Genetics:

A:Gene: plasmid pIB6

C:Keywords: membrane protein

F:1-49/Domain: signal sequence #status predicted <SIG>

F:50-1286/Product: adhesin AIDA-I #status predicted <MAT>

Query Match 9.0%; Score 185; DB 2; Length 1286;
Best Local Similarity 25.4%; Pred. No. 0.01;
Matches 107; Conservative 51; Mismatches 200; Indels 64; Gaps 19;

```
OY 1 MNKIRITWNSALNANVVSSELTNRHTRKASATVKTAVLA--TLLFATVQASANNVDFVR 58
DB 1 MNKAVSIIMSHSRQAMVAVASELARGH-----GFVLAKNTLLVLAIVSTIGNAFAVN 51
OY 59 TYDVEFLSADTKTTTAVVESKDKGKTEVKIGAKTSVIREKDGKLVTKRKGENGSTSD 118
DB 52 ISGTVSSGCTVSSGETQIVYSGRGNATVNSG--TQIV--NNGKTTATVNSSGQNV 108
OY 119 EGEGLVTAKEY---IDAVNKAQWRKMTTANGQTQGAQKFEVTSCTVTFVSGSGTFA 174
DB 109 GTSATISTIVNSGIIQHSVSG---VASATNLISGQNIYINLGHASNTVIFSG----- 159
OY 175 TVSKDDQGNITVMDVNVGDALNVN---QLONSGMNLDKRAVASSSGKVISGNVSPSKG 231
DB 160 -----GNQIT-PSGGITDSTNISGGQOQVSSSGVASTNTTINS--AQNILSEGA 208
OY 232 MDETVINAGNNIETTRNGKNIDTATSWTPOFSSVSLGAGADAPTLSDGDALNVGSKKD 291
DB 209 I-STHISSGQNOYISA-GANATEIYNSGQFQVNSGAVATGTVLSGCTQNVSSGSAI 265
OY 292 NKPVRTVAVAGVEGDVTNVAQLKVAQNLNRIIDVNDGNARAGIAO--AIAFAGLVQA 349
DB 266 STSVYNSGVQVFPAGATVTDVTNVSGGNQNTSS-----GGIYSETTVNVNSGTQNI 315
OY 350 YLPKSNMA-IGGGTYRGEAGYATGSSISDGNMWIK--GTASG---NSRNGHFGASASV 403
DB 316 YSGGSALSNIKGQIYNSEGTAIN-TLVSDGGIQLHNGIGIASGTYVNSGIVNIS-SG 373
OY 404 GY 405
DB 374 GY 375
```

RESULT 13

AB3486

cell surface protein [imported] - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002

C:Accession: AB3486

R:DelVecchio, V.G.; Kaparatl, V.; Redkar, R.J.; Patra, G.; Mujfer, C.; Los, T.; Ivanov

.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit

A:Reference number: AD3252; PMID:11756688

A:Accession: AB3486

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-365 <KUR>

A:Cross-references: GB:AE008917; PIDN:ALU53053.1; PID:917983913; GSPDB:GN00190

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BME1872

A:Map position: 1

Query Match 8.9%; Score 183.5; DB 2; Length 365;
Best Local Similarity 23.1%; Pred. No. 0.0027;
Matches 77; Conservative 38; Mismatches 82; Indels 137; Gaps 11;

```

0Y      179 DDQGNIT--VMYVNNVGDALNNVQLNSGNMIDSKAAGSSGKATISGNVSPSKRKMDETIV 237
           ::||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      29  ENLAINIDILHDIESGGGKIFYEHSNIG--ADSRAGTNSIAVSDSVASGEG-----S 80
           ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
0Y      238 INAGNNIETTRGKNIIDIAITSMTPQSSVSLGA-----DAP 275
           |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      81  ISVNGAQAASHAGSVALGENAPPAIDANSVALGSGTSEVYATKGTITNGQYIDFAGDAP 140
           ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
0Y      276 -----TLSVGDALNV-----286
           ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      141 SGTSVGDKGAERTITTNVAAGRISEVSTIAVNSQLNAANQALENLAAQTEMDKRSVKY 200
           |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
0Y      287 -----GSKKDN-----KPVRIITNVAPGYKEGDTVNAOLK--GVAONLNNRIDNVG 331
           ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      201 DRHSDGTKKNSMTLQGMDSATPVYLANVADGVHKNDNAVNVNSQLKAGLSTLLGSAKAYTDQ 260
           ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
0Y      332 NARAGIAQA-----IATAGLVQAYL-----PGKSMATIGG 362
           |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      261 TALQTLIDANAYTTDKKFGKLNEDIYATRIEAROAAAIGLAASLBRDPRCKISAAIGCG 320
           ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
0Y      363 TYRGEAGYALG-----YSSIDGGNMW 383
           ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      321 FWRGEGAAVALGLGHTSDEQRMRSNUSIAAATSGGWN 354
           ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

```

RESULT 14
HB3135
probable adhesin PA4082 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-dec-2000
C:Accession: HB3135
R:Stover, C.K., Plam, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: HB3135
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1*1018 <SRO>
A:Cross-references: GB:AE004824; GB:AE004091; NID:g9950277; PIDN:AA607469.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4082

```

Query Match	8.58;	Score 175.5;	DB 2;	Length 1018;
Best Local Similarity	20.38;	Pred. No. 0.026;		
Matches 113; Conservative	72;	Mismatches 209;	Indels 163;	Gaps 22;

```

0Y      1 MNKIYRIITWNSALNANVVYVSELTFRNHFRASATKTVLALLLEAT----- 46
      ||| : : : : : ||| : : : : : |||
Db      1 MNKCALVANNVSOQCMWNVSEGSRRRGKPAQAKAALASVLLALLGATLAPALYPSGGTV 60
0Y      47 VOASAN-----NVD-FVRYTDFVEELASDRTKTTTVNYESKNGKKTVEKI 90
      ||| : : : : : ||| : : : : : |||
Db      61 VGSANGNGIHLSGGMSLSVNOKVDKLIANMDS--FSAAGERYLFNPQSSSIALNR-I 117
0Y      91 GAKTSVVK--EKDGKLVYTKRDKG--ENGSTDEGEGLVTAKEVIDAV--NKAGWEMK 141
      ||| : : : : : ||| : : : : : |||
Db      118 GTKASDIDGRIIDANQVFLVNPNGVLFGRGAQVNVNGVLVASTLDTITDAEFNGNSRYRET 177
0Y      142 TTTANGQIGQADKFEYTVTSGTNVTFAS-----GKGTITAVSKDDOCNI 184
      ||| : : : : : ||| : : : : : |||
Db      178 GPSTNGVNLNHGGAITTAEGGSIALLAGAQVNDRGVTLVLAQMGGVGLGAGSDTLTLDNGNKL 237
0Y      185 TVMYDVANVGDA LN-----VNOLONSGGMNDUSKRVAGSSGKVI 221
      ||| : : : : : ||| : : : : : |||
Db      238 DIRVDAGVANNALASNGGLLKADGGRVYLMAAFTANALLTVVNSOGAITEARSLRGKNGKIV 297
0Y      222 SGNVSPSKGMDYEVNINA-----GNNIETTRNGKNIDATISMP----- 261
      ||| : : : : : ||| : : : : : |||

```

```

Dh      298 LDDGPPGKVMVGGALSLANMLNCPHGCTYEVRGQAVEALCTQYNTLASNGLNCTWKLIAA 357
      262 -----QESSYSIGACADAPTL-----VDGALNWSKRD 291
      : : : : :
      : : : : :
Dh      358 DKIDVRSAVSDCVTHADTLRNLSLSTNIELVSTKGLDLDGSVNMASGMRLLIGSAMAD 417
      292 ---NKPRITNVNAPGVK---EG-DVTYNAOLKGYAONLNRRID---AVDGNARAGIA 338
      : : : : :
      : : : : :
Dh      418 LTLNGRLMSGAKAGLELKAEGAIIDINDKTYIGGAGSL--AMDAEGSHRYNGLIASYLA 475
      339 QAIAT-----AGLVQAYLEPKSM--MAIGGTYRGEAGYAIGSYISDGGNMI 385
      : : : : :
      : : : : :
Dh      476 GANATVYSGGYTTVQNLQALQAIKRNKLDGLYVLGNMILGSSYCYTALQISG- GPAGVF 534
      386 KGTAS--GNSRGHFAS 400
      : : : : :
      : : : : :
Dh      535 SGTLDLIGNSIGNLSIS 551

```

RESULT 15
ydek protein - Escherichia coli (strain K-12)
A:Accession: A64905
N:Alternate names: protein T
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence-revision 17-Sep-1997 #text-change 01-Mar-2002
C:Accession: A64905; 152440; S34315
R:Blattner, F.N.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M...
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A>Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: A64905
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Crosses: 1-D325 <BLAT>
A:Cross-references: GB:A0000248; GB:U00096; NID:g1787783; PIDN:AAC74583.1; PID:g1787777
A:Experimental source: strain K-12, substrain M61655
R:Cartwright, P.; Tims, M.; Lithgow, T.; Hoj, P.; Hoogenraad, N.
Biochim. Biophys. Acta 1153, 345-347, 1993
A>Title: An Escherichia coli gene showing a potential ancestral relationship to the g
A:Reference number: 152440; MUID:94100243; PMID:8274505
A:Accession: 152440
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 685-883, 'K', 885-1316, 'S', 1318-1325 <RES>
A:Cross-references: EMBL:X73295; NID:g312392; PIDN:CAA51730.1; PID:g312393
A>Note: the difference in length is due to a frameshift error at pos 653
C:Genetics:
A:Gene: ydek
C:Function:
A:Description: probably involved in protein translocation apparatus
C:Keywords: nucleotide binding; P-loop
E:712-719/Region: nucleotide-binding motif A (P-loop)

Query Match	8.5%;	Score 175;	DB 2;	length 1325;
Best Local Similarity	21.5%;	Pred. No. 0.038;		
Matches 122; Conservative	58;	Mismatches 200;	Indels 188;	Gaps 23;

```

OY 1 MNKIYRIIMNSALMANVYVSELTR-----NHKRSATYKPAVLATTLFATVQASAN 52
   ||:||||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MNRIRYIMNCTQVQFQACSELTRRAGKTSTVNLKRSSGGLTTRSLVLGVLALLSGSAS 60
OY 53 -----NVDFEPTTYD-----TWELFSLADPTKTTT-T 74
   ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 GASLEVDNDQITIIDPDVAYDAYLWGYSTGVNLTLLAGSNASLTTITTSVIGANDEBEGT 120
OY 75 VNV-----ESKDNKRTTEV-KIGAKTSVIKE---DGLKLYTGKDKGENSGSTDEGE 121
   |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 VNVLGCGWRLRYDGSNNAPRLNVNGQSGSTGTLNKQGHGHDVGLRLGSGSTGVGVTVNEGE 180
OY 122 GLVYAKAEVD-----AVNKAG-WEMKTTT 155
   . ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 DSVLTTELEFPIGSGYGLSINTIDKGYSVSAIILGYQAGSNGGVVEKGEEMLIKINDS 240

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Oy 146 -----NGORGAOKFEIVNIGSTNVT-----ASCKGTATVSKDQGIITVMYD- 189
      | ||| | |
Db 241 SIEROIGNOGTEA---TIREGLVTAEWNTIIGGNATIGTLNVODODSVITVRRLYNG 296
      | ||| | |
Oy 190 -----VYNGDALN--VNOLONGMWL-----D 209
      | ||| | |
Db 297 YFGNCTVAINSNNGLINNKEYSLVGYQODSGHGVYVNTDKGHMNF LGTEAFRIY IODAGD 356
      | ||| | |
Oy 210 SKAVALSSGKYISGNVSPSKGMDT-----VINAGNNIETIRNGKNIDIAF 257
      | ||| | |
Db 357 GELNVSPSEKVDSGIITAG---MKETGNGTIVTKDKNSVTYMLGTMLGDGHGEMMISNQ 413
      | ||| | |
Oy 258 SMTPOFESSYISGAGDAPTLSDGALNVGSKD--NKPYRITNVAPEVGEADYTNVAOLK 316
      | ||| | |
Db 414 GLVYVNSGGSSJLGYG---ETGVGNYSITGGKMEVKNKYTTIGVAGVGNLMSDGG--K 467
      | ||| | |
Oy 317 GVAQNLNRRIDNVQSNARAGINQAATATAGVQAYLP--CKSMALIGCGYRREAGCAI-- 372
      | ||| | |
Db 468 FVSONITFLGKXASGIGTLMLMDAASSDETVGAINVGNFSGIIVVNSNGATLMSYTGFGTG 527
      | ||| | |
Oy 373 -----GYSSISDGGNMIITKFGASGNSR 394
      | ||| | |
Db 528 GNASCKGIYVNSTDSLMNLK--TSSINAQ 554

```

Search completed: October 6, 2003, 09:33:19
Job time : 13.6505 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2003, 09:06:20 ; Search time 6.28512 Seconds
(without alignments)
3045.266 Million cell updates/sec

Title: US-09-771-382-25
Perfect score: 2063
Sequence: 1 MNKIYRIIWSALNMAVYVS.....TASGNSRGHFGASASYGYOM 407

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	185	9.0	1286	1 AIDA_ECOLI	Q03155 escherichia
2	175	8.5	1325	1 YDEK_ECOLI	P32051 escherichia
3	171.5	8.3	1039	1 AG43_ECOLI	P39180 escherichia
4	155	7.5	2003	1 YDBA_ECOLI	P33666 escherichia
5	149.5	7.2	930	1 PMP8_CHLPN	O92393 chlamydia p
6	145.5	7.1	1300	1 120K_RICRI	P14914 rickettsia
7	145.5	7.1	1654	1 OMPB_RICRI	O53047 r outer mem
8	145	7.0	1953	1 BIGA_SALTY	P25927 salmonella
9	143	6.9	933	1 SLAP_CAME	P35827 campylobact
10	142.5	6.9	550	1 FLIC_SHIFL	O08860 shigella fl
11	141	6.8	1025	1 SLAP_CANCR	P35828 caulobacter
12	141	6.8	1645	1 OMPB_RICRY	P96989 r outer mem
13	141	6.8	1655	1 OMPB_RICCN	O9KX83 r outer mem
14	140.5	6.8	1608	1 HLVA_SERMA	P15330 serratia ma
15	139.5	6.8	1861	1 APU_THERU	P15836 t amylopull
16	139.5	6.8	3178	1 YS89_CABEL	O09634 caenorhabdl
17	138.5	6.7	1567	1 ICEN_XANCT	P18127 xanthomonas
18	138	6.7	2660	1 YEEB_ECO57	O8X877 escherichia
19	137.5	6.7	1569	1 YFJA_ECOLI	P52143 escherichia
20	136	6.6	497	1 FLIC_ECOLI	P04949 escherichia
21	136	6.6	2249	1 OMPA_RICRI	P15921 rickettsia
22	135	6.5	455	1 YADA_YEREN	P14499 yersinia en
23	135	6.5	1592	1 GTF2_STRPO	P27470 streptococc
24	135	6.5	1656	1 OMPB_RICJA	O06653 r outer mem
25	134	6.5	1928	1 HXA2_HAEIN	P45354 haemophilus
26	133	6.4	2021	1 OMPA_RICCN	O52657 rickettsia
27	131	6.3	434	1 YADA_YERPS	P10858 yersinia ps
28	131	6.3	928	1 PM10_CHLPN	O9B65 chlamydia p
29	131	6.3	1398	1 TOP2_PLAFL	P41001 plasmodium
30	130.5	6.3	1523	1 P60_LISSE	O01838 listeria se
31	130.5	6.3	1210	1 ICEN_PSEFL	P09815 pseudomonas
32	130.5	6.3	1577	1 HLVA_PROMI	P16466 proteus mir
33	129.5	6.3	575	1 FLA2_CAMJE	P22251 campylobact

34	129.5	6.3	716	1 CX80_EUPOC	O9N9X3 euplotes oc
35	127.5	6.2	367	1 FLIC2_PROMI	P42273 proteus mir
36	127.5	6.2	445	1 G6PI_BACTN	O8A5W2 bacteroides
37	127.5	6.2	880	1 LYTD_BACSU	P39848 bacillus su
38	127.5	6.2	1148	1 ICERK_PSEBX	O30611 pseudomonas
39	127.5	6.2	1153	1 PVDB_PLAKN	P50453 plasmodium
40	127	6.2	366	1 PGLB_ASPFL	P41750 aspergillus
41	127	6.2	461	1 US45_LACTIC	P22865 lactococcus
42	127	6.2	524	1 P60_LISME	O01839 listeria we
43	127	6.2	2358	1 YEEB_ECOLI	P76347 escherichia
44	126.5	6.1	1007	1 Y741_CHLMU	O9PJ16 chlamydia m
45	126	6.1	1076	1 NUP1_YEAST	P20676 saccharomyc

ALIGNMENTS

```

RESULT 1
AIDA_ECOLI
ID AIDA_ECOLI STANDARD; PRT; 1286 AA.
AC 003155;
DF 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adhesin aida-I precursor.
GN AIDA-I.
OS Escherichia coli.
OG plasmid PIB6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 50-56.
RC STRAIN=0126:H27 / 2787;
RX MEDLINE=9232636; PubMed=1625582;
RA Benz I., Schmidt M.A.;
RT "AIDA-I, the adhesin involved in diffuse adherence of the
RT diarrhoeagenic Escherichia coli strain 2787 (O126:H27), is
RT synthesized via a precursor molecule.";
RL Mol. Microbiol. 6:1539-1546(1992).
CC -!- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE
CC -!- ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI
CC TO EPITHELIAL CELLS.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; X65022; CAA46156.1; -.
CC PIR; S28634; S28634.
CC DR InterPro: IPR006315; Autotransport.
CC DR InterPro: IPR005546; Autotransporter.
CC DR InterPro: IPR004899; Peractin.
CC DR Pfam: PF03797; Autotransporter; 1.
CC DR Pfam: PF03212; Peractin; 1.
CC DR TIGRFAMs: TIGR01414; autotrans_parl; 2.
CC KW Cell adhesion; Signal; Outer membrane; Plasmid.
CC FT SIGNAL 1 49
CC FT CHAIN 50 1286 ADHESIN AIDA-I.
CC FT PROPEP ? 1286
CC SQ SEQUENCE 1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;

Query Match 9.0%; Score 185; DB 1; Length 1286;
Best Local Similarity 25.4%; Pred. No. 0.0048;
Matches 107; Conservative 51; Mismatches 200; Indels 64; Gaps 19;
OY 1 MNKIYRIIWSALNMAVYVSELTRNHTKRASATVKTAVLA--TLLEFTVQASANNDFVR 58
||| | ||| : ||:| ||| | ||| ||| | : : |

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```
DB 1 MNKAVSIWHSRQAMVIYASELARGH-----GVLAKTLLVLAVSTIGNAPAVN 51
QY 59 TYDVEFLADTKTTTNNVESKDKGKTEVIGAKTSYIKERDKLVTGDKGENSGSTD 118
DB 52 ISGTVSSGCVTSSTGFTQIVYSGRNSNATVNSGC-TQIV--NNGKTTATVYNSGSGNV 108
QY 119 EGEGLVTAKEY-----IDAVNKAQWPMKTTTANGTGQADKFTVTSNTVTFASKGTTA 174
DB 109 GTSQATISTIVNSGCIQHVSSSG-----VASATNLISGGAQNIYINLHASVTYLFSSG----- 159
QY 175 TVSKDQDNITVMYQVNVGDLNLNV--OLONSGMNLDSKAVAGSSGVISGNSPSSGK 231
DB 160 -----GNQTI-FEGGTTDSNTNISGGQQRVSSGCVASNTTINSG--FQNLISEBA 208
QY 232 MDETVINAGNNIETTRNGKNIDATSMTPQSSVSLGAGADAPPLSYDGDALVNSKRD 291
DB 209 I--STHISSGNGVYISA-GANATERIVNSGCFQVRVNSGVAATGVLTSGGTQVSSGSAI 265
QY 292 NKPVATITVAPGVKRGSDVTYNNVAQLKGVANLNLRIDNDGNARAGIAQ--AIATGLVOA 349
DB 266 STSVYNSGVQVFPAGATVTDPTVNSGNGQNTISS-----GGIVSETTVNVSGTQNI 315
QY 350 YLPGRKSMMA-IGGGTYRREGAGYAGYSSISDQGNMIR--GTPASG--NSRGHFGASASY 403
DB 316 YSGGSAISANIKSGQIVNSEGTALN-TLYSDGCTYHNRNGTASGTYVNSGTYNIS-SG 373
QY 404 GY 405
DB 374 GY 375

RESULT 2
YDEK_ECOLI STANDARD; PRT; 1325 AA.
ID YDEK_ECOLI STANDARD; PRT; 1325 AA.
AC P32051: P76140; P77168:
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical lipid protein ydek precursor (ORF1).
GN YDEK OR ORF1 OR B1510.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley J., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirovpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aliba H., Baba T., Fujita K., Hayashi K., Inada T., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakano S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Sampaio G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:365-377(1996).
RN [3]
RP SEQUENCE OF 595-1325 FROM N.A.
RX MEDLINE=94100243; PubMed=8274505;
RA Carwright P.J., Tims M.W., Lithgow T., Hoef P.B., Hoogenraad N.J.;
RT "An Escherichia coli gene showing a potential ancestral relationship
to the genes for the mitochondrial import site proteins ISP42 and
```

```
RT MON38."; Biophys. Acta 1153:345-347(1993).
RL Biochim. Biophys. Acta 1153:345-347(1993).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential).
CC -1- SIMILARITY: TO E-COLI YEAL.
CC -1- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
CC ISP42 AND MON38.
CC -1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 653.
CC -----
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CC or send an email to license@isb-sdb.ch).
CC -----
DR EMBL: AE000248; AAC74583.1; -.
DR EMBL: D90793; BAA15190.1; ALT_INIT.
DR EMBL: D90794; BAA15197.1; ALT_INIT.
DR EMBL: X73295; CAA51730.1; ALT_FRAME.
DR PIR: A64905; A64905.
DR Ecocyc: B31780; ydek.
DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
KW Hypothetical protein; Membrane; Lipoprotein; Signal;
KW Complete proteome.
FT SIGNAL 1 18
FT CHAIN 19 1325
FT LIPID 19 19
FT CONFLICT 884 884
FT CONFLICT 1317 1317
FT CONFLICT M -> S (IN REF. 3).
SQ SEQUENCE 1325 AA; 136514 MW; 26A3A06FA19AD7D CRC64;

Query Match 8.5%; Score 175; DB 1; Length 1325;
Best Local Similarity 21.5%; Pred. No. 0.018;
Matches 122; Conservative 58; Mismatches 200; Indels 188; Gaps 23;

QY 1 MNKAVSIWHSRQAMVIYASELARGH-----NHTKRASATVKTAVLATLTPATVQASAN 52
DB 1 MNRIYRVLINMCTLOQFQACSELTFRAGTSYVNLKSSGLTKFRLFLGVLALSGSAS 60
QY 53 -----NDVFRTYD-----TYEFLSADPKTT--T 74
DB 61 GASLEVDNDQITNIDTDVAYDAVLVGYGTGLNLIAAGNASLTITTSVIGANDSSET 120
QY 75 VNV-----ESKNGKRTVEY-KIGAKTSYIKER-----DGKLVGKDKGENSGSTDGE 121
DB 121 VAVLGCTMRKLDSDGNMARNPLVNGSGTGLTNIKQGHVDGTVLRGSGTGVYVNSGE 180
QY 122 GLVTAKEYID-----AVNKAG-WRMKTTTA 145
DB 181 DSVLTTEFLFEGISYGTGSLNITDKGYVTSIVAIIIGYQAGSNGYVVEKGEMLIKNDS 240
QY 146 -----NGQFGQAKFEYVTSCTVTF-----AGSKGTATVSDDDQNTITVMD- 189
DB 241 SIEFOIGNQGTGEA--TIREGGLVTAENTIIIGNAGTIGLNVQDDSVTVRLLYNG 296
QY 190 -----VNVGDALN--VNOLQNSGMNL-----D 209
DB 297 YPGNGTVINSNNGLINKKEYSIVGYQDSDSHGVVNTDGHWNFLGTGEAFRIYITGDACD 356
QY 210 SKAVAGSSGKVISGNVSPSKGMDT-----VINAGNNIETTRNGKNIDAT 257
DB 357 GELNVSSSGKVDSGIITAG--MKETGICNTIVKDKNSYITMLGTNLGYDGHGEMNISNQ 413
QY 258 SMTPOFSSVSLGAGADAPPLSYDGDALVNSKRD-NKPYRTITVAPGVKRGSDVTYNNVAQLK 316
DB 414 GLVNSNGSSSLGYG-----ETGVGNYSITTGGMMEVKNKYITIGVAGGNLINSISGG--K 467
QY 317 GVAONLNNRINDVDDNARAGIAQATATAGLVQAYLP--GKSMATIGGGTYRREGAGYAI-- 372
DB 468 FVSQNTITFLGDKRASGITGLNLMDATSSPDYGVINAGNGSGIYVNSGATNLNSTGTGFLG 527
```

OY 373 -----GYSSIDSGMNIINGTAGNSR 394
DB 528 GNASGKGIWNISFSLMNLK-TSSTNAQ 554

RESULT 3
AG43_ECOLI STANDARD; PRT: 1039 AA.
AC P39180; P75614; P76360; P97241; Q46771;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 43 precursor (AG43) (Fluffing protein).
GN FLU OR B2000.
OS Escherichia coli.
OC Bacteria: Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasei H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,
RA Sivasubramanian S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horiiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 4.0-1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ML 308-225;
RA Henderson I.R., Owen P.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PRELIMINARY SEQUENCE OF 53-78.
RC STRAIN=ML 308-225;
RX MEDLINE=99291704; PubMed=2661530;
RA Caffrey P., Owen P.;
RT "Purification and N-terminal sequence of the alpha subunit of antigen
43, a unique protein complex associated with the outer membrane of
Escherichia coli.";
RL J. Bacteriol. 171:3634-3640(1989).
RN [5]
RP SEQUENCE OF 53-63.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
RN [6]
RP GENE NAME.
RX MEDLINE=97257509; PubMed=9103983;
RA Henderson I.R., Meehan M., Owen P.;
RT "Antigen 43, a phase-variable bipartite outer membrane protein,
determines colony morphology and autoaggregation in Escherichia coli
K-12.";
RL FEMS Microbiol. Lett. 149:115-120(1997).
CC -1- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION. MAY

CC FUNCTION AS AN ADHESIN.
CC -1- SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA
CC CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA
CC CHAIN).
CC -1- SUBCELLULAR LOCATION: Outer membrane-associated.
CC -1- SIMILARITY: TO ADHESIN AID-1 AND TO BORDETELLA PERTACTIN.
CC -----
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CC -----
DR EMBL; AE000291; AAC75061.1; ALT_INIT.
DR EMBL; D90838; BAI15825.1; ALT_INIT.
DR EMBL; D90839; BAI15832.1; ALT_INIT.
DR EMBL; U24429; AAB47869.1; -.
DR HSSP; P07505; ISR.D.
DR Ecogene; EGI2686; flu.
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR InterPro; IPR004899; Pertactin.
DR Pfam; PF03797; Autotransporter; 1.
DR Pfam; PF03212; Pertactin; 1.
DR TIGRfams; TIGR01414; autotrans barl; 1.
DR Outer membrane; Signal; Complete proteome.
KW SIGNAL
FT 1 32
FT CHAIN
FT 53 551
FT FT 552 1039
FT VARIANT 2 2
FT VARIANT 41 42
FT VARIANT 46 46
FT VARIANT 157 157
FT VARIANT 188 188
FT VARIANT 303 305
FT VARIANT 320 320
FT VARIANT 372 372
FT VARIANT 493 493
FT VARIANT 497 497
FT VARIANT 585 585
FT VARIANT 709 709
FT VARIANT 721 721
FT VARIANT 751 753
FT VARIANT 803 803
FT VARIANT 815 815
FT VARIANT 824 824
FT VARIANT 829 835
FT VARIANT 845 847
FT VARIANT 855 855
FT VARIANT 888 888
FT VARIANT 1025 1025
FT CONFLICT 61 63
SQ SEQUENCE 1039 AA; 106841 MW; 5170D647C8DEBE0 CRC64;
Query Match 8.3%; Score 171.5; DB 1; Length 1039;
Best Local Similarity 20.3%; Pred. No. 0.021;
Matches 102; Conservative 57; Mismatches 195; Indels 149; Gaps 18;
OY 1 MNKIRIIMNSALNAVVSSELTNRNHTKRASATYKTVAVLATLPRATVOA-----SAN 52
DB 5 LNTCYRLVNMNMTCAPFYVASSLAARGRGVAVALSIAVATSLPVLAAADLVPRGETVN 64
OY 53 NVDFVRYDYVEFLISADTKTTTVNVE-SKDN-----GKTEVYKIG----- 91
DB 65 GGTLANHNDQIVFETGTNGMTSTGLEXPNDANTGQWQODGSTANKTFTVSGLORVN 124
OY 92 -----AKTSVIEKRGKXIVTQK--DKGENGSTDEGELVYNAKVEDVANNKAGMR----- 139
DB 125 PGGSVDPTVIVASGGQSLQGRNAVPTLLNGEGQNMHBEALATGTIVY---NDKGMQVVKPCT 181

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OY 140 MKTTTA-----NGTGQADKFEV-----TSGINVTASGK 171
DB 182 VAITDVVVTGAEAGDPDAENGDTGPGVRAVTTINKNGROIVRAEGTANTVYVAGGQ 241
OY 172 TTAATVSKDDGNTFYAVDVNVDALNVNOLQNSGANTL-DSKRVASSSGRVISGNSPSKG 230
DB 242 TVHGALDPTTLNGVGYVHNGSTASD-TVVNSDGMQIVKNGVAGNTVYNOKGRLOVDAG 300
OY 231 KMDETVINAG-----NNEITRNGKNIDTASMTPOF 263
DB 301 GTAFTVTLKGGALVSTAATVGTINRLGAFSVEGKADNV-VLENGGRDLVLTGHTATN 359
OY 264 SSVSISGA-----GADAPTLV-----DGDALNVGSKKNKRVRTITNAPVKEGDV 309
DB 360 TRVDGGGLDVNRNGTATTVSMGNGVLLADSGAIVSGTRSDGK-----AFSIGGQA 412
OY 310 TVNAOLKGVAAQNLNRINDVNDGNARAGIAQATATAGLVQAVYPRKSMALGGGTGREG 369
DB 413 DALMEKSSFTLN-----AGDTAIDTT-----VNGGLFTTARGG 446
OY 370 YAGYSISIDSGNMIIKGTASGN 392
DB 447 TLAGTTTLNNGAILFLSGKTVNN 469

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RESULT 4

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YD_BA_ECOLI STANDARD; PRT; 2003 AA.
ID YD_BA_ECOLI / MG1655;
AC P33666; P76087; P76088; P76856; P76857; P76859;
DT 01-FEB-1994 (Rel. 28, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ydBA.
GN YD_BA_OR_B1401/B1405.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RA MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RA MEDLINE=97251357; PubMed=9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Sempel G., Seki Y., Sivasubaram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 464-2003 FROM N.A.
RC STRAIN=K12;
RA MEDLINE=92190338; PubMed=1665988;
RA Moszer I., Glaser P., Danchin A.;
RT "Multiple IS insertion sequences near the replication terminus in
Escherichia coli K-12.";
RL Biochimie 73:1361-1374(1991).
CC -1- SIMILARITY: TO S.TYPHIMORIUM ORF NEAR CYSG (AC P25928).
CC CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR
CC THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT
CC BETWEEN AMINO ACIDS 839 AND 840.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE000237; AAC74483.1; ALT_SEQ.
DR EMBL; AE000237; AAC74487.1; ALT_SEQ.
DR EMBL; D90778; BAA15009.1; ALT_SEQ.
DR EMBL; D90778; BAA18880.1; ALT_SEQ.
DR EMBL; D90779; BAA18881.1; ALT_SEQ.
DR EMBL; X62680; -; NOT_ANNOTATED_CDS.
DR Ecocore; EG11307; ydBA.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 489 I -> V (IN REF. 2).
FT CONFLICT 495 495 I -> V (IN REF. 2).
SQ SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220DE CRC64;

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Query Match

Best local similarity 7.5%; Score 155; DB 1; Length 2003;
 Best local similarity 23.1%; Pred. No. 0.36;
 Matches 107; Conservative 59; Mismatches 164; Indels 134; Gaps 25;

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OY 26 HTKRASATV---KTAVALTLLEATVQASANNVDFRYDYVELISADTKT----- 72
DB 164 YTENADGTISLSDSGNRKATINLMQIDEANNV-----ALEGVSADGATKWOYNHNGE 216
OY 73 ---TVNVESKNGKTEKIGAKTSV---IKEDGKIYTGDKENG-----SS 116
DB 217 LVITGDNATVNNNGKTT---VDGKSTGTETLNGNGKVIQDGDLDVSGGHCIDITGDSA 273
OY 117 TDEGGLVYAKE-----VIDA---VKNAGRMKTTTANGTGQADKFEVTVT----- 159
DB 274 TVDNKGTMTVYDPESMGIIQDGAIVNNEG---ESTITNGGTQINGDATTANNNGKT 330
OY 160 -----SGTNVTFASGK-----GTTATVSKDDGNTITVMDVAVG 193
DB 331 TVDGKDSGTETLNGNGKVIQDGDLDVSGGHCIDITGDSATV---DNKGTMTVYDPESIG 388
OY 194 DALANNO---LQNSGNNLSKAAVAGSSKAVISGN---VSPDSK-----MDEFININAGNN- 243
DB 389 IOVDDQAVVNNEG---ESAITNGGTQIINGDDATTANNNGKTTVYDGKDSGTETETAGNNG 445
OY 244 -----IEITRNGKNIDI-ATSMTPQFSVSIAGADAPTLTVSDGDLNVGSKKDNRPV 295
DB 446 KVIQDGDLDVSGGHCIDITGDSATVYDNKGTMTVYDPESIGIQIDGDAIVNNEGES--- 502
OY 236 RITNVAPGVKESDVTNVAOLKGVAAQNLNNR-IDNVGNARAGIAQATATAGLVQAVYLRGK 354
DB 503 TITNGGTG-----TQINGNDATTANNNGKTTVYDGKDSGTG-TRIAGNIGIVN-LDG- 549
OY 355 SMMAIAGGTYREAGVYAGYSISIDSGNMIIKGTASGNSRGHFG 398
DB 550 SLTVTGG-----AHGVENIGNGVYNNKGDIVSDTSGIG 584

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RESULT 5

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PMP8_CHLPN STANDARD; PRT; 930 AA.
ID PMP8_CHLPN /
AC Q92393; Q9RB66;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable outer membrane protein pmp8 precursor (Polymorphic membrane
protein 8) (Outer membrane protein 11).
GN PMP8 OR OMP11 OR CPN0446 OR CP0307.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_Taxid=83558;
RN [1]
RP SEQUENCE FROM N.A.

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CC STRAIN-VRI310;
 RX MEDLINE=20007584; PubMed=10539856;
 RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
 RA Madsen A.S., Knudsen K., Falk E., Birkeland S.;
 RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
 RL role in immunopathogenicity.";
 RN Am. Heart J. 138:S491-S495(1999).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CWL029;
 RX MEDLINE=99206606; PubMed=10192388;
 RA Kaiman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
 RN Nat. Genet. 21:385-389(1999).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AR39;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Uitterback T., Berry K., Bass S.,
 RA Linher K., Weiman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gattin M., Nelson W., Deboy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MOpn and Chlamydia
 RL pneumoniae AR39.";
 RN Nucleic Acids Res. 28:1397-1406(2000).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-J138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RL from Japan and CWL029 from USA.";
 CC Nucleic Acids Res. 28:2311-2314(2000).
 CC -1- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
 CC (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: AJ13034; CAB37068.1; -;
 DR EMBL: AE001627; AD18590.1; -;
 DR EMBL: AE002193; AF38164.1; -;
 DR EMBL: AP002546; BA98654.1; -;
 DR PIR: A81591; A81591;
 DR PIR: D72078; D72078;
 DR PIR: D72078; D72078;
 DR PIR: Q92393; -;
 DR TIGR: CP0307; -;
 DR InterPro: IPR006315; Autotransport.
 DR InterPro: IPR005546; Autotransporter.
 DR InterPro: IPR003368; Chlamydia_PMP.
 DR Pfam: PF03797; Autotransporter; 1.
 DR Pfam: PF02415; DUF145; 2.
 DR TIGRPFAMS: TIGR01414; autotrans_pam1.
 DR TIGRPFAMS: TIGR01376; POMP-repeat; 6.
 KM Outer membrane: Signal; Multigene family; Complete proteome.
 FT STGNL 1 26 POTENTIAL.
 FT CHAIN 27 930 PROBABLE OUTER MEMBRANE PROTEIN PMP8.
 FT CONFLICT 177 177 T -> A (IN REF. 3 AND 4).
 SQ SEQUENCE 930 AA; 97669 MW; 46A9B5E3BB913C4C CRC64;

Query Match 7.2%; Score 149.5; DB 1; Length 930;
 Best Local Similarity 22.4%; Pred. No. 0.3; 171; Indels 105; Gaps 19;
 Matches 95; Conservative 54; Mismatches 171; Indels 105; Gaps 19;

QY 26 HTRKASATVKTAVLATLLFATVQASANNVDFVRYDVEELISADTKTTTVNVEBKDKK 85
 Db 6 HKLLISLTVPILLSLTATGADASLSPTD-----SPDGAGGSGFTFKSTADANG-- 55
 QY 86 TEVKIGAKTSYIKEDKLVYCKDKE-NSSSTDEGGGLYAKVDAVNAKGRMKTIT 144
 Db 56 TNYVLSGNVYINDAGKGTALTGCCFETTTDILFTFGKGSFSEFTVDAGSNAGAASTT- 114
 QY 145 ANGTQADKFEFTVSTNTVTPASGKTGTATVSKD-----DQGNITVYDVNV- 192
 Db 115 -----ADKALFTFGSNLSFTAPGTIVASGKSTYSAGALMLTNG--TLFSQNV 165
 QY 193 -----GDALNVOLONGSNNLDSKAVAGSGKVISGNSPKGKMDETVINAGNIEI 246
 Db 166 MEANNNGGALTITTKLTSIG-NTSSITFTSSAKKLGAIISSAA--ASISGNTGOLVFM 221
 QY 247 TRNGK-----NIDIATSMTPQSSV-----SLGAG-----ADAPILSVGDA 283
 Db 222 NNKGETGGALGEFASSSIT-ONSLEFSGNTATDAAGKGAIIYCEKTEGTPTLTISG-- 278
 QY 284 LNVGSKKDNKPRVTNTNAPGVKEDV-TNVAQLKVAQNL--NNRIDVGNMARAIAQA 340
 Db 279 -----NKSLEPAENSVTGGCAICAHGLDLSAAGPTLPSNNRC---GNTAAGGGA 326
 QY 341 IATAGLVQAVLPKSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRC--HFG 398
 Db 327 IATAD-----SGSLSLSANOGDITPLGNTLTITSASPTSTNATYLG 367
 QY 399 ASASV 403
 Db 368 SSAKI 372
 RESULT 6
 ID 120K_RICRI STANDARD; PRT; 1300 AA.
 AC P14914;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 26-FEB-2003 (Rel. 41, Last annotation update)
 DE 120 kDa surface-exposed protein.
 GN P120.
 OS Rickettsia rickettsii.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 CC Rickettsiaceae; Rickettsiae; Rickettsia.
 CC NCBI_TaxID=783;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-R;
 RX MEDLINE=90136087; PubMed=2515418;
 RA Gilmore R.D., Jr., Joste N., McDonald G.A.;
 RT "Cloning, expression and sequence analysis of the gene encoding the
 RL 120 kDa surface-exposed protein of Rickettsia rickettsii.";
 RL Mol. Microbiol. 3:1579-1586(1989).
 CC -1- FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS
 CC RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
 CC S-LAYER WITH HEXAGONAL SYMMETRY.
 CC -1- MISCELLANEOUS: ITS C-TERMINUS POTENTIALLY MAY BEAR THE EPTOPES
 CC CONFERRING ANTIGENICITY TO THE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.
 CC -----
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 CC -----
 DR EMBL: X16353; CA34402.1; -;
 DR PIR: S07575; S07575;
 DR InterPro: IPR006315; Autotransport.

InterPro: IPR005546; Autotransporter.
 DR Pfam: PF03797; Autotransporter; 1.
 DR TIGRfams: TIGR01414; autotrans_bar1; 2.
 KM Antigen; Glycoprotein; Cell wall; S-layer.
 FT CAROYD 66 66 N-LINKED (POTENTIAL).
 FT CAROYD 86 86 N-LINKED (POTENTIAL).
 FT CAROYD 103 103 N-LINKED (POTENTIAL).
 FT CAROYD 147 147 N-LINKED (POTENTIAL).
 FT CAROYD 268 268 N-LINKED (POTENTIAL).
 FT CAROYD 330 330 N-LINKED (POTENTIAL).
 FT CAROYD 375 375 N-LINKED (POTENTIAL).
 FT CAROYD 415 415 N-LINKED (POTENTIAL).
 FT CAROYD 424 424 N-LINKED (POTENTIAL).
 FT CAROYD 430 430 N-LINKED (POTENTIAL).
 FT CAROYD 436 436 N-LINKED (POTENTIAL).
 FT CAROYD 444 444 N-LINKED (POTENTIAL).
 FT CAROYD 515 515 N-LINKED (POTENTIAL).
 FT CAROYD 547 547 N-LINKED (POTENTIAL).
 FT CAROYD 593 593 N-LINKED (POTENTIAL).
 FT CAROYD 655 655 N-LINKED (POTENTIAL).
 FT CAROYD 698 698 N-LINKED (POTENTIAL).
 FT CAROYD 710 710 N-LINKED (POTENTIAL).
 FT CAROYD 799 799 N-LINKED (POTENTIAL).
 FT CAROYD 800 800 N-LINKED (POTENTIAL).
 FT CAROYD 826 826 N-LINKED (POTENTIAL).
 FT CAROYD 844 844 N-LINKED (POTENTIAL).
 FT CAROYD 861 861 N-LINKED (POTENTIAL).
 FT CAROYD 879 879 N-LINKED (POTENTIAL).
 FT CAROYD 920 920 N-LINKED (POTENTIAL).
 FT CAROYD 926 926 N-LINKED (POTENTIAL).
 FT CAROYD 1116 1116 N-LINKED (POTENTIAL).
 FT CAROYD 1128 1128 N-LINKED (POTENTIAL).
 FT CAROYD 1140 1140 N-LINKED (POTENTIAL).
 FT CAROYD 1146 1146 N-LINKED (POTENTIAL).
 FT CAROYD 1211 1211 N-LINKED (POTENTIAL).
 SQ SEQUENCE 1300 AA; 132801 MW; E09F52C3F67243D CRC64;
 Query Match 7.1%; Score 145.5; DB 1; Length 1300;
 Best Local Similarity 22.5%; Pred. No. 0.74;
 Matches 100; Conservative 50; Mismatches 177; Indels 117; Gaps 19;

RESULT 7
 OMPB_RICRI
 ID OMPB_RICRI STANDARD; PRT; 1654 AA.
 AC 053047;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Outer membrane protein B precursor (168 kDa surface-layer protein)
 DE (Surface protein antigen) (Cell surface antigen 5) (Scas5) (ompB)
 DE (omp.B) [Contains: 120 kDa surface-exposed protein (Surface protein
 antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
 GN OMPB.
 OS Rickettsia rickettsii.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Rickettsiaceae; Rickettsiasee; Rickettsia.
 OX NCBI_Taxid=783;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R;
 RX MEDLINE=92167802; PubMed=1724278;
 RA Gilmore R.D., Jr., Cleplak W., Jr., Pollicastro P.F., Hackstadt T.;
 RT "The 120 kilodalton outer membrane protein (omp B) of Rickettsia
 rickettsii is encoded by an unusually long open reading frame:
 RT evidence for protein processing from a large precursor.";
 RT Mol. Microbiol. 5:2361-2370(1991).
 RL [2]
 RP SEQUENCE OF 279-1654 FROM N.A.
 RC STRAIN=R;
 RX MEDLINE=90136087; PubMed=2515418;
 RA Gilmore R.D., Jr., Joste N., McDonald G.A.;
 RT "Cloning, expression and sequence analysis of the gene encoding the
 RT 120 kD surface-exposed protein of Rickettsia rickettsii.";
 RL Mol. Microbiol. 3:1579-1586(1989).
 CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
 CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
 CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
 CC LAYER WITH HEXAGONAL SYMMETRY.
 CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPB/OMPB FAMILY.
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 CC
 DR EMBL: X16353; CAA34403.1; -.
 DR PIR: S18227; S18227.
 DR InterPro: IPR006315; Autotransport.
 DR InterPro: IPR005546; Autotransporter.
 DR Pfam: PF03797; Autotransporter; 1.
 DR TIGRfams: TIGR01414; autotrans_bar1; 2.
 KM Antigen; S-layer; Cell wall.
 FT CHAIN 1 1333 120 KDA SURFACE-EXPOSED PROTEIN.
 FT CHAIN 1334 1654 32 KDA BETA PEPTIDE.
 FT DOMAIN 1181 1188 POLY-THR.
 FT SEQUENCE 1654 AA; 168184 MW; D7AB70B7087F518 CRC64;
 SQ
 Query Match 7.1%; Score 145.5; DB 1; Length 1654;
 Best Local Similarity 22.5%; Pred. No. 0.98;
 Matches 100; Conservative 50; Mismatches 177; Indels 117; Gaps 19;


```

DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE S-layer protein (Surface array protein) (SAP).
GN SAP.
OS Campylobacter fetus.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteriaceae; Campylobacter.
OX NCBI_TaxID=196;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
RC STRAIN-84-32 / 23D;
RX MEDLINE=90354448; PubMed=2387868;
RA Blaser M.J., Gotschlich E.C.;
RT "Surface array protein of Campylobacter fetus. Cloning and gene
RT structure."
RL J. Biol. Chem. 265:14529-14535(1990).
RN [2]
RP ERRATUM.
RX MEDLINE=91035477; PubMed=2229082;
RA Blaser M.J., Gotschlich E.C.;
RL J. Biol. Chem. 265:19372-19372(1990).
CC -I- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS
CC CRITICAL FOR VIRULENCE.
CC -I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: J05577; AAA3032.1; -
KW Cell wall; S-layer.
SQ SEQUENCE 933 AA; 96757 MW; F88C729B4B5B1E9 CRC64;

Query Match 6.9%; Score 143; DB 1; Length 933;
Best Local Similarity 24.7%; Pred. No. 0.7;
Matches 100; Conservative 50; Mismatches 151; Indels 104; Gaps 20;

OY 28 KRASATVY-TAVLATLFAVYQASANNVDVRYDYVEFLSADTKTTVNVESKDKNGKT 86
DB 475 KRAAKVYVLTNTAATDQTVTLKANA-----TNSLEFDSATKTSVTASG----- 520
OY 87 EVKIGAKTSVKEKDKLVTKGDKGENSSSTDESGTLTAKVIDAVKAGRMKMTTAN 146
DB 521 -----SGKLVTKGAEVETLVNID-----TTAFNALQSV-----SF 551
OY 147 GGTGADKFEVTSCTNTVTFASGKTATVSK--DDOGNITVYVYVNGDALNVQLONS 204
DB 552 GKTGGGKGF-SVKTGTGDDKIEPVGTTLIEGVIDAPNDPIAMSAALTSANFMINI 610
OY 205 GWNLDKRVAG-----SSGKVIISGNVSPSKGKMDVYNINAGNNEITRNGKN----- 252
DB 611 ENVALISDAVATADSSSAFKNSVITITKEADDTTLTKDKDVIYNFTADAGSVKLITVKL 670
OY 253 -----IDIAVSMTPQFSSVLSAGADAPTLSDVC--DALNVS-KKNKKPRPRTNV 300
DB 671 NDVYALMIVYKIVIDAAKKDTINIALGTAADKALVIDIGIEITLNTSLVKATSPETTANT 730
OY 301 APGVKEDPTNV---AQL---KGAQNLNRRIDNVGNA-RAGI---AQAATAGLVQ 348
DB 731 V-NMKLVDVTSIIIDGMQITLGHAGTACTDYSKYMDASALKAGLTFDASAI-TLG--- 785
OY 349 AYLPEKSMALGGTGTGEGAGTAIGYSIS--DGNMIIKGTASGN 392
DB 786 -----ANATTKGGS-----GADSIYVKGNIIVDLVAGCD 815

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RESULT 10
ID FLIC_SHIFL STANDARD; PRT; 550 AA.
AC 008860;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Flagellin.
DE FLIC OR SF1966.
GN Shigella flexneri.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ID642;
RX MEDLINE=94335647; PubMed=8057852;
RA Tomlinaga A., Mahmoud M.A.-H., Mukaihara T., Enomoto M.;
RT "Molecular characterization of intact, but cryptic, flagellin genes
RT in the genus Shigella."
RL Mol. Microbiol. 12:277-285(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157."
RL Nucleic Acids Res. 30:4432-4441(2002).
CC -I- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
CC FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: D16819; BAA04093.1; -
DR EMBL: AE015215; AAN43516.1; -
DR PIR: S44980; S44980.
DR InterPro: IPR001029; Flagellin_C.
DR InterPro: IPR001492; Flagellin_N.
DR Pfam: PF00700; Flagellin_C_1.
DR Pfam: PF00669; Flagellin_N_1.
DR PRINTS: PR00207; FLAGELLIN.
KW Flagella.
SQ SEQUENCE 550 AA; 56636 MW; CC921C9ABEF200B6 CRC64;

Query Match 6.9%; Score 142.5; DB 1; Length 550;
Best Local Similarity 21.9%; Pred. No. 0.4;
Matches 79; Conservative 55; Mismatches 165; Indels 61; Gaps 15;

OY 46 TVOASA-----NNVDFVR-----TYDYVEFLSADTKTTVNVESKDKNKEVKGATGS 95
DB 96 TVOASTGNSDSDSIDDEIKSRIDETDRVSGOTFNGVAVLADGSMK--IOVGANDG 153
OY 96 VIKEDKGLVTKGDKGENSSSTDEGEGL---VTAKEVIDAVNKAQWRKRTTANGQTS-- 150
DB 154 QTITIDLKIDSDTLGLNGFNVNGGAVANAAASADLVANATPYVGGKTYVSAGYDAK 213
OY 151 QADKFEVTSCTNV--TFASGKTATVVS--KDDGNITVYVYVNGDALNVQLONSQW 206
DB 214 ASDLAGVSDGDDVQATITNNGFPAASATNYKYSASKSYSFDDTTASAADQVKLTPG- 272
OY 207 NLDSKAVAGSSGK---VISGNVSPSKGKMDVYNINAGNNI-----ETTRNGKNIDLAT 257

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OMP_RICTY
ID OMP_RICTY STANDARD: PRT: 1645 AA.
AC P96989;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scas5) (rOmpB)
DE (Omp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB OR SLIP.
OS Rickettsia typhi.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=785;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Williamington;
RX MEDLINE=94040787; PubMed=8224886;
RA Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;
RT "Cloning and sequence analysis of the gene encoding the crystalline surface layer protein of Rickettsia typhi.";
RL Gene 133:129-133(1993).
RN [2]
RP PARTIAL SEQUENCE.
RC STRAIN=Williamington;
RX MEDLINE=92114896; PubMed=1370573;
RA Chung W.M., Carl M., Dasch G.A.;
RT "Mapping of monoclonal antibody binding sites on CNBr fragments of the S-layer protein antigens of Rickettsia typhi and Rickettsia prowazekii.";
RL Mol. Immunol. 29:95-105(1992).
RN [3]
RP IDENTIFICATION OF CLEAVAGE SITE.
RX MEDLINE=92104668; PubMed=1729180;
RA Hackstadt T., Messer R., Cieplak W., Peacock M.G.;
RT "Evidence for proteolytic cleavage of the 120-kilodalton outer membrane protein of rickettsiae: identification of an avirulent mutant deficient in processing.";
RL Infect. Immun. 60:159-165(1992).
CC -I- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -I- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.
CC -I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.
CC -I- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
CC -----
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CC -----
DR EMBL: L04661; ABA8987.1; -.
DR PIR: JN0896.
DR InterPro: IPR005415; Autotransporter.
DR Pfam: PF03797; Autotransporter; 1.
DR TIGRFAMs: TIGR01414; autotrans_bar1.1.
RW Antigen: S-layer; Transmembrane; Cell wall.
FT CHAIN 1 1353 120 KDA SURFACE-EXPOSED PROTEIN.
FT TRANSMEM 1354 1645 32 KDA BETA PEPTIDE.
FT TRANSMEM 1415 1429 MEMBRANE ANCHOR (POTENTIAL).
FT CONFLICT 657 657 H -> N (IN REF. 2).
FT CONFLICT 842 842 V -> I (IN REF. 2).
FT CONFLICT 1071 1071 G -> A (IN REF. 2).
FT CONFLICT 1306 1306 G -> S (IN REF. 2).
SQ SEQUENCE 1645 AA; 169698 MW; 0CB5641C7EE185EE CRC64;

Query Match

6.8%; Score 141; DB 1; Length 1645;

Best Local Similarity 21.4%; Pred. No. 1.7;
Matches 100; Conservative 67; Mismatches 172; Indels 128; Gaps 22;
QY 14 NAMVVSELTNRHNRASATVKTAVLAT---LFFATQVQSANNNVFVTFDVEFLSDT 70
DB 218 NGFVAVSOKT-----FAGIKTTINIGNOGIMFTTTPDAANALWLOGGGNTINGRDG 270
QY 71 KTTVNVSKDNKGKKEVEKI---GAKTSVIREKD---GKL-----VYGRDKGE 112
DB 271 TGLVLVGR--NGNTEFNVTGSLGSGNLKGVIEFPTTAAGLLANGAANNVIGTDGCA 328
QY 113 NGS-----STDEG---EGLVTAKEVIDAVNKKAGMRKKTYYANGQT-----GOA 152
DB 329 GRAAGFIIVSDNGNNAATISGOVYAKDIV-----IOSANAGGVTFEHLVDVGLGCK 379
QY 153 DKFEVTSGTNTVFASGKGTATVASKDQGNITVYVDV-----VGDALVNNQNLN 203
DB 380 TNEKTAADSKVIITENASFGST-----DFGNLAVQIVPNKKILTGNFIGDA-----KN 427
QY 204 SGWNIDSKAVAGSSGKVIISGVNPS-----GKMDETVNI-----NAGNN 243
DB 428 NG-NTAGVITTNANGTLVSGMTDPNIVVTNKAIEVEGAGIVQSLGIGHGALRLGNAGSI 486
QY 244 IETTRNGKNIDIASTMTQFSSVSLGACADAPTLSDGDAL---NVGSKDKNKPVRITNV 300
DB 487 FKLA-DGTVINGPVNQNPLVNNMALAAG---SIOLDSSAIIITGIGAVNAALQDITL 541
QY 301 APGVGEQVTVAOLKGVANQNLNRRIDVWDNARAGINQATATAGLVQAVLPKSMMAIG 360
DB 542 A-----NDASKILTLSGA-----NIGANMGAIHPQANGSTTDTLTQNNITLDF 587
QY 361 GGYVGEAGVAYIGVSSISDGNMIKGT-----ASGNSRGHGASAS 402
DB 588 DLDVTTDQTVGDASLTNNQTLFTINGSIGTIGANTKTLGRPNWSS 634
RESULT 13
OMP_RICCN
ID OMP_RICCN STANDARD: PRT: 1655 AA.
AC 09KRA3; 09KR98; 09XC45;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scas5) (rOmpB)
DE (Omp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB OR RC1085.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cosserat P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
RN [2]
RP SEQUENCE OF 33-1649 FROM N.A.
RC STRAIN=Indian tick typhus, and Malish 7;
RX MEDLINE=20393643; PubMed=10939649;
RA Roux V., Raoult D.;
RT "Phylogenetic analysis of members of the genus Rickettsia using the
RT gene coding the outer-membrane protein rOmpB (ompB)";
RL Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
RN [3]
RP SEQUENCE OF 353-1655 FROM N.A.
RC STRAIN=Malish 7;
RA Stenos J., Walker D.;


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OY 176 VSKDQGNITWYDVNVDALNVNOLNSGMNLSKANAAGSSGKVCISGVSPSKGMDT 235
DB 822 SSGDVKGNLT-----INARDKLTQOGASHGVGAYENMAGVYDHLAADASTTTTKTDVG 877
OY 226 VINAGNNIETRNKNKNDIATSMTPQSSVSLGA-----GADATLTLDVGD 283
DB 878 VNI-----GANDYSAVTRPVERAVGAKAKLDATGVYINDIGGADNVGLDGA 926
OY 284 LNVGSKR--DNKPRVITNVAPGV-----KEGDV-----TNVAOLKGYAONIN----- 323
DB 927 QCGSSEKSSSSQAVVSSVQASIDIMAKGEVRDQGTQVQASKG-AVNTLTADSHRSEAA 985
OY 324 NRIDNVGNAKAGTGAATAGLVAYLPKGSMAIG-----CGTRGEGAGTATGSSSID 379
DB 966 NMQDQSRDTR-----GSAG-VRYVYTTTGSDDLVDVDAKGEQGTQRSNSASQAVTGSID 1037
OY 380 GGNW-----IIGTASGNSRGHFGASA 401
DB 1038 AANGINNVKKDAITYGTALNGRGKRTAVNA 1068

RESULT 15
APU_THETU STANDARD; PRT: 1861 AA.
AC P38536;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Amylopullulanase precursor (Alpha-amyglase/pullulanase) (Pullulanase
DE type II) [includes: Alpha-amyglase (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase), Pullulanase (EC 3.2.1.41) (1,4-alpha-D-glucan
DE glucanohydrolase), (Alpha-dextrin endo-1,6-alpha-glucosidase)].
GN AMY.
OS Thermoanaerobacter thermosulfurogenes (Clostridium
OS thermosulfurogenes).
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacterium.
OX NCBI_TaxID=33950;
RN [1]
RP SEQUENCE FROM N.A..
RC STRAIN=DSM 3896 / EML;
RX MEDLINE=9425298; PubMed=8195085;
RA Matuschek M., Butchardt G., Sahm K., Bahl H.;
RT Pullulanase of Thermoanaerobacterium thermosulfurogenes EML
RT (Clostridium thermosulfurogenes): molecular analysis of the gene,
RT composite structure of the enzyme, and a common model for its
RT attachment to the cell surface."
RL J. Bacteriol. 176:3295-3302(1994).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of (1->6)-alpha-D-glucosidic
CC linkages in pullulan and in amylopectin and glycogen, and the
CC alpha and beta-limit dextrans of amylopectin and glycogen.
CC -1- SUBCELLULAR LOCATION: CELL-BOUND. IT C-TERMINUS MAY SERVE AS AN
CC S-LAYER ANCHOR.
CC -1- PM: GLYCOSYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
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CC -----
CC EMBL: M57692; AAB00841.1; .
CC DR HSSP: 008751; 1BVZ.
CC DR InterPro: IPR006589; Alp_amy1_cat_sub.
CC DR InterPro: IPR006048; Alp_amy1_C.

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DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR004185; Glyco_hydro_131g.
DR InterPro: IPR004193; Glyco_hydro_13N.
DR InterPro: IPR001119; SLH.
DR Pfam: PF00128; alpha-amyglase; 1.
DR Pfam: PF02806; alpha-amyglase; 1.
DR Pfam: PF02903; alpha-amyglase; 1.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF02922; Isoamylase; N; 1.
DR Pfam: PF00395; SLH; 3.
DR SMART: SM00642; Amy; 1.
DR SMART: SM00632; Amy-C; 1.
DR SMART: SM00060; FN3; 2.
DR PROSITE: PS01072; SLH_DOMAIN; 3.
DR Hydrolyase: Glycosidase; Carbohydrate metabolism; signal; Repeat;
KW Multifunctional enzyme; Glycoprotein.
FT SIGNAL 1 35
FT CHAIN 36 1861
FT DOMAIN 928 1018
FT DOMAIN 1157 1248
FT ACT_SITE 628 628
FT ACT_SITE 657 657
FT ACT_SITE 734 734
FT DOMAIN 1681 1739
FT DOMAIN 1740 1803
FT DOMAIN 1804 1861
FT CONFLICT 1734 1734
FT SEQUENCE 1861 AA; 206104 MW; 06C23070E453B574 CRC64;

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Query Match 6.8%; Score 139.5; DB 1; Length 1861;
Best Local Similarity 20.1%; Pred. No. 2.4;
Matches 101; Conservative 74; Mismatches 204; Indels 123; Gaps 24;

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OY 2 NKIYRIINNSALNA-----WVVSSELTNRNHRFRASATYKFAVLATLLEATYQASANNDF 56
DB 1208 NEVNYIDTSTYINGVYTKVAVDLSEFRRESNVYTIKPDVPIKVFJNTVPDYTPDA 1267
OY 57 VR-----TYD--TVEFLSADTKTTTVNVEKSKNGKKEVEKI--GAKTSYKEKDG-- 102
DB 1268 VNLACTFFNATWDPDAQOMTKRIDNNTYTITL-TDEGTOIEKVKARGSMDEVKEQYENE 1326
OY 103 ----KLVTGDKDKENGSSSTDE-----GEGLVTAKEVIDAVNKAAG--WRMKT 142
DB 1327 FASNKKVITVYVNGNMEMINDVYRWRDIPFIYSPSSNMVYDWSNISTMEVKGNTYKCAK 1386
OY 143 TTANGQFOQADKFEETVTSGFNTVFASGK-----GTFAPVSKDDGNT-----V 186
DB 1387 VTINDSRYQDKNGVFTKDVSLNIVGNKIKIHVEPNDSVYGNDDGRITELTKDIEIYI 1446
OY 187 MYDVAVGDALNVNOLNSGMNLSKRAVAGSSGKV-ISGNVSPSKGKMDETVNI--NAGNN 243
DB 1447 RQENNSGGGTGNNNTSTGGSN-SSSTGSGTSGTSTISNIS-NTSNTSNTIGVITKGNV 1504
OY 244 IEITRN-GKNIDTATSMTPQ---ESSVSLGACADAPTLSDGDALNVGS-----KKD 291
DB 1505 ITLTADKAKADLVNSKDKKVPDITTTIGEG-QQKVVOISKIDILDTSAANGKDIVIKSD 1563
OY 292 NKPRVIT-----NVAPEGKGVTVNAQLKGYAONLNRIIDVNDG----- 332
DB 1564 NASIALTLDALNOLNOLNSGMNLSKRAVAGSSGKV-PSNTVYSLNVDITTSIGSGVTLAKVE 1623
OY 333 ----ARAGIAQATAGLVAYLPKGSMAIGGCTYGEAG-----YA 371
DB 1624 VTLNISKANDPRKVA-----VYYNNTTQOMEVYGVKVDASSGTTFENATHRSQVAAFXD 1679
OY 372 IGYNISDGNW---IIGTAS 390
DB 1680 KTFNDIKD--NMAKDVIEVLAS 1699

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Search completed: October 6, 2003, 09:24:00
Job time : 8.28512 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:10 ; Search time 29.8927 Seconds
(without alignments)
3513.485 Million cell updates/sec

Title: US-09-771-382-25

Perfect score: 2063

Sequence: 1 MNKYRIINMSALNMAWVVS.....TASGNSRGHFGASASVGYQM 407

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP viirus:*
16: SP bacteriap:*
17: SP archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	1961	95.1	591	09JRI8	09jri8 neisseria m
2	1957	94.9	591	09JPS7	09jps7 neisseria m
3	1956.5	94.8	592	09AQF0	09aqf0 neisseria m
4	1949	94.5	591	093QY3	093qy3 neisseria m
5	1909.5	92.6	600	09JPS6	09jps6 neisseria m
6	1903.5	92.3	592	09JPS9	09jps9 neisseria m
7	1893.5	91.8	592	09JQW4	09jqw4 neisseria m
8	1890.5	91.6	590	09JPS3	09jps3 neisseria m
9	1890.5	91.6	598	09JPS7	09jps7 neisseria m
10	1890	91.6	595	09JPH0	09jph0 neisseria m
11	1888.5	91.5	594	09JPS2	09jps2 neisseria m
12	1887.5	91.5	594	09JQY4	09jqy4 neisseria m
13	1886	91.4	599	09JPS8	09jps8 neisseria m
14	1884.5	91.3	594	09JPI3	09jpi3 neisseria m
15	1883	91.3	599	09JPS8	09jps8 neisseria m
16	1879.5	91.1	594	09JPH7	09jph7 neisseria m

17	1877.5	91.0	598	09JPS9	09jps9 neisseria m
18	1869.5	90.6	592	093QY2	093qy2 neisseria m
19	1865.5	90.4	600	09JPS5	09jps5 neisseria m
20	1864.5	90.4	598	09JPS0	09jps0 neisseria m
21	1864.5	90.4	598	09JPS0	09jps0 neisseria m
22	1860	90.2	599	09JPI0	09jpi0 neisseria m
23	1855.5	89.9	598	093QY5	093qy5 neisseria m
24	1848	89.6	589	093QY1	093qy1 neisseria m
25	1801	87.3	526	09JPS4	09jps4 neisseria m
26	1801	87.3	530	09JPS1	09jps1 neisseria m
27	660.5	32.0	1098	048152	048152 haemophilus
28	659.5	32.0	1096	098M79	098m79 haemophilus
29	638	30.9	2353	P71401	P71401 haemophilus
30	592.5	28.7	1210	098M75	098m75 haemophilus
31	583.5	28.3	1210	098M75	098m75 haemophilus
32	575.5	27.9	1204	098M76	098m76 haemophilus
33	413.5	20.0	1004	098M77	098m77 haemophilus
34	393.5	19.1	1002	098M78	098m78 haemophilus
35	379	18.4	1299	09F3X6	09f3x6 pasteurella
36	341	16.5	1190	09PC04	09pc04 xylella fas
37	332.5	16.1	2059	09PD50	09pd50 xylella fas
38	331	16.0	1588	08XDG4	08xdg4 escherichia
39	331	16.0	1778	08FCB2	08fcb2 escherichia
40	321	15.6	1461	08ZU64	08zu64 salmonella
41	320	15.5	1107	09F2D8	09f2d8 salmonella
42	315.5	15.3	2314	08KOM8	08kom8 moraxella c
43	307.5	14.9	641	08CKM1	08ckm1 yersinia pe
44	307.5	14.9	658	08ZHJ0	08zhj0 yersinia pe
45	301.5	14.6	2712	09F3X5	09f3x5 pasteurella

ALIGNMENTS

RESULT 1

ID	09JRI8	PRELIMINARY:	PRT:	591 AA.
AC	09JRI8:			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	Outer membrane protein GNA992 (Adhesin) (Nmha outer membrane protein).			
GN	GNA992 OR NMH0992 OR NMHA.			
OS	Neisseria meningitidis, and			
OC	Neisseria meningitidis (serogroup B).			
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;			
OC	Neisseriaceae; Neisseria.			
OX	NCBI_Taxid=487, 491;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MC58 / Serogroup B, BZ169, BZ83, and H44/76;			
RX	MEDLINE=20175756; PubMed=10710306;			
RA	Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,			
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,			
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,			
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,			
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,			
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,			
RA	Moxon E.R., Grandi G., Rappuoli R.;			
RT	"Identification of Vaccine Candidates Against Serogroup B			
RT	Meningococcus by Whole-Genome Sequencing.";			
RL	Science 287:1816-1820(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MC58 / Serogroup B;			
RX	MEDLINE=20175755; PubMed=10710307;			
RA	Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,			
RA	Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,			
RA	Nelson W.C., Gwinn M.L., Deboy R., Peterson J.D., Hickey E.K.,			
RA	Hart D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,			
RA	Mason T., Ciecko A., Parksey D.S., Blair E., Ciftone H., Clark E.B.,			
RA	Cotton M.D., Uitterback T.R., Khouri H., Olin H., Vamathevan J.,			

RA Gill J., Scarlato V., Maignani V., Pizzo M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,
RT "Complete genome sequence of *Neisseria meningitidis* serogroup B strain
MC58.";
RL Science 287:1809-1815(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=*N.meningitidis*; STRAIN=PMC21;
RA Peak I.R., Srikanta Y., Dieckelman M., Moxon R., Jennings M.P.,
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of *Neisseria meningitidis*.";
RL Submitted (JUN-1999) to the EMBL/Genbank/DBD databases.
DR EMBL: AF226375; AAF42524.1; -
DR EMBL: AF226375; AAF41395.1; -
DR EMBL: AF226367; AAF42516.1; -
DR EMBL: AF226370; AAF42519.1; -
DR EMBL: AF226374; AAF42523.1; -
DR EMBL: AF157611; AAK68872.1; -
DR TIGR: MMB0992; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
KW Complete proteome.
SQ SEQUENCE 591 AA; 62112 MW; 7C22F3CAE7F73EC6 CRC64;

Query Match 95.1%; Score 1961; DB 16; Length 591;
Best Local Similarity 68.9%; Pred. No. 2,1e-86;
Matches 407; Conservative 0; Mismatches 0; Indels 184; Gaps 1;

OY 1 MNKIRIIMNSALNMAVYSELTRNHTKRASATVAVATLTLFATVOASAN----- 52
DB 1 MNKIRIIMNSALNMAVYSELTRNHTKRASATVAVATLTLFATVOASANNEQEDL 60
OY 53 ----- 52
DB 61 YLDPVQRTAVALIYNSDEKGEKEKEVEENSDMAVYFNEKGYLTAREITLKAGDNLKIK 120
OY 53 ----- 52
DB 121 NGTNETYSLKRDLDLTDSVTEKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVALN 180
OY 53 -----NYDF 56
DB 181 GIGSLTDTLNTGATNTVNDNTVDDEKKRAASVYKDVNLNAGMNIKGVKPGTTASDNDF 240
OY 57 VRTDYVEFLSADRTTTTVNVEESKDKNGKTEVKIGAKTSVIREKDGKLVTEGDKGENSS 116
DB 241 VRTDYVEFLSADRTTTTVNVEESKDKNGKTEVKIGAKTSVIREKDGKLVTEGDKGENSS 300
OY 117 TDEGGGLTAKAEVIDAVKAGRMKTTTANGOTGADKFEVYTSNTNTPFASGKGTATV 176
DB 301 TDEGGGLTAKAEVIDAVKAGRMKTTTANGOTGADKFEVYTSNTNTPFASGKGTATV 360
OY 177 SKDDGNTITVYDVVNGDALVNLQNSGMNLSKAVALSSGKTVSGNVSPSKGMDETV 236
DB 361 SKDDGNTITVYDVVNGDALVNLQNSGMNLSKAVALSSGKTVSGNVSPSKGMDETV 420
OY 237 NINAGNNIETIRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDGALNVSSKDKNKPVR 296
DB 421 NINAGNNIETIRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDGALNVSSKDKNKPVR 480
OY 297 ITTNAVPGKEGDVYTNVQALKGVAQNLNRRINDVGNANAGIAQAATATAGLVQAYLPGRSM 356
DB 481 ITTNAVPGKEGDVYTNVQALKGVAQNLNRRINDVGNANAGIAQAATATAGLVQAYLPGRSM 540
OY 357 MAIGGGTYRGEAGYAIIGYSSISDGGNWIITKGASNSGHRFGASASVGYOW 407
DB 541 MAIGGGTYRGEAGYAIIGYSSISDGGNWIITKGASNSGHRFGASASVGYOW 591

RESULT 2
ID 09JPS7 PRELIMINARY: PRT: 591 AA.
AC 09JPS7;
AC 09JPS7;

DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA92.
GN GNA92.
OS *Neisseria meningitidis*.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_Taxid=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B2147;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizzo M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.,
RT "Identification of Vaccine Candidates Against Serogroup B.
RT *Meningococcus* by Whole-genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226366; AAF42515.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;

Query Match 94.9%; Score 1957; DB 2; Length 591;
Best Local Similarity 68.7%; Pred. No. 3,3e-86;
Matches 406; Conservative 1; Mismatches 0; Indels 184; Gaps 1;

OY 1 MNKIRIIMNSALNMAVYSELTRNHTKRASATVAVATLTLFATVOASAN----- 52
DB 1 MNKIRIIMNSALNMAVYSELTRNHTKRASATVAVATLTLFATVOASANNEQEDL 60
OY 53 ----- 52
DB 61 YLDPVQRTAVALIYNSDEKGEKEKEVEENSDMAVYFNEKGYLTAREITLKAGDNLKIK 120
OY 53 ----- 52
DB 121 NGTNETYSLKRDLDLTDSVTEKLSFSANGKNVITSDTKGLNFAKETAGTNGDTTVALN 180
OY 53 -----NYDF 56
DB 181 GIGSLTDTLNTGATNTVNDNTVDDEKKRAASVYKDVNLNAGMNIKGVKPGTTASDNDF 240
OY 57 VRTDYVEFLSADRTTTTVNVEESKDKNGKTEVKIGAKTSVIREKDGKLVTEGDKGENSS 116
DB 241 VRTDYVEFLSADRTTTTVNVEESKDKNGKTEVKIGAKTSVIREKDGKLVTEGDKGENSS 300
OY 117 TDEGGGLTAKAEVIDAVKAGRMKTTTANGOTGADKFEVYTSNTNTPFASGKGTATV 176
DB 301 TDEGGGLTAKAEVIDAVKAGRMKTTTANGOTGADKFEVYTSNTNTPFASGKGTATV 360
OY 177 SKDDGNTITVYDVVNGDALVNLQNSGMNLSKAVALSSGKTVSGNVSPSKGMDETV 236
DB 361 SKDDGNTITVYDVVNGDALVNLQNSGMNLSKAVALSSGKTVSGNVSPSKGMDETV 420
OY 237 NINAGNNIETIRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDGALNVSSKDKNKPVR 296
DB 421 NINAGNNIETIRNGKNIDIASMTPOFSSVSLGAGADAPTLISVDGALNVSSKDKNKPVR 480
OY 297 ITTNAVPGKEGDVYTNVQALKGVAQNLNRRINDVGNANAGIAQAATATAGLVQAYLPGRSM 356
DB 481 ITTNAVPGKEGDVYTNVQALKGVAQNLNRRINDVGNANAGIAQAATATAGLVQAYLPGRSM 540
OY 357 MAIGGGTYRGEAGYAIIGYSSISDGGNWIITKGASNSGHRFGASASVGYOW 407
DB 541 MAIGGGTYRGEAGYAIIGYSSISDGGNWIITKGASNSGHRFGASASVGYOW 591

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RESULT 3
09AOF0 PRELIMINARY: PRT; 592 AA.
AC 09AOF0:
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Outer membrane protein.
GN NHA.
OS Neisseria meningitidis.
OC Bacteria: Proteobacteria; Betaproteobacteria; Neisseriales.
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon E.R., Jennings M.P.;
RT Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF153375; AAK09243.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;

Query Match 94.8%; Score 1956.5; DB 2; Length 592;
Best Local Similarity 68.6%; Pred. No. 3.5e-86;
Matches 406; Conservative 0; Mismatches 1; Indels 185; Gaps 1;

QY 1 MNKIYRIINNSALNAVWVSELTRNHTKRASATVKTAVLATLTFATVQASAN----- 52
DB 1 MNKIYRIINNSALNAVWVSELTRNHTKRASATVKTAVLATLTFATVQASANERPCKD 60
QY 53 ----- 52
DB 61 LVIDPVQRTVAVLIVNSDKEGTGEKEVEENSDMAVYFNEKGVLTAREITLKAGDNLKIK 120
QY 53 ----- 52
DB 121 QNGTNTYSLKNDLDTLTSVGTETKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHL 180
QY 53 -----NVD 55
DB 181 NGIGSTLTDLTLNTGATTTNTNDVYTDDEKKRAASVQDVLNAGNNIKGVKPGTTASDNVD 240
QY 56 FVRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYIKEDGKLVYTGDKGENGS 115
DB 241 FVRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYIKEDGKLVYTGDKGENGS 300
QY 116 STDEGGLVYTAKEVIDAVNKAAGWRMKTJTANGQTGAADKFEYVTSGTNTVFASGKGTAT 175
DB 301 STDEGGLVYTAKEVIDAVNKAAGWRMKTJTANGQTGAADKFEYVTSGTNTVFASGKGTAT 360
QY 176 VSKDDGNTITVMDVNVGDALNVNQLNSGWNLDKRAVAGSSGKVIISGNVSPSKGMDET 235
DB 361 VSKDDGNTITVMDVNVGDALNVNQLNSGWNLDKRAVAGSSGKVIISGNVSPSKGMDET 420
QY 236 VTNAGNNIETTRNGKNIDATISMTPOFSSVSLGAGADAPTLISVDGDALNVGSKKNKP 295
DB 421 VTNAGNNIETTRNGKNIDATISMTPOFSSVSLGAGADAPTLISVDGDALNVGSKKNKP 480
QY 296 RITNVAPGVKEGDTVVAQLKGVQNLNNRIDVNDGNARAGIAQALATAGLVQAYLPKGS 355
DB 481 RITNVAPGVKEGDTVVAQLKGVQNLNNRIDVNDGNARAGIAQALATAGLVQAYLPKGS 540
QY 356 MAAGGTTVRGEAGYVAGISISDGNWIIKGTASGNSRHFASASVGYQW 407
DB 541 MAAGGTTVRGEAGYVAGISISDGNWIIKGTASGNSRHFASASVGYQW 592

RESULT 4
0930Y3 PRELIMINARY: PRT; 591 AA.
ID 0930Y3
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AC 0930Y3;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE NHA outer membrane protein.
GN NHA.
OS Neisseria meningitidis.
OC Bacteria: Proteobacteria; Betaproteobacteria; Neisseriales.
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG329;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF157606; AAK68867.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 591 AA; 62048 MW; C0DC600798859C65 CRC64;

Query Match 94.5%; Score 1949; DB 2; Length 591;
Best Local Similarity 68.5%; Pred. No. 8e-86;
Matches 405; Conservative 1; Mismatches 1; Indels 184; Gaps 1;

QY 1 MNKIYRIINNSALNAVWVSELTRNHTKRASATVKTAVLATLTFATVQASAN----- 52
DB 1 MNKIYRIINNSALNAVWVSELTRNHTKRASATVKTAVLATLTFATVQASANEDEEDL 60
QY 53 ----- 52
DB 61 YIDPVLTVAVLIVNSDKEGTGEKEVEENSDMAVYFNEKGVLTAREITLKAGDNLKIK 120
QY 53 ----- 52
DB 121 NGTNTYSLKNDLDTLTSVGTETKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN 180
QY 53 -----NVD 56
DB 181 GIGSTLTDLTLNTGATTTNTNDVYTDDEKKRAASVQDVLNAGNNIKGVKPGTTASDNVD 240
QY 57 VRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYIKEDGKLVYTGDKGENGS 116
DB 241 VRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSYIKEDGKLVYTGDKGENGS 300
QY 117 TDEGGLVYTAKEVIDAVNKAAGWRMKTJTANGQTGAADKFEYVTSGTNTVFASGKGTAT 176
DB 301 TDEGGLVYTAKEVIDAVNKAAGWRMKTJTANGQTGAADKFEYVTSGTNTVFASGKGTAT 360
QY 177 SKDDGNTITVMDVNVGDALNVNQLNSGWNLDKRAVAGSSGKVIISGNVSPSKGMDET 236
DB 361 SKDDGNTITVMDVNVGDALNVNQLNSGWNLDKRAVAGSSGKVIISGNVSPSKGMDET 420
QY 237 NINAGNNIETTRNGKNIDATISMTPOFSSVSLGAGADAPTLISVDGDALNVGSKKNKP 296
DB 421 NINAGNNIETTRNGKNIDATISMTPOFSSVSLGAGADAPTLISVDGDALNVGSKKNKP 480
QY 297 ITNVAPGVKEGDTVVAQLKGVQNLNNRIDVNDGNARAGIAQALATAGLVQAYLPKGS 356
DB 481 ITNVAPGVKEGDTVVAQLKGVQNLNNRIDVNDGNARAGIAQALATAGLVQAYLPKGS 540
QY 357 MATGGTTVRGEAGYVAGISISDGNWIIKGTASGNSRHFASASVGYQW 407
DB 541 MATGGTTVRGEAGYVAGISISDGNWIIKGTASGNSRHFASASVGYQW 591

RESULT 5
09JPS6 PRELIMINARY: PRT; 600 AA.
ID 09JPS6
AC 09JPS6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
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DT 01-OCr-2002 (TREMBLrel. 22, last annotation update)
DE Outer membrane protein GMA992.
GN GMA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E26;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizzia M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Commanduci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RL EMBL: AF226371; AAF2520.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada. 1
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0596CD1 CRC64;

Query Match	92.6%	Score 1909.5	DB 2	Length 600
Best Local Similarity	66.5%	Pred. No. 6.4e-84		
Matches 399	Conservative 2	Mismatches 6	Indels 193	Gaps 1

QY	1	MNKIYRIIMNSALNAWVYVSELTRNHTKRASVYTAVALATLFTPTVOASA-----	51
Dd	1	MNKIYRIIMNSALNAWVYVSELTRNHTKRASVYTAVALATLFTPTVOASADN	60
QY	52	-----	51
Dd	61	EEEEYLEPVRTAPVLSFYSDAEDTGEKEVENTNMGIYFPKNGVYKAGTITLKAGDNLK	120
QY	52	-----	51
Dd	121	IKONTIDENTNASSFTYSLKKELTDLTSVYTEKLSFGANGKNVNTSDTKGLNFAKETAGT	180
QY	52	-----	51
Dd	181	NGDPTVHLNGISGTLDTLTLNFATNTVNTDNTDDEKKRAASVKDVLINAGNINIKGVKPG	240
QY	52	---NNVDPVYTYTVEFLSADTKTTTVNVESSDKGKTEYKIGAKTSVIREKDGKLYTG	107
Dd	241	TTASDNDVDFVHTYDTVEFLSADTKTTTVNVESSDKGKTEYKIGAKTSVIREKDGKLYTG	300
QY	108	KDKCEGSSSTDEGBGLVTAKEVIDAVNKAQNRMKTTTANGOTGQADKEFYVTSGTNVTFPA	167
Dd	301	KKGKENGSSSTDEGBGLVTAKEVIDAVNKAQNRMKTTTANGOKGQADKEFYVTSGTNVTFPA	360
QY	168	SGKGTPTATVSKDDOGNTTVMYDVNVGDLANTNOLONGSWMNDSKVAASSGCVTISGNVSP	227
Dd	361	SGKGTPTATVSKDDOGNTTVMYDVNVGDLANTNOLONGSWMNDSKVAASSGCVTISGNVSP	420
QY	228	SKGKMDTEVNIINAGNNIEITFRNGKNIDTATSMTPQFSSVSLGAGADAFTLSYDGDALVNG	287
Dd	421	SKGKMDTEVNIINAGNNIEITFRNGKNIDTATSMTPQFSSVSLGAGADAFTLSYDGDALVNG	480
QY	288	SKKDNKEPVRTITNVAPEGKGDVTNVAQLKGVAONLNBRIDNVGDNARAGIAQAIATAGLV	347
Dd	481	SKDNKKEPVRTITNVAPEGKGDVTNVAQLKGVAONLNBRIDNVGDNARAGIAQAIATAGLV	540
QY	348	QAYIPLGSSMAIGGCTYRGEAGYALIGVSSISDGGWMIITKGASGNSRHFAGASAVGYQW	407
Dd	541	QAYIPLGSSMAIGGCTYRGEAGYALIGVSSISDGGWMIITKGASGNSRHFAGASAVGYQW	600

RESULT 6
Q9JPS9

TD	09JPS9	PRELIMINARY;	PRT;	592 AA.
AC	09JPS9.			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	Outer membrane protein GNA92.			
GN	GNA92.			
OS	Neisseria meningitidis.			
CC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;			
CC	Neisseriaceae; Neisseria.			
OX	NCBI_TaxID=487;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=860800;			
RX	MEDLINE=20175756; PubMed=10710308;			
RA	Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,			
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,			
RA	Galeotti C.L., Iuzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,			
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,			
RA	Broeker M., Hundt E., Knapp B., Blahr E., Mason T., Tettelin H.,			
RA	Hood D.W., Ueffing A.C., Saunders N.J., Granoff D.M., Venter C.,			
RA	Moxon E.R., Grandi G., Rappuoli R.;			
RT	"Identification of Vaccine Candidates Against Serogroup B			
RT	Meningococcus by Whole-Genome Sequencing.";			
RL	Science 287:1816-1820(2000).			
DR	EMBL; AF226361; AAF42510.1; -			
DR	InterPro: IPR005594; Yada.			
DR	Pfam; PF03895; Yada, 1.			
QO	SEQUENCE 592 AA; 61917 MW; 4A347151AFD3C879 CRC64;			

Query Match	92.38;	Score 1903.5;	DB 2;	Length 592;
Best Local Similarly	67.48;	Pred. No. 1.2e-83;		
Matches 399;	Conservative 2;	Mismatches 6;	Indels 185;	Gaps 2;

QY	1	MNKIYRIIMNSALNAAVVYSELTRNHTKRASATYKTAVALADLEFETVOASA-----	51
Dp	1	MNKIYRIIMNSALNAAVASELTRNHTKRASATYKTAVALADLEFETVOANAATEDDEEBEL	60
QY	52	-----	51
Dp	61	ESVQRSVYGSIQASWESGSELETJLSMTNDSKEFVPIYVTLKAGDNLKI KONTNENT	120
QY	52	-----	51
Dp	121	NASSFTYSLKKDLYGLINVEFEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTHLN	180
QY	52	-----	51
Dp	181	GIGSTLTDMLINFGATTNTNDNVTDEDEKRAASVKDYLANGMNITKGVKPGCTYASDNDF	240
QY	57	VRTDPVEEFLSADPTKRTTVNVESKDNGCKTEVKGAKTSVYKEDGKLVTKDKDENSS	116
Dp	241	VRTDPVEEFLSADPTKRTTVNVESKDNGCKTEVKGAKTSVYKEDGKLVTKDKDENSS	300
QY	117	TDESEGLVTAKEVIDAANKAGRMKRTTANGQTOGADKFEVYTSCTNVTFAISGCKTATV	176
Dp	301	TDESEGLVTAKEVIDAANKAGRMKRTTANGQTOGADKFEVYTSCTNVTFAISGCKTATV	360
QY	177	SKDQGNITWYDVNVDGDLNVNOLNONGMWLDSKAVVSGSGKVISGVNPSFKGMDETV	236
Dp	361	SKDQGNITWYDVNVDGDLNVNOLNONGMWLDSKAVVSGSGKVISGVNPSFKGMDETV	420
QY	237	NINAGNNIETLRNCKNIDIASMTPOFSSVSLGAGADPTLSYDG-DALNYSKKDKNKPV	295
Dp	421	NINAGNNIETLRNCKNIDIASMTPOFSSVSLGAGADPTLSYDDKGLNYSKKRANKPV	480
QY	296	RITNVAEYKEGDVTNVAOLKGVAQNLNRIIDNVGNARAGIAQAIATAGLVQAYLPKS	355
Dp	481	RITNVAEYKEGDVTNVAOLKGVAQNLNRIIDNVGNARAGIAQAIATAGLVQAYLPKS	540
QY	356	MMALGGSTYKREAGATGYSISISDGGWNIIGCTASGNSRGHFGASASVGYOM	407
Dp	541	MMALGGSTYKREAGATGYSISISDGGWNIIGCTASGNSRGHFGASASVGYOM	592

```
RESULT 7
09JOM4
ID 09JOM4 PRELIMINARY; PRT: 592 AA.
AC 09JOM4;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Putative surface fibril protein (Outer membrane protein GNA992).
GN MNA1200 OR GNA992
OS Neisseria meningitidis (serogroup A), and
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699, 487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Keehill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Hasham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Felkwell T., Hamlin N., Holroyd S.,
RA Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis 2491."
RL Nature 404:502-506(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=205900, B2133, F6124, AND 22491;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Masiagnani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Ntli S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knap B., Blair E., Mason T., Tettein H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL: AL162755; CAB84461.1; -.
DR EMBL: AF226357; AAF42506.1; -.
DR EMBL: AF226365; AAF42514.1; -.
DR EMBL: AF226373; AAF42522.1; -.
DR EMBL: AF226386; AAF42535.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
KW Complete proteome.
SQ SEQUENCE 592 AA; 61745 MW; AD22E255EEF8F754 CRC64;

Query Match 91.8%; Score 1893.5; DB 16; Length 592;
Best Local Similarity 66.9%; Pred. No. 3.7e-83;
Matches 396; Conservative 4; Mismatches 7; Indels 185; Gaps 2;

QY 1 MNKTYRLINNSALNANVAVVSELTRNHTKRASATVKTAVLATLLFAVVOASA----- 51
DB 1 MNKTYRLINNSALNANVAVVSELTRNHTKRASATVKTAVLATLLFAVVOANATDEDEEEL 60
QY 52 ----- 51
DB 61 ESVQRSVVGSIQASMEGSGLELTISLMTNDSKEFDPYIVYTLAKAGDNLIKQNTNENT 120
QY 52 ----- 51
DB 121 NASSFTYSLKDLJGLINNETEKLSPGANGKKVNIISDTKGLNFAKETAGTNGDTVHLN 180
QY 52 -----NNVDF 56
DB 181 GIGSTLTDLTLGSSASHVDAGNOSTHYTRAASTIKVDLNGWNIKGVKGTGSTGQSENVDP 240
```

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QY 57 VRTYDVEEISADTKTTTNNVESKDNKKTEVKIGAKTSYIKKDKLTKGKGENSS 116
DB 241 VRTYDVEEISADTKTTTNNVESKDNKKRTEVKIGAKTSYIKKDKLTKGKGENSS 300
QY 117 TDEGELVYRAKEVIDAVNKRAGMKTTTANGTGQADKPEFTVSGTNVTFASKGTTAVY 176
DB 301 TDEGELVYRAKEVIDAVNKRAGMKTTTANGTGQADKPEFTVSGTNVTFASKGTTAVY 360
QY 177 SKDDGNITVYVYVNGDALNVNQLNSGNNLDSKRVAGSSGAVISGNVSPSKGMDYV 236
DB 361 SKDDGNITVYVYVNGDALNVNQLNSGNNLDSKRVAGSSGAVISGNVSPSKGMDYV 420
QY 237 NINAGNNIETTRGNKIDATSMTPQFSVSLGAGADAPTLVSQGD-ALNVGSKKDNKPV 295
DB 421 NINAGNNIETTRGNKIDATSMAPQFSVSLGAGADAPTLVSQGDALNVGSKDANKPV 480
QY 296 RITNVAPGVKEGVTVAQLKGYAQLNLRIDVNGNARAGIAQAIATAGLVQATYLPKGS 335
DB 481 RITNVAPGVKEGVTVAQLKGYAQLNLRIDVNGNARAGIAQAIATAGLVQATYLPKGS 540
QY 356 MMAIGGTYRGEAGVAGYSISDGNWITKTPASGNSRHFASASVGYOW 407
DB 541 MMAIGGTYRGEAGVAGYSISDGNWITKTPASGNSRHFASASVGYOW 592

RESULT 8
09JPS3
ID 09JPS3 PRELIMINARY; PRT: 590 AA.
AC 09JPS3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE28;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Masiagnani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Ntli S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knap B., Blair E., Mason T., Tettein H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL: AF226378; AAF42527.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 91.6%; Score 1890.5; DB 2; Length 590;
Best Local Similarity 67.1%; Pred. No. 5.1e-83;
Matches 396; Conservative 4; Mismatches 7; Indels 183; Gaps 2;

QY 1 MNKTYRLINNSALNANVAVVSELTRNHTKRASATVKTAVLATLLFAVVOASA----- 51
DB 1 MNKTYRLINNSALNANVAVVSELTRNHTKRASATVKTAVLATLLSAVVOANATDEDEEEL 60
QY 52 ----- 51
DB 61 DPOQRTVAVLIVNSDKETGEKEKEVENSMDAVYFNEKGVLTAGITLAKAGDNLIKQNG 120
QY 52 ----- 51
DB 121 TNFTYSLKDLJDLTJVSGETEKLSPSANGKNVNTSDTKGLNFAKETAGTNGDTVHLNGI 180
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OY 52 -----NNVDPR 58
DB 181 GSTLTDTLLTNGATNTVNDVDEKKRAASVKDVLNAGNNIKGVPGTTASDNVDPR 240
OY 59 TYDVEFLSADPTKTTTVNVEESKDNKTEYKIGAKTSYKEDKGLVTKDKGENGSSTD 118
DB 241 TYDVEFLSADPTKTTTVNVEESKDNKTEYKIGAKTSYKEDKGLVTKDKGENGSSTD 300
OY 119 EGBELVTAKEVIDAVNKAQRMKTTTANGOTGADKFEYTVSGTNVTFASGKGTATVSK 178
DB 301 EGBELVTAKEVIDAVNKAQRMKTTTANGOTGADKFEYTVSGTNVTFASGKGTATVSK 360
OY 179 DDGQNTVMYDNNVGDALNVNOLNONGMNLDSKAVAGSSGKVISGNVSPSKGMDENVTI 238
DB 361 DDGQNTVMYDNNVGDALNVNOLNONGMNLDSKAVAGSSGKVISGNVSPSKGMDENVTI 420
OY 239 NAGNNIETTRNGKNIDTATSMTPQSSSVSLGAGADAPTLSDYGD-ALNVGSKDKPKPVRI 297
DB 421 NAGNNIETTRNGKNIDTATSMTPQSSSVSLGAGADAPTLSDYGDALNVGSKDKPKPVRI 480
OY 298 TNVAPGVKEDVTNVAOLKGYAQNLRNRIIDVNGNARAGIAQAIATAGLVQAYLPKSKM 357
DB 481 TNVAPGVKEDVTNVAOLKGYAQNLRNRIIDVNGNARAGIAQAIATAGLVQAYLPKSKM 540
OY 358 AIGGTYRGEAGYALGYSSISDGGNMTIKGTASGNSRGHFGASASVGYQW 407
DB 541 AIGGTYRGEAGYALGYSSISDGGNMTIKGTASGNSRGHFGASASVGYQW 590
```

RESULT 9

```
O9JPR7 PRELIMINARY: PRT: 598 AA.
AC O9JPR7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SW2107;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundi E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rapupoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226385; AAF42534.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 598 AA; 62431 MW; 0881CC094F33B4D4 CRC64;
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Query Match 91.6%; Score 1890.5; DB 2; Length 598;
Best Local Similarity 66.4%; Pred. No. 5.1e-83;
Matches 397; Conservative 2; Mismatches 8; Indels 191; Gaps 2;
OY 1 MNKIYRIIWNLSALNAAVYVSELTRNHTKRASATYKTAVALATLTFATVOASA----- 50
DB 1 MNKIYRIIWNLSALNAAVYVSELTRNHTKRASATYKTAVALATLTFATVOASTTDDDDLYLE 60
OY 51 ----- 50
DB 61 PVQRTAPVLSFHADESGTEGKEVIGNTNLGIYFDEKRVLKAGTTTLKAGDNLIKQNDDE 120
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OY 51 ----- 50
DB 121 NFDENTNASSFTYSLKNDLIDLVSETEKLSFGANGKKNVITSDTKGLNFAKETAAGTNGD 180
OY 51 ----- 50
DB 181 TTVALNGISLTLPDTLNGSSASHVDAGNOSTHYTRAASIKDVLNAGNNIKGVKGTGSTTQ 240
OY 51 ANNDVFRYDVTVEFLSADPTKTTTVNVEESKDNKTEYKIGAKTSYKEDKGLVTKDK 110
DB 241 SENDDVFRYDVTVEFLSADPTKTTTVNVEESKDNKTEYKIGAKTSYKEDKGLVTKDK 300
OY 111 GENGSSTDEGGLVTAKEVIDAVNKAQRMKTTTANGOTGADKFEYTVSGTNVTFASGK 170
DB 301 GENGSSTDEGGLVTAKEVIDAVNKAQRMKTTTANGOTGADKFEYTVSGTNVTFASGK 360
OY 171 GTTATVSKDDGNTVMYDNNVGDALNVNOLNONGMNLDSKAVAGSSGKVISGNVSPSKG 230
DB 361 GTTATVSKDDGNTVMYDNNVGDALNVNOLNONGMNLDSKAVAGSSGKVISGNVSPSKG 420
OY 231 KMDETVNIAGNNIETTRNGKNIDTATSMTPQSSSVSLGAGADAPTLSDYGD-DLNVGSK 289
DB 421 KMDETVNIAGNNIETTRNGKNIDTATSMTPQSSSVSLGAGADAPTLSDYGDALNVGSK 480
OY 290 KDNKPVRTTNVAPGVKEDVTNVAOLKGYAQNLRNRIIDVNGNARAGIAQAIATAGLVQ 349
DB 481 DANKPVRTTNVAPGVKEDVTNVAOLKGYAQNLRNRIIDVNGNARAGIAQAIATAGLVQ 540
OY 350 YLPKSKMAIIGGTYRGEAGYALGYSSISDGGNMTIKGTASGNSRGHFGASASVGYQW 407
DB 541 YLPKSKMAIIGGTYRGEAGYALGYSSISDGGNMTIKGTASGNSRGHFGASASVGYQW 598
```

RESULT 10

```
O9JPH0 PRELIMINARY: PRT: 595 AA.
AC O9JPH0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=528; and 1000;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundi E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rapupoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226385; AAF42505.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 595 AA; 62120 MW; 8212C96380142BFC CRC64;
```

```
Query Match 91.6%; Score 1890; DB 2; Length 595;
Best Local Similarity 66.6%; Pred. No. 5.4e-83;
Matches 396; Conservative 4; Mismatches 7; Indels 188; Gaps 2;
OY 1 MNKIYRIIWNLSALNAAVYVSELTRNHTKRASATYKTAVALATLTFATVOASA----- 51
DB 1 MNKIYRIIWNLSALNAAVYVSELTRNHTKRASATYKTAVALATLTFATVOANNTDDEDEL 60
```


QY 52 ----- 51
Db 61 EPVRSALVQFMIDKEGCEIESTDIGNSTYDDHNTLHGATVTLKAGDNLIKONTD 120
QY 52 ----- 51
Db 121 ENTNASSFTYSLKKDLTDLTSVGTSELSFGANGKNVNTSDTKGLNFAKKTAGTNGDTTV 180
QY 52 -----NN 53
Db 181 HLMGISTLTDLTLAGSSASHVDAGNOSTHYTRAASIKDVLNAGMNKGVKGTGSTGSEN 240
QY 54 VDFRTYDTVEFLSADTKTTTVNESKDNKTEVKIGAKTSVKEKDKGLVTKGKGEN 113
Db 241 VDFRTYDTVEFLSADTKTTTVNESKDNKTEVKIGAKTSVKEKDKGLVTKGKGEN 300
QY 114 GSSTDEGEGLVTAKEVIDAVNKAQWMTKTTTANGOTGQADKFEVTSSTNTVTFASGKGT 173
Db 301 GSSTDEGEGLVTAKEVIDAVNKAQWMTKTTTANGOTGQADKFEVTSSTNTVTFASGKGT 360
QY 174 ATYSKDDGNTTYVMYVNGDALNVNOLONGSMNLSKAVAGSSGKVISGNVSPSKGMD 233
Db 361 ATYSKDDGNTTYVMYVNGDALNVNOLONGSMNLSKAVAGSSGKVISGNVSPSKGMD 420
QY 234 ETVNINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKKN 292
Db 421 ETVNINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKDN 480
QY 293 KPVRTNVAPEVKEGDTVNVQALKGVAQNLNRIIDVNGNARAGIAQAIATAGLVQAYLP 352
Db 481 KPVRTNVAPEVKEGDTVNVQALKGVAQNLNRIIDVNGNARAGIAQAIATAGLVQAYLP 540
QY 353 GKSMALIGGTYRGEGAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 407
Db 541 GKSMALIGGTYRGEGAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 595

RESULT 11

Q9JPS2 PRELIMINARY; PRT; 594 AA.
AC Q9JPS2; 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TremBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE31;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B., Galeotti C.L., Iuzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tellelli H., Hood D.W., Jeffries A.C., Saunders N.J., Grassoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226379; AAF42528.1; -;
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 91.5%; Score 1888.5; DB 2; Length 594;
Best Local Similarity 66.7%; Pred. No. 6,4e-83;
Matches 396; Conservative 3; Mismatches 8; Indels 187; Gaps 2;

QY 1 MNKIYRIINMSALNAVVSSELPNNHTKRASATYKATVATLLEFATVOAS----- 50
Db 1 MNKIYRIINMSALNAVVSSELPNNHTKRASATYKATVATLLEFATVOASSTDDDLYLE 60
QY 51 ----- 50
Db 61 PVQRTAPVLSFHADSEGTGKEVTEEDSNMCKVYFDKKGVLTAGTTTLKAGNLKIKONTDE 120
QY 51 ----- 50
Db 121 NTNASSFTYSLKKDLTDLTSVETEKLSEFGANGKNVNTSDTKGLNFAKKTAGTNGDTTVH 180
QY 51 -----ANNV 54
Db 181 LMGISTLTDLTLAGTNTVNDNTDDEKRRASVYKDVLMGNMKNKVPPTTASDNV 240
QY 55 DFRYDTVEFLSADTKTTTVNESKDNKTEVKIGAKTSVKEKDKGLVTKGKGEN 114
Db 241 DFRYDTVEFLSADTKTTTVNESKDNKTEVKIGAKTSVKEKDKGLVTKGKGEN 300
QY 115 SSTDEGEGLVTAKEVIDAVNKAQWMTKTTTANGOTGQADKFEVTSSTNTVTFASGKGT 174
Db 301 SSTDEGEGLVTAKEVIDAVNKAQWMTKTTTANGOTGQADKFEVTSSTNTVTFASGKGT 360
QY 175 TVSKDDGNTTYVMYVNGDALNVNOLONGSMNLSKAVAGSSGKVISGNVSPSKGMD 234
Db 361 TVSKDDGNTTYVMYVNGDALNVNOLONGSMNLSKAVAGSSGKVISGNVSPSKGMD 420
QY 235 TVNINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKKN 293
Db 421 TVNINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKDN 480
QY 294 PVRTNVAPEVKEGDTVNVQALKGVAQNLNRIIDVNGNARAGIAQAIATAGLVQAYLP 353
Db 481 PVRTNVAPEVKEGDTVNVQALKGVAQNLNRIIDVNGNARAGIAQAIATAGLVQAYLP 540
QY 354 KSMALIGGTYRGEGAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 407
Db 541 KSMALIGGTYRGEGAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 594

RESULT 12

Q93QY4 PRELIMINARY; PRT; 594 AA.
AC Q93QY4; 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TremBLrel. 22, Last annotation update)
DE NHA outer membrane protein.
GN NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG327;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF157605; AAK68866.1; -;
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62297 MW; 9DD48B04B3A8EA2 CRC64;

Query Match 91.5%; Score 1887.5; DB 2; Length 594;
Best Local Similarity 66.5%; Pred. No. 7.1e-83;
Matches 395; Conservative 5; Mismatches 7; Indels 187; Gaps 2;
QY 1 MNKIYRIINMSALNAVVSSELPNNHTKRASATYKATVATLLEFATVOAS----- 50
|||||

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Db      1 MNKIRIITWNSALNMAVAVSELTNRNHTKRASATVATAVLATLLPFTVQASTTDDDDLYLE 60
QY      51 -----
Db      61 PVORTAVVLSFRSDKEGTEKEVEDSNMGVYFDKGVLYFAGTITLKGAGDNLIKIKONTNE 120
QY      51 -----
Db      121 NTNASSFTYSLKDLTDLTTSVTEKLSFSANSNKVNITSDTKGLNFAKTAETNGDTVH 180
QY      51 -----
Db      181 LMGIGSTLDTLLTGATTNTNDVYDDEKKRAASVQVNLNAGNIGKVPRTTASDV 240
QY      55 DFTVRYDVEFLSADTKTTTVNVESSKNGKTEVKIGAKTSVKEKDKLVTGKDGENG 114
Db      241 DFTVRYDVEFLSADTKTTTVNVESSKNGKTEVKIGAKTSVKEKDKLVTGKDGEND 300
QY      115 SSTDEGEGVYTAKEVIDAVNKAQRMKTTTANGOTGADKFEYVTSNTNTPFASGKTGA 174
Db      301 SSTKGEGLVYTAKEVIDAVNKAQRMKTTTANGOTGADKFEYVTSNTNTPFASGKTGA 360
QY      175 TVSKDDGNTVMDVNVGDALNVNQLNSGMNLSKAVAGSSGKVISGNVSPSKGKME 234
Db      361 TVSKDDGNTVMDVNVGDALNVNQLNSGMNLSKAVAGSSGKVISGNVSPSKGKME 420
QY      235 TVNINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADPTLSVDG-ALNVGSKDKNK 293
Db      421 TVNINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADPTLSVDGALNVGSKDKNK 480
QY      294 PVRTTNVAPGVKEDVTVNAQLKGYAQNLRNIDVNGNARAGIAQAIATAGLVAYLP 353
Db      481 PVRTTNVAPGVKEDVTVNAQLKGYAQNLRNIDVNGNARAGIAQAIATAGLVAYLP 540
QY      354 KSMAIGGCTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 407
Db      541 KSMAIGGCTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 594

RESULT 13
Q9JPR8 PRELIMINARY: PRT: 599 AA.
AC 09JPR8:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
GN Outer membrane protein GNA992 (Nhha outer membrane protein).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG38;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scariato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capeccchi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H38;
RX Piza M., Scariato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capeccchi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AF226383; AAF42532.1; -.
DR EMBL: AF157608; AAK68869.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 599 AA; 62844 MW; BBA16BEBF53C1970C CRC64;

Query Match      91.4%; Score 1886; DB 2; Length 599;
Best Local Similarity 66.1%; Pred. No. 8; Se-83;
Matches 396; Conservative 3; Mismatches 8; Indels 192; Gaps 2;

QY      1 MNKIRIITWNSALNMAVAVSELTNRNHTKRASATVATAVLATLLPFTVQASA----- 51
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QY      52 -----
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QY      52 -----
Db      121 KNTNENTDSSFTYSLKDLTDLTTSVTEKLSFGANGKNKVNITSDTKGLNFAKETAGTNG 180
QY      52 -----
Db      181 DTTVHLNGIGSTLDTLLTGATTNTNDVYDDEKKRAASVQVNLNAGNIGKVPRTT 240
QY      52 --NNVDFTVRYDVEFLSADTKTTTVNVESSKNGKTEVKIGAKTSVKEKDKLVTKGD 109
Db      241 ASDNVDFVHTYDVEFLSADTKTTTVNVESSKNGKTEVKIGAKTSVKEKDKLVTKGD 300
QY      110 KGENSSSTDEGEGVYTAKEVIDAVNKAQRMKTTTANGOTGADKFEYVTSNTNTPFASG 169
Db      301 KGENSSSTDEGEGVYTAKEVIDAVNKAQRMKTTTANGOTGADKFEYVTSNTNTPFASG 360
QY      170 KGTATVSKDDGNTVMDVNVGDALNVNQLNSGMNLSKAVAGSSGKVISGNVSPSK 229
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Db      421 GKMDFTVNIAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADPTLSVDGKALNVGS 480
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AC 09JPI3:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
GN Outer membrane protein GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88; B2232;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scariato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capeccchi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

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RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226376; AAF42525.1; -;
DR EMBL: AF226369; AAF42518.1; -;
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04B6 CRC64;

Query Match 91.3%; Score 1884.5; DB 2; Length 594;
Best Local Similarity 66.5%; Pred. No. 9, 9e-83;
Matches 395; Conservative 3; Mismatches 9; Indels 187; Gaps 2;

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QY 51 ----- 50
DB 121 NTNASSFTYSLKDLTLDTLTVETEKLSFGANGKRVNITSDTKGLNFAKETAGTNGDTVH 180
QY 51 -----ANV 54
DB 181 LNCIGSTLTDLTLNTGATTNTNDVNTDEKKRAASVYKDVNLNAGMNKGVKPGTTASDNY 240
QY 55 DEVRTYDVEFLSADTKTTTVNVESEKDNKTEVKIGAKTSVIREKDKLVTGDKGENG 114
DB 241 DEVRTYDVEFLSADTKTTTVNVESEKDNKTEVKIGAKTSVIREKDKLVTGDKGENG 300
QY 115 SSTDEGELVTAKVIDAVNKAQRMKTTTANGQTQADKFEVTSVSGTNVTFASGKGT 174
DB 301 SSTDEGELVTAKVIDAVNKAQRMKTTTANGQTQADKFEVTSVSGTNVTFASGKGT 360
QY 175 TVSKDQDGNITVYVNVGDALNVNOLNSGMNLDKSAVAGSSGVISGNSVPSKGMDE 234
DB 361 TVSKDQDGNITVYVNVGDALNVNOLNSGMNLDKSAVAGSSGVISGNSVPSKGMDE 420
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DB 421 TVNINAGNNIETTRNGKNIDIAATSMTPQFSSVSLGAGADAPTLISVDDEBALVSGSKDANK 480
QY 294 PVRTITNAPGVKEGDTVNVVQOLKGYAQNLRIDVNGNARAGIAQAIATAGLVQAYLP 353
DB 481 PVRTITNAPGVKEGDTVNVVQOLKGYAQNLRIDVNGNARAGIAQAIATAGLVQAYLP 540
QY 354 KSMMAIGGTYRGEGYVAGYVAGYVAGYVAGYVAGYVAGYVAGYVAGYVAGYVAGYV 407
DB 541 KSMMAIGGTYRGEGYVAGYVAGYVAGYVAGYVAGYVAGYVAGYVAGYVAGYV 594

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AC Q9JPS8:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBL_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A22;
RX MEDLINE=20175756; PubMed=10710308;

RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,
RA Galotti C.L., Iuzzo E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarelli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Moxon E.R., Grandi G., Saunders N.J., Granoff D.M., Venter C.,
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226364; AAF42513.1; -;
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 599 AA; 62693 MW; 46C2E974AF7F78E9 CRC64;

Query Match 91.3%; Score 1883; DB 2; Length 599;
Best Local Similarity 66.1%; Pred. No. 1, 2e-82;
Matches 396; Conservative 3; Mismatches 8; Indels 192; Gaps 2;

QY 1 MNKIYRIIWNLSALNMAVYVSELTRNHTKRASATVATLTLFATVOAS----- 50
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QY 51 ----- 50
DB 61 EPVKRTAVVLSFRSDEKTEGEKEVTEEDSHMGVYFDEKGVLLAKGTTTLKAGDNLKIKQNTD 120
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QY 51 ----- 50
DB 181 DPTVHLNGIGSTLTDLTLASSASHVDAGNOSTHYTPAASIKVNLNAGMNKGVKKTSTNG 240
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DB 241 QSENVDFVRTYDVEFLSADTKTTTVNVESEKDNKTEVKIGAKTSVIREKDKLVTGKG 300
QY 110 KGENSGSTDEGEGLVYAKVIDAVNKAQRMKTTTANGQTQADKFEVTSVSGTNVTFASG 169
DB 301 KGENSGSTDEGEGLVYAKVIDAVNKAQRMKTTTANGQTQADKFEVTSVSGTNVTFASG 360
QY 170 KGTATVSKDQDGNITVYVNVGDALNVNOLNSGMNLDKSAVAGSSGVISGNSVPSK 229
DB 361 KGTATVSKDQDGNITVYVNVGDALNVNOLNSGMNLDKSAVAGSSGVISGNSVPSK 420
QY 230 GRMDETUNINAGNNIETTRNGKNIDIAATSMTPQFSSVSLGAGADAPTLISVDG- DALNVGS 288
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QY 289 KKDNRPVRTITNAPGVKEGDTVNVVQOLKGYAQNLRIDVNGNARAGIAQAIATAGLVQ 348
DB 481 KKDNRPVRTITNAPGVKEGDTVNVVQOLKGYAQNLRIDVNGNARAGIAQAIATAGLVQ 540
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Job time : 32.8927 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2003, 09:05:45 ; Search time 37.1842 Seconds
(without alignments)
1848.329 Million cell updates/sec

Title: US-09-771-382-26

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:	Minimum Match 0%
	Maximum Match 100%
	Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2197	100.0	433	22	AAU06185	N. meningitidis PM
2	2147.5	97.7	512	22	AAU06182	N. meningitidis PM
3	2108	95.9	591	20	AAV27202	Amino acid sequenc
4	2108	95.9	591	20	AAV23746	A surface protein
5	2108	95.9	591	22	AAU06171	N. meningitidis PM
6	2103.5	95.7	592	20	AAV23737	A surface protein
7	2101	95.6	591	21	AAV57045	BASB029 amino acid
8	2098.5	95.5	502	22	AAU06186	N. meningitidis PM
9	2096	95.4	591	20	AAV23741	A surface protein

10	2096	95.4	591	22	AAU06185	N. meningitidis EG
11	2095	93.5	513	22	AAU06183	N. meningitidis H4
12	2040	92.9	407	22	AAU06184	N. meningitidis PM
13	2032.5	92.5	594	20	AAI23740	A surface protein
14	2032.5	92.5	594	21	AAI23704	BAS029 amino acid
15	2032.5	92.5	594	22	AAU06174	N. meningitidis EG
16	2032	92.5	599	20	AAU03743	A surface protein
17	2032	92.5	599	22	AAU06176	N. meningitidis H3
18	2025.5	92.2	594	20	AAI23739	A surface protein
19	2025.5	92.2	594	22	AAU06179	N. meningitidis B2
20	2015.5	91.7	592	20	AAU03744	A surface protein
21	2015.5	91.7	592	22	AAU06172	N. meningitidis H4
22	2010.5	91.5	598	20	AAU03742	A surface protein
23	2010.5	91.5	598	22	AAU06177	N. meningitidis H1
24	2009.5	91.5	592	22	AAU06180	N. meningitidis Z2
25	2001.5	91.1	598	20	AAI23738	A surface protein
26	2001.5	91.1	598	22	AAU06178	N. meningitidis B2
27	1979.5	90.1	592	20	AAU037203	Amino acid sequenc
28	1964	89.4	589	20	AAU03745	A surface protein
29	1964	89.4	589	22	AAU06173	N. meningitidis P2
30	1852.5	84.3	604	22	AAU06181	N. meningitidis su
31	776.5	35.3	1098	17	AAU09332	Haemophilus adhe
32	748.5	34.1	1094	21	AAU03858	Haemophilus influe
33	736	33.5	2411	21	AAU03860	Haemophilus influe
34	734	33.4	2353	17	AAU09393	Haemophilus adhe
35	600	27.3	116	21	AAU037832	Neisserial conserv
36	562	25.6	679	17	AAU09394	Haemophilus adhe
37	562	25.6	679	21	AAU03855	Haemophilus influe
38	487.5	22.2	1002	21	AAU03854	Haemophilus influe
39	475.5	21.6	1104	21	AAU03857	Haemophilus influe
40	397.5	18.1	1104	21	AAU03856	Haemophilus influe
41	397.5	18.1	1104	21	AAU03859	Haemophilus influe
42	378	17.2	245	20	AAU072201	Amino acid sequenc
43	366	16.7	72	21	AAU037830	Neisserial conserv
44	359	16.3	2139	24	ABP11294	M. catarrhalis sur
45	357.5	16.3	2314	22	AAU06136	M. catarrhalis sur

ALIGNMENTS

RESULT 1	ID	AAU06185	AAU06185 standard; Protein; 433 AA.
XX	AC	AAU06185;	
XX	DT	24-OCT-2001 (first entry)	
XX	DE	N. meningitidis PMC21 Nhha deletion mutant #3.	
XX	KW	Surface antigen Nhha; meningococcal disease; meningitis vaccine mutant; muteln.	
XX	OS	Neisseria meningitidis strain PMC21.	
XX	OS	Synthetic.	
XX	FT	Key	Location/Qualifiers
XX	FT	Peptide	1..51
XX	FT	Protein	/label= Signal_peptide
XX	FT		52..433
XX	FT		/label= Mature_Nhha_deletion_mutant_#3
XX	FT		/note= "predicted mature protein, specifically claimed in claim 12"
XX	PN	WO20015182-A1.	
XX	PD	02-AUG-2001.	
XX	PF	25-JAN-2001; 2001WO-AU00069.	
XX	PR	25-JAN-2000; 2000US-0177917.	

PA (UYOU) UNIV QUEENSLAND.
 XX
 PI Peak IRA, Jennings MP;
 XX
 DR WPI: 2001-488774/53.
 DR N-PSDB: AAS09175.
 XX
 PT New Nhba surface antigen polypeptides and polynucleotides from
 PT Neisseria meningitidis, useful in producing vaccines for treating or
 PT preventing broad spectrum of Neisseria meningitidis -
 XX
 PS Claim 12; Fig 8; 91pp; English.
 XX
 CC The present invention relates to the isolation of novel Neisseria
 CC meningitidis mutant polypeptides of the surface antigen Nhba
 CC (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are
 CC characterised by deletions of non-conserved amino acids, particularly
 CC the deletion of variable regions. The deletion mutants are useful in
 CC diagnostics, therapeutic and prophylactic vaccines against a broader
 CC spectrum of N. meningitidis, and in designing and/or screening of
 CC immunisations. The mutant proteins when used as a vaccine can effectively
 CC immunise against a broader spectrum of N. meningitidis strains than
 CC would be expected from a corresponding wild-type surface antigen.
 CC The present sequence represents N. meningitidis strain PMC21 surface
 CC antigen Nhba deletion mutant #3.
 CC
 SO Sequence 433 AA;

Query Match 100.0%; Score 2197; DB 22; Length 433;
 Best Local Similarity 100.0%; Pred. No. 5.7e-137;
 Matches 433; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 61 LNAAGNNTKGVKPGTTASDNDVFRITDVEFLSADTKTTVNVESKNGKTEYKIGAKT 120
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 DB 121 SVIEKEDGKLVTKDGENSGSTDEGEGLVTAKEVIDAVNKAAGNMTKTTTANGOTGQADK 180
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 QY 241 GSSGKVISGNVSPSKGKDETVNINAGNNEITRNGKNIDTATSPTPSSVSLGAGADA 300
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 QY 241 GSSGKVISGNVSPSKGKDETVNINAGNNEITRNGKNIDTATSPTPSSVSLGAGADA 300
 DB 241 GSSGKVISGNVSPSKGKDETVNINAGNNEITRNGKNIDTATSPTPSSVSLGAGADA 300
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 QY 421 GHFGASASVGYOW 433
 DB 421 GHFGASASVGYOW 433

RESULT 2
 ID AAU06182 standard; Protein: 512 AA.
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 AC AAU06182;
 XX
 DT 24-OCT-2001 (first entry)
 XX

DE N. meningitidis PMC21 Nhba deletion mutant #1.
 XX
 KW Surface antigen Nhba; meningococcal disease; meningitis vaccine;
 KW mutant; muten.
 XX
 OS Neisseria meningitidis strain PMC21.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FH Peptide 1..51
 FH Protein /label= Signal_peptide
 FH 52..512
 FH /note= "Mature_Nhba_deletion_mutant_#1
 FH /label= Predicted mature protein, specifically
 FH claimed in claim 12"
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 PN WO200155182-A1.
 XX
 PD 02-AUG-2001.
 XX
 PP 25-JAN-2001; 2001WO-AU00069.
 XX
 PR 25-JAN-2000; 2000US-0177917.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 XX
 PI Peak IRA, Jennings MP;
 XX
 DR WPI: 2001-488774/53.
 DR N-PSDB: AAS09172.
 XX
 PT New Nhba surface antigen polypeptides and polynucleotides from
 PT Neisseria meningitidis, useful in producing vaccines for treating or
 PT preventing broad spectrum of Neisseria meningitidis -
 XX
 PS Claim 12; Fig 5; 91pp; English.
 XX
 CC The present invention relates to the isolation of novel Neisseria
 CC meningitidis mutant polypeptides of the surface antigen Nhba
 CC (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are
 CC characterised by deletions of non-conserved amino acids, particularly
 CC the deletion of variable regions. The deletion mutants are useful in
 CC diagnostics, therapeutic and prophylactic vaccines against a broader
 CC spectrum of N. meningitidis, and in designing and/or screening of
 CC immunisations. The mutant proteins when used as a vaccine can effectively
 CC immunise against a broader spectrum of N. meningitidis strains than
 CC would be expected from a corresponding wild-type surface antigen.
 CC The present sequence represents N. meningitidis strain PMC21 surface
 CC antigen Nhba deletion mutant #1.
 CC
 SO Sequence 512 AA;

Query Match 97.7%; Score 2147.5; DB 22; Length 512;
 Best Local Similarity 84.6%; Pred. No. 1.3e-133;
 Matches 433; Conservative 0; Mismatches 0; Indels 79; Gaps 1;

QY 1 MNKIYRIIMNSALNAAVYSELTRNHTKRASATVKTAVLATLLEFATVQASAN----- 52
 DB 1 MNKIYRIIMNSALNAAVYSELTRNHTKRASATVKTAVLATLLEFATVQASANNETDLTSV 60
 QY 53 -----
 DB 53 -----
 QY 61 GTEKLSFSGANGKNVITSDFKGLNFAKETAGTNGDTVHLNGISLTDLTLNLTGATTNV 120
 DB 61 GTEKLSFSGANGKNVITSDFKGLNFAKETAGTNGDTVHLNGISLTDLTLNLTGATTNV 120
 QY 53 -----
 DB 53 -----
 QY 121 TNDNVTDEKRRASAVKDYLNAGNNTKGVKGTASDNDVFRITDVEFLSADTKTTTV 180
 DB 121 TNDNVTDEKRRASAVKDYLNAGNNTKGVKGTASDNDVFRITDVEFLSADTKTTTV 180
 QY 102 NVESKDNKKTTEYKIGAKTSYIKEDGKLVTKDGENSGSTDEGEGLVTAKEVIDAVNK 161
 DB 102 NVESKDNKKTTEYKIGAKTSYIKEDGKLVTKDGENSGSTDEGEGLVTAKEVIDAVNK 161
 QY 181 NVESKDNKKTTEYKIGAKTSYIKEDGKLVTKDGENSGSTDEGEGLVTAKEVIDAVNK 240
 DB 181 NVESKDNKKTTEYKIGAKTSYIKEDGKLVTKDGENSGSTDEGEGLVTAKEVIDAVNK 240
 QY 162 AGWRMKTTTANGOTGQADKDFETVTSIGTVTFASGKGTATVSKDDGNTVMYDVNVDGA 221

Db 241 AGWRMKTATTANGOTGADKFEETVTSCTNTVFASGKGTATVSKDDGNTITMTDVNWGDA 300
QY 222 LNVNQLQNSGWNLDKAAVAGSSGKVISGNVSPSKGKDETVNTNAGNNIEITRNGKNIDI 281
Db 301 LNVNQLQNSGWNLDKAAVAGSSGKVISGNVSPSKGKDETVNTNAGNNIEITRNGKNIDI 360
QY 282 ATSMTPQFSSVSLGAGADAPTLISVDGDLNVGSKKNPKPVRTTNVAPGVKESDVTVAOL 341
Db 361 ATSMTPQFSSVSLGAGADAPTLISVDGDLNVGSKKNPKPVRTTNVAPGVKESDVTVAOL 420
QY 342 KGVANQLNNRINDVNDGNARAGIAQAATAGLVQAYLPGRKSMAIGGTYRGEAGYAIGYS 401
Db 421 KGVANQLNNRINDVNDGNARAGIAQAATAGLVQAYLPGRKSMAIGGTYRGEAGYAIGYS 480
QY 402 SISDGGNMIITKGTASGNSRGHFGASASVGYOW 433
Db 481 SISDGGNMIITKGTASGNSRGHFGASASVGYOW 512

RESULT 3
AA27202
ID AA27202 standard; Protein; 591 AA.
XX
AC AA27202;
XX
DT 24-SEP-1999 (first entry)
XX
DE Amino acid sequence of N. meningitidis protein ORF40-1.
XX
KM Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;
KW bacterial infection; treatment.
OS Neisseria meningitidis.
XX
PN WO936544-A2.
PD 22-JUL-1999.
XX
PF 14-JAN-1999; 99MO-IB00103.
PR 09-OCT-1998; 98GB-0022143.
PR 14-JAN-1998; 98GB-0000760.
PR 01-SEP-1998; 98GB-0019015.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Grandi G, Maignani V, Pizza M, Rappuoli R, Scarlato V;
XX
DR MPI; 1999-444400/37.
DR N-PSDB; AAX99124.
XX
PT New protein and its nucleotide sequence, useful in vaccines or
PT diagnostic compositions for treating and/or preventing Neisseria
PT meningitidis infections
XX
PS Claim 1; Page 62; 123pp; English.
XX
CC The invention provides proteins (AA27201-245) from Neisseria
CC meningitidis (strains A and B) and nucleic acid sequences (AA29123-167)
CC encoding the proteins. Compositions comprising the protein, nucleic acid
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a
CC vaccine composition or a diagnostic composition. The composition is also
CC useful for treating or preventing an infection due to Neisseria
CC bacteria, especially Neisseria meningitidis.
XX
SQ Sequence 591 AA;

Query Match 95.9%; Score 2108; DB 20; Length 591;
Best Local Similarity 73.3%; Pred. No. 6.2e-131;
Matches 433; Conservative 0; Mismatches 0; Indels 158; Gaps 1;
QY 1 MNKTYRIWNSALNANWVWVSELTNRNHTKRASATVKTAVLATLTFATVQASAN-----52

Db 1 MNKTYRIWNSALNANWVWVSELTNRNHTKRASATVKTAVLATLTFATVQASANNEQEDL 60
QY 53 -----52
Db 61 YLDPVORTAVAVLIVNSDKREGTGEKEVEENSMDAVYFNEKGLTAREITLKAGDNLIKQ 120
QY 53 -----52
Db 121 NGTNFTYSLKKDLTLTSVGTETKLSFSAANGKNYNTSDTKGLNFAKETAGTNGDITVHLN 180
QY 53 -----RAASVADVNLNAGNNINGVAPGTTASDNVDF 82
Db 181 GIGSTLTDPLTNGATTNTNDVNTDDEKKRAASVADVNLNAGNNINGVAPGTTASDNVDF 240
QY 83 VRTYDVEEFLSADTKTTTNNVESKDKGKTEVIGAKTSYIKEDKLVTKGDKGENGSS 142
Db 241 VRTYDVEEFLSADTKTTTNNVESKDKGKTEVIGAKTSYIKEDKLVTKGDKGENGSS 300
QY 143 TDEGEGLVTAKEVIDAVNKRAGMRKTTTANGOTGADKFEETVTSCTNTVFASGKGTATV 202
Db 301 TDEGEGLVTAKEVIDAVNKRAGMRKTTTANGOTGADKFEETVTSCTNTVFASGKGTATV 360
QY 203 SKDDGNTITVMDVNVGDALNVNQLQNSGWNLDKAAVAGSSGKVISGNVSPSKGKDETV 262
Db 361 SKDDGNTITVMDVNVGDALNVNQLQNSGWNLDKAAVAGSSGKVISGNVSPSKGKDETV 420
QY 263 NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLISVDGDLNVGSKKNPKPV 322
Db 421 NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLISVDGDLNVGSKKNPKPV 480
QY 323 ITNVAPGVKESDVTVAOLKGVANQLNNRINDVNDGNARAGIAQAATAGLVQAYLPGRKS 382
Db 481 ITNVAPGVKESDVTVAOLKGVANQLNNRINDVNDGNARAGIAQAATAGLVQAYLPGRKS 540
QY 383 MAIGGTYRGEAGYAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 433
Db 541 MAIGGTYRGEAGYAIGYSSISDGGNMIITKGTASGNSRGHFGASASVGYOW 591

RESULT 4
AA23746
ID AA23746 standard; Protein; 591 AA.
XX
AC AA23746;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KM Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
OS Neisseria meningitidis.
XX
PN WO931132-A1.
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98MO-AU01031.
PR 12-DEC-1997; 97GB-0026398.
PR (ISIS-) ISIS INNOVATION LTD.
PA (UYOU) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX
DR MPI; 1999-418754/35.
DR N-PSDB; AAX85798.
XX
PT Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections

XX Claim 1; Page 127-128; 132pp; English.

PS The present sequence represents a surface protein of *Neisseria*
 CC meningitidis which is approximately 62 kDa. The *N. meningitidis*
 CC surface glycoproteins, nucleic acids, the primers and optionally
 CC a thermostable polymerase, or antibodies are useful in a kit for
 CC the detection or diagnosis of *N. meningitidis* infection in humans.
 CC The *N. meningitidis* surface glycoproteins can also be used to
 CC prevent or treat *N. meningitidis* infection in humans, especially
 CC in the form of vaccines. The proteins and antibodies can also
 CC be used to identify immunoreactive peptides.

XX Sequence 591 AA;

Query Match 95.9%; Score 2108; DB 20; Length 591;

Best Local Similarity 73.3%; Pred. No. 6 2e-131; Matches 433; Conservative 0; Mismatches 0; Indels 158; Gaps 1;

```

QY 1 MNKIRIIMNSALNMMVYSELTRNHTKRASATVAVLATLLEFATVQASAN----- 52
DB 1 MNKIRIIMNSALNMMVYSELTRNHTKRASATVAVLATLLEFATVQASANNEQEDL 60
QY 53 ----- 52
DB 61 YIDPVQRTVAVLIIVNSDEKGEKGEKVEENSDMAVYFNEKGVLTAREITLKAGDNLKIQ 120
QY 53 ----- 52
DB 121 NGTFNTYSIKKDLTDLTSVTEKLSFSAANGKNVNTSDTKGLNFAKETAGTNGDTTVHIN 180
QY 53 -----RAASVKDVLNAGWNIKGVKPGTTASDNVE 82
DB 181 GIGSTLTDTLLNTGATFNTVNDNTDDEKKRAASKVDVNLNAGWNIKGVKPGTTASDNVE 240
QY 83 VETVDTVEFLSADTETTVNVESKNGKKEVYKIAKTSVYKEKKGKLVTKGDKENGSS 142
DB 241 VETVDTVEFLSADTETTVNVESKNGKKEVYKIAKTSVYKEKKGKLVTKGDKENGSS 300
QY 143 TDEGGLVTAKEVIDAVNKAQRMTTANQOTGADKFEYVTSNTVTFASGKGTATV 202
DB 301 TDEGGLVTAKEVIDAVNKAQRMTTANQOTGADKFEYVTSNTVTFASGKGTATV 360
QY 203 SKDDGNTVTMDVNVGDLNVLNOLNSGWNLSKRAVAGSSGKVIISGVNPSKGMDET 262
DB 361 SKDDGNTVTMDVNVGDLNVLNOLNSGWNLSKRAVAGSSGKVIISGVNPSKGMDET 420
QY 263 NINAGNNEITRNKGNIDATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKNKPYR 322
DB 421 NINAGNNEITRNKGNIDATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKNKPYR 480
QY 333 ITNVAQVKEGDDVTVAOLKGYAQNLLNNRIDVDGNARAGIAQALATAGLVQAYLPKGS 382
DB 481 ITNVAQVKEGDDVTVAOLKGYAQNLLNNRIDVDGNARAGIAQALATAGLVQAYLPKGS 540
QY 383 MAIGGGTYRGEAGVYAGYSSISDGGNWIITKGTASGNSRCHFGASASVGYQW 433
DB 541 MAIGGGTYRGEAGVYAGYSSISDGGNWIITKGTASGNSRCHFGASASVGYQW 591

```

RESULT 5
 AAU06171
 ID AAU06171 standard; Protein; 591 AA.

XX AAU06171;

DT 24-OCT-2001 (first entry)

DE N. meningitidis PMC21 surface antigen Noha polypeptide sequence.

KV Surface antigen Noha; meningococcal disease; meningitis vaccine.

OS *Neisseria meningitidis* strain PMC21.

```

XX Key
FH Peptide
FT 1..51
FT /label= Signal_peptide
FT 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT 51..108
FT /label= V1
FT /note= "Variable region 1"
FT 52..591
FT /label= Mature_Noha
FT /note= "Predicted mature protein, specifically
FT claimed in claim 12"
FT 109..120
FT /label= C2
FT /note= "Conserved region 2"
FT 121..124
FT /label= V2
FT /note= "Variable region 2"
FT 125..188
FT /label= C3
FT /note= "Conserved region 3"
FT 189..210
FT /label= V3
FT /note= "Variable region 3"
FT 211..229
FT /label= C4
FT /note= "Conserved region 4"
FT 230..236
FT /label= V4
FT /note= "Variable region 4"
FT 237..591
FT /label= C5
FT /note= "Conserved region 5"

```

WO20015182-A1.

PD 02-AUG-2001.

XX 25-JAN-2001; 2001WO-AU00069.

XX 25-JAN-2000; 2000US-0177917.

XX (UYOU) UNIT QUEENSLAND.

PI Peak IRA, Jennings MP;

XX WPI: 2001-488774/53.

DR N-PSDB; AAS09161.

XX New Noha surface antigen polypeptides and polynucleotides from

PT *Neisseria meningitidis*, useful in producing vaccines for treating or

PT preventing broad spectrum of *Neisseria meningitidis* -

XX Claim 9; Fig 1; 91pp; English.

PS The present invention relates to the isolation of novel *Neisseria*

CC meningitidis mutant polypeptides of the surface antigen Noha

CC (AAU06182-AAU06186). The modified or mutant Noha polypeptides are

CC characterised by deletions of non-conserved amino acids, particularly

CC the deletion of variable regions. The deletion mutants are useful in

CC diagnostics, therapeutic and prophylactic vaccines against a broader

CC spectrum of *N. meningitidis*, and in designing and/or screening of

CC medicaments. The mutant proteins when used as a vaccine can effectively

CC immunise against a broader spectrum of *N. meningitidis* strains than

CC would be expected from a corresponding wild-type surface antigen.

CC The present sequence representing the wild type surface antigen Noha

CC from *N. meningitidis* strain PMC21 is 1 of 10 Noha polypeptide sequences

CC (AAU06171-AAU06180) from 10 different *N. meningitidis* strains given in

CC the present invention.

XX Sequence 591 AA;

Query Match 95.9%; Score 2108; DB 22; Length 591;
Best Local Similarity 73.3%; Pred. No. 6.2e-131;
Matches 433; Conservative 0; Mismatches 0; Indels 158; Gaps 1;

```
QY 1 MNKITYIINNSALNANVWVSELTRNHTKRASATVKTAVALATLLEFATVOASAN----- 52
DB 1 MNKITYIINNSALNANVWVSELTRNHTKRASATVKTAVALATLLEFATVOASANNEQEDDL 60
QY 53 ----- 52
DB 61 YLDPVQRTVAVLIVNSDKEGTGEKEVEENSDMAVYFNEKGYLTAREITLKAGDNLIK 120
QY 53 ----- 52
DB 121 NGTNFTYSLKQDLTDLTSVGTETKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLN 180
QY 53 -----RAASVQDVNLNAGNINIKGVKPGTTASDNVD 82
DB 181 GIGSTLTDLTNTGATTNTVNDVTDDEKKRAASVQDVNLNAGNINIKGVKPGTTASDNVD 240
QY 83 VRTYDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIREKDKLVTGKDKGENSS 142
DB 241 VRTYDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIREKDKLVTGKDKGENSS 300
QY 143 TDEGEGLYTAKKEYIDAVNKAQWPKRTTTANGOTGQADKFEYTSCTNTVFASGKGTATY 202
DB 301 TDEGEGLYTAKKEYIDAVNKAQWPKRTTTANGOTGQADKFEYTSCTNTVFASGKGTATY 360
QY 203 SKDDOGNTVMDVNVGDLNVLNOLONGSMNLDKSAVAGSSGKVISGNVSPSKGMDY 262
DB 361 SKDDOGNTVMDVNVGDLNVLNOLONGSMNLDKSAVAGSSGKVISGNVSPSKGMDY 420
QY 263 NINAGNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKKPY 322
DB 421 NINAGNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKKPY 480
QY 323 ITNVAPEVEGDTVNAQLKGYAQNLRIDNVGNARAGIAQAITAGLVQAYLPKGS 382
DB 481 ITNVAPEVEGDTVNAQLKGYAQNLRIDNVGNARAGIAQAITAGLVQAYLPKGS 540
QY 383 MAIGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 433
DB 541 MAIGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 591

RESULT 6
AA23737
ID AAY23737 standard; Protein; 592 AA.
XX
AC AAY23737;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KM Surface protein; surface glycoprotein; infection; vaccine;
XX
OS Immunoreactive peptide.
XX
XX Neisseria meningitidis.
XX
PN MO9931132-A1.
PD 24-JUN-1999.
XX
PE 14-DEC-1998; 98WO-AU01031.
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX (ORQV) UNITV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
```

```
XX WP1: 1999-418754/35.
DR N-PSDB; AAX85788.
XX
PT Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
PS Claim 1; Page 86-87; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 592 AA;
```

Query Match 95.7%; Score 2103.5; DB 20; Length 592;
Best Local Similarity 73.0%; Pred. No. 1.2e-130;
Matches 432; Conservative 0; Mismatches 1; Indels 159; Gaps 1;

```
QY 1 MNKITYIINNSALNANVWVSELTRNHTKRASATVKTAVALATLLEFATVOASAN----- 52
DB 1 MNKITYIINNSALNANVWVSELTRNHTKRASATVKTAVALATLLEFATVOASANRRPKRD 60
QY 53 ----- 52
DB 61 YLDPVQRTVAVLIVNSDKEGTGEKEVEENSDMAVYFNEKGYLTAREITLKAGDNLIK 120
QY 53 ----- 52
DB 121 QNCTNFTYSLKQDLTDLTSVGTETKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHL 180
QY 53 -----RAASVQDVNLNAGNINIKGVKPGTTASDNVD 81
DB 181 NGIGSTLTDLTNTGATTNTVNDVTDDEKKRAASVQDVNLNAGNINIKGVKPGTTASDNVD 240
QY 82 FVRTYDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIREKDKLVTGKDKGENS 141
DB 241 FVRTYDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIREKDKLVTGKDKGENS 300
QY 142 STDEGEGLYTAKKEYIDAVNKAQWPKRTTTANGOTGQADKFEYTSCTNTVFASGKGTAT 201
DB 301 STDEGEGLYTAKKEYIDAVNKAQWPKRTTTANGOTGQADKFEYTSCTNTVFASGKGTAT 360
QY 202 VSKDDOGNTVMDVNVGDLNVLNOLONGSMNLDKSAVAGSSGKVISGNVSPSKGMDY 261
DB 361 VSKDDOGNTVMDVNVGDLNVLNOLONGSMNLDKSAVAGSSGKVISGNVSPSKGMDY 420
QY 262 VNINAGNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKKPY 321
DB 421 VNINAGNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKKPY 480
QY 322 RITNVAPEVEGDTVNAQLKGYAQNLRIDNVGNARAGIAQAITAGLVQAYLPKGS 361
DB 481 RITNVAPEVEGDTVNAQLKGYAQNLRIDNVGNARAGIAQAITAGLVQAYLPKGS 540
QY 382 MAIGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 433
DB 541 MAIGGTYRGEAGYAIIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 592

RESULT 7
AAY57045
ID AAY57045 standard; Protein; 591 AA.
XX
AC AAY57045;
XX
DT 21-FEB-2000 (first entry)
```

```

XX BASB029 amino acid sequence from N. meningitidis strain H44/76.
DE
XX
XX BASB029: Neisseria meningitidis; surface fibril protein; HSF; diagnosis;
KM infection; treatment; prevent; antibacterial drug.
XX
XX Neisseria meningitidis.
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 90
FT /note= "Encoded by AAT"
FT Misc-difference 92
FT /note= "Encoded by GAT"
FT Misc-difference 98
FT /note= "Encoded by AAC"
FT Misc-difference 108
FT /note= "Encoded by AATC"
FT Misc-difference 123
FT /note= "Encoded by ACA"
FT Misc-difference 269
FT /note= "Encoded by AAA"
FT Misc-difference 389
FT /note= "Encoded by CGT"
XX
XX WO958683-A2.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-EP03255.
XX
XX 13-MAY-1998; 98GB-0010276.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX
XX Ruelle J;
XX
XX WPI: 2000-053103/04.
XX
XX N-PSDB: AA239865.
XX
XX
XX New polypeptide from neisseria meningitidis useful for diagnosis,
PT treatment or prevention of bacterial infections in mammal
XX
XX
XX Claim 4; Fig 2; 74pp; English.
XX
XX
XX This is the Neisseria meningitidis BASB029 amino acid sequence from
CC serogroup B strain H44/76. The BASB029 protein is homologous to the
CC Haemophilus influenzae surface fibril (HSF) protein. The invention
CC relates to BASB029 polynucleotide sequences (AA239864-239865) and
CC polypeptide sequences (AA57044-57045) and their immunogenic fragments.
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria
CC meningitidis infection in a mammal. Compositions containing BASB029
CC polynucleotides and polypeptides are useful for generating an immune
CC response in an animal. A therapeutic composition comprising an antibody
CC directed against BASB029 is useful in treating humans with Neisseria
CC meningitidis disease. The polynucleotide is useful in the diagnosis of
CC the stage of infection, type of infection, susceptibility to an
CC infection which results from increased or decreased expression of the
CC polynucleotide, and for therapeutic or prophylactic purposes.
CC particularly genetic immunisation. Antibodies against BASB029
CC polynucleotides and polypeptides are also useful for treating infections
CC particularly bacterial infections. The protein is useful in the
CC screening and development of antibacterial drugs. Fused recombinant
CC protein is useful for the stimulation of the immune system of an organism
CC receiving the protein.
XX
XX
XX Sequence 591 AA:
XX
XX Query Match 95.6%; Score 2101; DB 21; Length 591;
XX Best Local Similarity 72.9%; Pred. No. 1.8e-130;
XX Matches 431; Conservative 1; Mismatches 1; Indels 158; Gaps 1;
XX
XX 1 MKKIRITWNSALNMAVAVSELTRNHTKRASATVTAVALTLLEFATVQASAN----- 52
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

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Db 1 MKKIRITWNSALNMAVAVSELTRNHTKRASATVTAVALTLLEFATVQASANNEQEEDL 60
QY 53 ----- 52
Db 61 YLDPVORTVAVLIVNSDEKGEKKEVEEDSNMAYFPEDEKGLVTAAREITLAKGDLKIKO 120
QY 53 ----- 52
Db 121 NGSNFTYSLKKDLFDLTLSVTEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTYHLN 180
QY 53 -----RAASVKDVLNMGWNTKGVKPGTTASDNDVF 240
Db 181 GIGSTLTDLTLLNTGATTVTNDVNTDDEKKRAASVAVDLNMGWNTKGVKPGTTASDNDVF 240
QY 83 VRTYDVEFLSADFTKTVTVNVESSKNGKTEVKIGAKTSYVKEKDKLVTEGDKGENGSS 142
Db 241 VRTYDVEFLSADFTKTVTVNVESSKNGKTEVKIGAKTSYVKEKDKLVTEGDKGENGSS 300
QY 143 TDEGGLVTAREVIDAVKAKGRMKTGTANGOTGQADKFEETVSGTNVTFASGKTATV 202
Db 301 TDEGGLVTAREVIDAVKAKGRMKTGTANGOTGQADKFEETVSGTNVTFASGKTATV 360
QY 203 SKDDOGNTTVMYDVAVGALNVNQLONGSNMUDSAVAGSSGKVTISGVNPSKGMDET 262
Db 361 SKDDOGNTTVMYDVAVGALNVNQLONGSNMUDSAVAGSSGKVTISGVNPSKGMDET 420
QY 263 NINAGNNIETIRNGKNIDIASMPPOFSSVSLGACADAPTLISVDDALNVGSKDKNRYR 322
Db 421 NINAGNNIETIRNGKNIDIASMTPOFSSVSLGACADAPTLISVDDALNVGSKDKNRYR 480
QY 323 ITNVAPEGKEDVTNVAOLKGAONLNNRIDNVGDNARAGIAQAIATAGLVQAVLPGKSM 382
Db 481 ITNVAPEGKEDVTNVAOLKGAONLNNRIDNVGDNARAGIAQAIATAGLVQAVLPGKSM 540
QY 383 MAIGGCTYRGEAGYALIGYSSISDGGNWTIKTAAGNSRSGHGASASVGYOW 433
Db 541 MAIGGCTYRGEAGYALIGYSSISDGGNWTIKTAAGNSRSGHGASASVGYOW 591

RESULT 8
AAU06186
ID AAU06186 standard; Protein; 502 AA.
XX
XX AAU06186;
AC
XX
XX 24-OCT-2001 (first entry)
DE N. meningitidis PMC21 Nhba deletion mutant #4.
XX
XX Surface antigen Nhba; meningococcal disease; meningitis vaccine;
KM mutant; muteln.
XX
XX Neisseria meningitidis strain PMC21.
OS Synthetic.
XX
XX
XX Key Location/Qualifiers
FH Peptide 1..49
FT /label= signal_peptide
FT Protein 50..502
FT /label= Mature_Nhba_deletion_mutant_#4
FT /note= "Predicted mature protein, specifically
XX claimed in claim 12"
XX
XX
XX WO200155182-A1.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU00069.
XX
XX 25-JAN-2000; 2000US-0177917.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX
XX

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PI Peak IRA, Jennings MP;
 XX
 DR WPI: 2001-488774/53.
 N-PSDB; AAS09176.
 XX
 PT New Nhba surface antigen polypeptides and polynucleotides from
 PT Neisseria meningitidis, useful in producing vaccines for treating or
 PT preventing broad spectrum of Neisseria meningitidis -
 XX
 PS Claim 12: Fig 9; 91pp; English.
 CC The present invention relates to the isolation of novel Neisseria
 CC meningitidis mutant polypeptides of the surface antigen Nhba
 CC (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are
 CC characterised by deletions of non-conserved amino acids, particularly
 CC the deletion of variable regions. The deletion mutants are useful in
 CC diagnostics, therapeutic and prophylactic vaccines against a broader
 CC spectrum of N. meningitidis, and in designing and/or screening of
 CC medicaments. The mutant proteins when used as a vaccine can effectively
 CC immunise against a broader spectrum of N. meningitidis strains than
 CC would be expected from a corresponding wild-type surface antigen
 CC The present sequence represents N. meningitidis strain PMC21 surface
 CC antigen Nhba deletion mutant #4.
 CC
 XX Sequence 502 AA;
 SQ
 Query Match 95.5%; Score 2098.5; DB 22; Length 502;
 Best Local Similarity 83.7%; Pred. No. 2.2e-130; Indels 83; Gaps 2;
 Matches 426; Conservative 0; Mismatches 0;
 QY 1 MNKIRIIMNSALANAWVWVSELTNRNHTKRASATVKTAVLATLLFATVQASAN----- 52
 DB 1 MNKIRIIMNSALANAWVWVSELTNRNHTKRASATVKTAVLATLLFATVQASANLTKAGDNL 60
 QY 53 ----- 52
 DB 61 KIKQFTYSLKKDLTDLTSVGTETKLSFANGKNVITSDTKGLNFAKETAGTNGDTTVHLN 120
 QY 53 -----RASVYKDVNLNGMNIKGVKPGTTASDNDFVRYTVTFELSDTCTTVNVE 104
 DB 121 GIGSTLTLDRAASVYKDVNLNGMNIKGVK-----NDFVRYTVTFELSDTCTTVNVE 173
 QY 105 SKDNGKRTVEYKIGAKTSVIEKDKLVYTKDKGENSSSTDEGEGLVTAKEDVAVNKA 164
 DB 174 SKDNGKRTVEYKIGAKTSVIEKDKLVYTKDKGENSSSTDEGEGLVTAKEDVAVNKA 223
 QY 165 RAKTTTANGOTGQADKFEYVTSNTVFPASGKTATVSKDQGNITVMDVAVGALNV 224
 DB 234 RAKTTTANGOTGQADKFEYVTSNTVFPASGKTATVSKDQGNITVMDVAVGALNV 293
 QY 225 NOLONGMNLDSKA VAGSSGKTVISGNVSPSKGMDDEVININAGNNIEITRNGKNIDIAT 284
 DB 294 NOLONGMNLDSKA VAGSSGKTVISGNVSPSKGMDDEVININAGNNIEITRNGKNIDIAT 353
 QY 285 MPPOFSSVSLGAGADAPTLSDVDALNVGSKDKNKPVRITNVAPGVKEGDTVAADLKV 344
 DB 354 MPPOFSSVSLGAGADAPTLSDVDALNVGSKDKNKPVRITNVAPGVKEGDTVAADLKV 413
 QY 345 AONLNNRIDNVGNARAGIAQAIAATAGVQAYLPGKSMAIGGGTYRGEAGVAGYSSIS 404
 DB 414 AONLNNRIDNVGNARAGIAQAIAATAGVQAYLPGKSMAIGGGTYRGEAGVAGYSSIS 473
 QY 405 DGGNMIITKGTASGNSRGHGASASVGYOW 433
 DB 474 DGGNMIITKGTASGNSRGHGASASVGYOW 502
 RESULT 9
 ID AAY23741
 AC AAY23741 standard; Protein; 591 AA.
 XX AAY23741;
 XX

DT 08-SEP-1999 (first entry)
 XX
 DE A surface protein of Neisseria meningitidis.
 XX
 KW Surface protein; surface glycoprotein; infection; vaccine;
 XX immunoreactive peptide.
 XX
 OS Neisseria meningitidis.
 XX
 PN WO9931132-A1.
 XX
 PD 24-JUN-1999.
 XX
 PF 14-DEC-1998; 98WO-AU01031.
 XX
 PR 12-DEC-1997; 97GB-0026398.
 XX
 PA (ISIS-) ISIS INNOVATION LTD.
 XX (UYOU) UNIV QUEENSLAND.
 XX
 PI Jennings MP, Moxon ER, Peak IRA;
 XX
 DR WPI: 1999-418754/35.
 DR N-PSDB; AAX85793.
 XX
 PT Neisseria meningitidis surface proteins useful for treating N.
 PT meningitidis infections
 XX
 PS Claim 1: Page 104-106; 132pp; English.
 CC The present sequence represents a surface protein of Neisseria
 CC meningitidis which is approximately 62 kDa. The N. meningitidis
 CC surface glycoproteins, nucleic acids, the primers and optionally
 CC a thermostable polymerase, or antibodies are useful in a kit for
 CC the detection or diagnosis of N. meningitidis infection in humans.
 CC The N. meningitidis surface glycoproteins can also be used to
 CC prevent or treat N. meningitidis infection in humans, especially
 CC in the form of vaccines. The proteins and antibodies can also
 CC be used to identify immunoreactive peptides.
 CC
 XX Sequence 591 AA;
 SQ
 Query Match 95.4%; Score 2096; DB 20; Length 591;
 Best Local Similarity 72.9%; Pred. No. 3.9e-130;
 Matches 431; Conservative 1; Mismatches 1; Indels 158; Gaps 1;
 QY 1 MNKIRIIMNSALANAWVWVSELTNRNHTKRASATVKTAVLATLLFATVQASAN----- 52
 DB 1 MNKIRIIMNSALANAWVWVSELTNRNHTKRASATVKTAVLATLLFATVQASANNEDEEDL 60
 QY 53 ----- 52
 DB 61 YLDPVLTAVAVLI VNSDKEGTGKEKEVENSMDAVYFNEKGVLTAREITLAKGDNLIK 120
 QY 53 ----- 52
 DB 121 NGTNFTYSLKKDLTDLTSVGTETKLSFANGKNVITSDTKGLNFAKETAGTNGDTTVHLN 180
 QY 53 -----RAASVYKDVNLNGMNIKGVKPGTTASDNDF 82
 DB 181 GIGSTLTDLTLNLTGATVNTNDVNTDDEKRAASVYKDVNLNGMNIKGVKPGTTASDNDF 240
 QY 83 VRTYDIVERLSADTKTTTVNVEKDKGKTEYKIGAKTSVIEKDKLVYTKDKGENSS 142
 DB 241 VRTYDIVERLSADTKTTTVNVEKDKGKTEYKIGAKTSVIEKDKLVYTKDKGENSS 300
 QY 143 TDEGEGLVTAKEDVAVNKA VAGSSGKTVISGNVSPSKGMDDEVININAGNNIEITRNGKNIDIAT 202
 DB 301 TDEGEGLVTAKEDVAVNKA VAGSSGKTVISGNVSPSKGMDDEVININAGNNIEITRNGKNIDIAT 360
 QY 203 SKDDQGNITVMDVAVGALNVNOLONGMNLDSKA VAGSSGKTVISGNVSPSKGMDDEVININAGNNIEITRNGKNIDIAT 262
 DB 361 SKDDQGNITVMDVAVGALNVNOLONGMNLDSKA VAGSSGKTVISGNVSPSKGMDDEVININAGNNIEITRNGKNIDIAT 420

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OY 263 NINAGNNIETIRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVGDALNVGSKDKNKFVR 322
|||
DB 421 NINAGNNIETIRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVGDALNVGSKDKNKFVR 480
|||
OY 323 ITNVA PGVEGDVTNVAOLKGVAVQNLNRRINDVGNARAGIAQAIATAGLVQAVYLPKSKM 382
|||
DB 481 ITNVA PGVEGDVTNVAOLKGVAVQNLNRRINDVGNARAGIAQAIATAGLVQAVYLPKSKM 540
|||
OY 383 MAIGGTYRGAGYALIGYSSISDGNWIIKGTASGNSGHRGASASVGYQW 433
|||
DB 541 MAIGGTYRGAGYALIGYSSISDGNWIIKGTASGNSGHRGASASVGYQW 591
|||
RESULT 10
AAU06175
ID AAU06175 standard; Protein: 591 AA.
XX AC AAU06175;
XX DT 24-OCT-2001 (first entry)
XX DE N. meningitidis EG329 surface antigen NhbA polypeptide sequence.
XX KM Surface antigen NhbA; meningococcal disease; meningitis vaccine.
XX OS Neisseria meningitidis strain EG329.
XX FH
XX FH Key location/Qualifiers
FT 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT 51..108
FT /label= V1
FT /note= "Variable region 1"
FT 109..120
FT /label= C2
FT /note= "Conserved region 2"
FT 121..124
FT /label= V2
FT /note= "Variable region 2"
FT 125..188
FT /label= C3
FT /note= "Conserved region 3"
FT 189..210
FT /label= V3
FT /note= "Variable region 3"
FT 211..229
FT /label= C4
FT /note= "Conserved region 4"
FT 230..236
FT /label= V4
FT /note= "Variable region 4"
FT 237..591
FT /label= C5
FT /note= "Conserved region 5"
PN WO200155182-A1.
PD 02-AUG-2001.
XX 25-JAN-2001; 2001WO-AU00069.
XX 25-JAN-2000; 2000US-0177917.
XX PA (UYOU ) UNITV QUEENSLAND.
XX PI Peak IRA, Jennings MP;
XX DR MPI: 2001-488774/53.
XX DR N-PSDB; AAS09165.
XX PT New NhbA surface antigen polypeptides and polynucleotides from
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PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
PS Claim 9; Fig 1; 91pp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen NhbA
CC (AAU06182-AAU06186). The modified or mutant NhbA polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen NhbA
CC from N. meningitidis strain EG329 is 1 of 10 NhbA polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
XX SQ Sequence 591 AA;
XX
XX Query Match 95.4%; Score 2096; DB 22; Length 591;
XX Best Local Similarity 72.9%; Pred. No. 3.9e-130;
XX Matches 431; Conservative 1; Mismatches 1; Indels 158; Gaps 1;
OY 1 MNKTYRIITWNSALNAAVYVSELTRNHTKRAATYKTAVALTLTLPATVQASAN----- 52
DB 1 MNEITRIITWNSALNAAVYVSELTRNHTKRAATYKTAVALTLTLPATVQASANNEQERDL 60
OY 53 ----- 52
DB 61 YLDEPLRTAVLIVNSDEKTEGKEKEVENSMAVYENKGVLTAREITLKAGDNLKIKQ 120
OY 53 ----- 52
DB 121 NGTNETYSLKRLDLTISVTEKLSFSANGKNVITSDTKGLNFAKETAGTNGDTYHLN 180
OY 53 ----- -RAASVKDVLNAGWNIKGVKPGTASDNDVF 82
DB 181 GIGSTLDTLNTGATNTVTDNNVTDDKKRAASVKDVLNAGWNIKGVKPGTASDNDVF 240
OY 83 VRTYDVEFLSADTKTTTVNVEESKDNKKTVEKIGAKTSYKEKDGKLVYTKDGENGSS 142
DB 241 VRTYDVEFLSADTKTTTVNVEESKDNKKTVEKIGAKTSYKEKDGKLVYTKDGENGSS 300
OY 143 TDEGEGLYTAKEVIDAVNKAAGMRKTTTANGOTGOADKFEFVTSNTVTFASGKGTATV 202
DB 301 TDEGEGLYTAKEVIDAVNKAAGMRKTTTANGOTGOADKFEFVTSNTVTFASGKGTATV 360
OY 203 SKDDGNTTVWYDVNVGDALNVNOLQNSGWNLDKSAVAGSSGKVIISGNVSPSKGMDETV 262
DB 361 SKDDGNTTVWYDVNVGDALNVNOLQNSGWNLDKSAVAGSSGKVIISGNVSPSKGMDETV 420
OY 263 NINAGNNIETIRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVGDALNVGSKDKNKFVR 322
DB 421 NINAGNNIETIRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVGDALNVGSKDKNKFVR 480
OY 323 ITNVA PGVEGDVTNVAOLKGVAVQNLNRRINDVGNARAGIAQAIATAGLVQAVYLPKSKM 382
DB 481 ITNVA PGVEGDVTNVAOLKGVAVQNLNRRINDVGNARAGIAQAIATAGLVQAVYLPKSKM 540
OY 383 MAIGGTYRGAGYALIGYSSISDGNWIIKGTASGNSGHRGASASVGYQW 433
DB 541 MAIGGTYRGAGYALIGYSSISDGNWIIKGTASGNSGHRGASASVGYQW 591
|||
RESULT 11
AAU06183
ID AAU06183 standard; Protein: 513 AA.
XX AC AAU06183;
XX
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DT 24-OCT-2001 (first entry)
XX N. meningitidis H41 Nhha deletion mutant.
DE Surface antigen Nhha; meningococcal disease; meningitis vaccine;
XX mutant; mutcin.
XX Neisseria meningitidis strain H41.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..51
FT Protein /label= Signal_peptide
FT /label= Mature_Nhha_deletion_mutant
FT /note= "Predicted mature protein, specifically
FT claimed in claim 12"
XX
XX WO200155182-A1.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001: 2001WO-AU00069.
XX
XX 25-JAN-2000: 2000US-0177917.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX
XX Peak IRA, Jennings MP;
XX
XX WPI: 2001-488774/53.
XX
XX N-PSDB: AAS09173.
XX
XX New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 12; Fig 6; 91pp: English.
XX
XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence represents N. meningitidis strain H41 surface
CC antigen Nhha deletion mutant.
XX
XX Sequence 513 AA:
SQ
Query Match 93.5%; Score 2055; DB 22; Length 513;
Best Local Similarity 81.7%; Pred. No. 1.6e-127;
Matches 419; Conservative 3; Mismatches 11; Indels 80; Gaps 2;
QY 1 MKKIYIINNSALNMAVYVSELTNRHTKRASATVKTAVLATLFAVQASA----- 51
DB 1 MKKIYIINNSALNMAVAVSELTNRHTKRASATVKTAVLATLFAVQANADDEGLIN 60
QY 52 ----- 51
DB 61 ETEKLSFGANGKKVNIISPTKGLNFAKETAGTNGDTTVAHLNIGSTLTMLNTGATTNV 120
QY 52 -----NRAASYKDVNLNAGWNKIGVKGPTTASDNVDFVETDVEFLSADTFTTV 101
DB 121 TNDNVTDBDKKRAASYKDVNLNAGWNKIGVKGPTTASDNVDFVETDVEFLSADTFTTV 180
QY 102 NRESKNGKTEVKIAKTSVYKEKDGKLVGTGDKKESSSDDEGGGLYTAKEVIDAVNK 161
DB 181 NRESKNGKTEVKIAKTSVYKEKDGKLVGTGDKKESSSDDEGGGLYTAKEVIDAVNK 240

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QY 162 AGRMRKTTTANGOTGADKFEETVTSQNTVPFASGKGTATVASKDOGNITVMYDVAVGDA 221
DB 241 AGRMRKTTTANGOTGADKFEETVTSQNTVPFASGKGTATVASKDOGNITVMYDVAVGDA 300
QY 222 LNVNQLNSGNWLDKRAVAGSSGKYISGNVSPSKGMEFTVINAGNNIEITRNGKNIDI 281
DB 301 LNVNQLNSGNWLDKRAVAGSSGKYISGNVSPSKGMEFTVINAGNNIEITRNGKNIDI 360
QY 282 ATSKTPQESSVSLGADAPTLISVDCD-ALNNGSKDKKPKVRIITNVAPGVKGGDVYVNAQ 340
DB 361 ATSKTPQESSVSLGADAPTLISVDEGALNNGSKDKKPKVRIITNVAPGVKGGDVYVNAQ 420
QY 341 LKGVAQNLNRRIDNDVGNARAGIAQAIATAGLVQAVLPGKSMMAIGGTYRSEAGYAIQY 400
DB 421 LKGVAQNLNRRIDNDVGNARAGIAQAIATAGLVQAVLPGKSMMAIGGTYRSEAGYAIQY 480
QY 401 SSISDGGNWIIRKGTASGNSRGHFGASASVGYQW 433
DB 481 SSISAGGNWIIRKGTASGNSRGHFGASASVGYQW 513

RESULT 12
AAU06184
ID AAU06184 standard; Protein: 407 AA.
XX
XX AAU06184:
AC
XX
XX 24-OCT-2001 (first entry)
DE
XX N. meningitidis PMC21 Nhha deletion mutant #2.
XX
XX Surface antigen Nhha; meningococcal disease; meningitis vaccine;
XX mutant; mutcin.
XX
XX Neisseria meningitidis strain PMC21.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Peptide 1..51
FT Protein /label= Signal_peptide
FT /label= Mature_Nhha_deletion_mutant_#2
FT /note= "Predicted mature protein, specifically
FT claimed in claim 12"
XX
XX WO200155182-A1.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001: 2001WO-AU00069.
XX
XX 25-JAN-2000: 2000US-0177917.
XX
XX (UYOU ) UNIV QUEENSLAND.
XX
XX Peak IRA, Jennings MP;
XX
XX WPI: 2001-488774/53.
XX
XX N-PSDB: AAS09174.
XX
XX New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 12; Fig 7; 91pp: English.
XX
XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader

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CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence represents N. meningitidis strain PMC21 surface
CC antigen Nmba deletion mutant #2.

XX Sequence 407 AA:

Query Match 92.9%; Score 2040; DB 22; Length 407;
Best Local Similarity 94.0%; Pred. No. 1,2e-126;
Matches 407; Conservative 0; Mismatches 0; Indels 26; Gaps 1;

QY 1 MNKYRIIWSALNAAVVSSELTFRNHTKRASATVATAVATLLEFATVOASAAASVADV 60
DB 1 MNKYRIIWSALNAAVVSSELTFRNHTKRASATVATAVATLLEFATVOASAAAN----- 52
QY 61 LNAGNINIGVAPGTTASNDVDFRYDVEFLSADTKTTYNVESKDKGTEVIGAKT 120
DB 53 -----NDFPVRYDVEFLSADTKTTYNVESKDKGTEVIGAKT 94
QY 121 SVIREKDKLVTKDKGENSGSTDEGEGLVTAKEVIDAVNKRAGMRKTTTANGOTGQADK 180
DB 95 SVIREKDKLVTKDKGENSGSTDEGEGLVTAKEVIDAVNKRAGMRKTTTANGOTGQADK 154
QY 181 FEYVTSGTNTVPASGKGTATVSKDDGNTVMTDVNVGDLNVLNQLONSGMNLDKAVA 240
DB 155 FEYVTSGTNTVPASGKGTATVSKDDGNTVMTDVNVGDLNVLNQLONSGMNLDKAVA 214
QY 241 GSSGKVISGNSPSKGMDETVNINAGNIEITRGNKIDATATMTPOFSSVSLGAGADA 300
DB 215 GSSGKVISGNSPSKGMDETVNINAGNIEITRGNKIDATATMTPOFSSVSLGAGADA 274
QY 301 PTLSDVDGALNVGSKDKNPKVRIITNVAAPGVEGDVTNVAQLKGAQNLNNRIDVNGAR 360
DB 275 PTLSDVDGALNVGSKDKNPKVRIITNVAAPGVEGDVTNVAQLKGAQNLNNRIDVNGAR 334
QY 361 AGIAQAIATAGLVQAYLTPGKSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSR 420
DB 335 AGIAQAIATAGLVQAYLTPGKSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSR 394
QY 421 GHFGASASVGYOW 433
DB 395 GHFGASASVGYOW 407

RESULT 13

AAV23740
ID AAY23740 standard; Protein: 594 AA.

XX AAY23740;
AC 08-SEP-1999 (first entry)
DT
XX A surface protein of Neisseria meningitidis.
DE
XX Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX Neisseria meningitidis.
OS
XX WO9931132-A1.
PN
XX 24-JUN-1999.
PD
XX 14-DEC-1998; 98WO-AU01031.
PE
XX 12-DEC-1997; 97GB-0026398.
PR
XX (ISIS-) ISIS INNOVATION LTD.
PA (UYOU) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;

XX WP1: 1999-418754/35.
DR N-PSDB; AAX85792.
XX

PT Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections

XX Claim 1; Page 100-101; 132pp; English.

XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.

XX Sequence 594 AA:

Query Match 92.5%; Score 2032.5; DB 20; Length 594;
Best Local Similarity 70.9%; Pred. No. 6e-126;
Matches 421; Conservative 3; Mismatches 9; Indels 161; Gaps 2;

QY 1 MNKYRIIWSALNAAVVSSELTFRNHTKRASATVATAVATLLEFATVOASA----- 51
DB 1 MNKYRIIWSALNAAVVSSELTFRNHTKRASATVATAVATLLEFATVOASTTDDDDLYLE 60
QY 52 ----- 51
DB 61 PVQRTAVVLSFRSDKEGTEKEVTEDSNMWGYFDKGVLTAGTTLAAGNLIKIKONTNE 120
QY 52 ----- 51
DB 121 NTNASSFTSLKDLTDLTISVTEKLSFANSKNVNTISDPLGKLNFAKKTAEETNGDTTVA 180
QY 52 -----NRAASVQDVLAAGMNIKGVPGTTASDNV 80
DB 181 LINGIGSTLDTLTNTGATTNTVNDNVDEKKRAASVADVLAAGMNIKGVPGTTASDNV 240
QY 81 DFVRTYDVEFLSADTKTTYNVESKDKGTEVIGAKTSVIREKDKLVTKDKGENG 140
DB 241 DFVRTYDVEFLSADTKTTYNVESKDKGTEVIGAKTSVIREKDKLVTKDKGEND 300
QY 141 SSTDEGEGLVTAKEVIDAVNKRAGMRKTTTANGOTGQADKPEYVTSGTNTVPASGKGT 200
DB 301 SSTDEGEGLVTAKEVIDAVNKRAGMRKTTTANGOTGQADKPEYVTSGTNTVPASGKGT 360
QY 201 TVSKDDGNTVMTDVNVGDLNVLNQLONSGMNLDKRAVAGSSGKVISGNSVPSKGMDE 260
DB 361 TVSKDDGNTVMTDVNVGDLNVLNQLONSGMNLDKRAVAGSSGKVISGNSVPSKGMDE 420
QY 261 TVNINAGNIEITRGNKIDATATMTPOFSSVSLGAGADATLTVDDG-ALNNSKDKN 319
DB 421 TVNINAGNIEITRGNKIDATATMTPOFSSVSLGAGADATLTVDDGALNNSKDKN 480
QY 320 PVRIITNVAAPGVEGDVTNVAQLKGAQNLNNRIDVNGARAGIAQAIATAGLVQAYLPG 379
DB 481 PVRIITNVAAPGVEGDVTNVAQLKGAQNLNNRIDVNGARAGIAQAIATAGLVQAYLPG 540
QY 380 KSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 433
DB 541 KSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 594

RESULT 14

AAV57044
ID AAY57044 standard; Protein: 594 AA.

XX AAY57044;
AC 21-FEB-2000 (first entry)
DT

XX BASB029 amino acid sequence from N. meningitidis strain ATCC13090.
 DE
 XX
 KM BASB029; *Neisseria meningitidis*; surface fibrin protein; HSF; diagnosis;
 KM infection; treatment; prevent; antibacterial drug.
 XX
 OS *Neisseria meningitidis*.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 104
 FT /note= "Encoded by AATC"
 XX
 PN MO958683-A2.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99MO-EP03255.
 XX
 PR 13-MAY-1998; 98GB-0010276.
 XX
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI Ruella J;
 XX
 DR WPI; 2000-053103/04.
 DR N-PSDB; AA239864.
 XX
 PT New polypeptide from *neisseria meningitidis* useful for diagnosis,
 PT treatment or prevention of bacterial infections in mammal
 XX
 PS Claim 4; Fig 2; 74pp; English.

CC This is the *Neisseria meningitidis* BASB029 amino acid sequence from
 CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the
 CC Hemophilus influenzae surface fibrin (HSF) protein. The invention
 CC relates to BASB029 polynucleotide sequences (AA239864-239865) and
 CC polypeptide sequences (AAV57044-Y57045) and their immunogenic fragments.
 CC BASB029 polypeptides are useful in a method of diagnosing a *Neisseria*
 CC meningitidis infection in a mammal. Compositions containing BASB029
 CC polynucleotides and polypeptides are useful for generating an immune
 CC response in an animal. A therapeutic composition comprising an antibody
 CC directed against BASB029 is useful in treating humans with *Neisseria*
 CC meningitidis disease. The polynucleotide is useful in the diagnosis of
 CC the stage of infection, type of infection, susceptibility to an
 CC infection which results from increased or decreased expression of the
 CC polynucleotide, and for therapeutic or prophylactic purposes,
 CC particularly genetic immunisation. Antibodies against BASB029
 CC polynucleotides and polypeptides are also useful for treating infections
 CC particularly bacterial infections. The protein is useful in the
 CC screening and development of antibacterial drugs. Fused recombinant
 CC protein is useful for the stimulation of the immune system of an organism
 CC receiving the protein.
 CC
 XX

SQ Sequence 594 AA;

Query Match 92.5%; Score 2032.5; DB 21; Length 594;

Best Local Similarity 70.9%; Pred. No. 6e-126;
 Matches 421; Conservative 3; Mismatches 9; Indels 161; Gaps 2;

QY 1 MNKIYRIIMNSALNAMYVSELTRNHTKRASATVATLTLFATVQASA----- 51
 DB 1 MNKIYRIIMNSALNAMYVSELTRNHTKRASATVATLTLFATVQASTDDDDLYLE 60
 QY 52 ----- 51
 DB 61 PVORTAVVLSFRSDKDEGTGEKEVTEDSNMGVYEDDKGVLTAAGTTTLKAGDNLIKIKONTNE 120
 QY 52 ----- 51
 DB 121 NTNASSFTYSLKKDLDTJTSVTEKLSFSANSKNKVNITSDTKGINKFAKKTAEINQDTVH 180
 QY 52 -----NRAASYKDVLMNGWNIKGVKPGTTASDNV 80
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 181 LNCIGSTLPTDLLNTGATVTNTNDNTYDDEKKRASVYKDVLMNGWNIKGVKPGTTASDNV 240
 QY 81 DFRVTYTVPELISADPTTNNVNESKNGKTEKIGAKTSVKEKXGLVTGDKGENG 140
 DB 241 DFRVTYTVPELISADPTTNNVNESKNGKTEKIGAKTSVKEKXGLVTGDKGEND 300
 QY 141 SSTDEGEGLYTAKEVIDAVNKKAGRMKTTTANGCOTGADFEFTVSGTNTFFASGKCTTA 200
 DB 301 SSTDKGEGLYTAKEVIDAVNKKAGRMKTTTANGCOTGADFEFTVSGTNTFFASGKCTTA 360
 QY 201 TVSKDQGNITTVMDVNVGALNVNOLNSGWNIDSKAVAGSGKVISGVNPSKGMDE 260
 DB 361 TVSKDQGNITTVMDVNVGALNVNOLNSGWNIDSKAVAGSGKVISGVNPSKGMDE 420
 QY 261 TVNINAGNNIEITRNGKNIDIAISMTPOFSSVSLGACADAPTLISVDDEGLNAGSKDANK 319
 DB 421 TVNINAGNNIEITRNGKNIDIAISMTPOFSSVSLGACADAPTLISVDDEGLNAGSKDANK 480
 QY 320 PVRTTNVAPGVKEDGVNVAQLKGAONLNRRIDNVGDNARAGIAQAIAATAGLVQAVLP 379
 DB 481 PVRTTNVAPGVKEDGVNVAQLKGAONLNRRIDNVGDNARAGIAQAIAATAGLVQAVLP 540
 QY 380 KSMMAIGGTYRGEGAGYAGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 433
 DB 541 KSMMAIGGTYRGEGAGYAGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 594

RESULT 15
 AAU06174
 ID AAU06174 standard; Protein: 594 AA.
 AC AAU06174;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE N. meningitidis EG327 surface antigen Nha polypeptide sequence.
 XX
 KM Surface antigen Nha; meningococcal disease; meningitis vaccine.
 XX
 OS *Neisseria meningitidis* strain EG327.
 XX
 FH Key Location/Qualifiers
 FT Region 1..50
 FT /label= C1
 FT /note= "Conserved region 1"
 FT 51..104
 FT /label= V1
 FT /note= "Variable region 1"
 FT 105..116
 FT /label= C2
 FT /note= "Conserved region 2"
 FT 117..126
 FT /label= V2
 FT /note= "Variable region 2"
 FT 127..190
 FT /label= C3
 FT /note= "Conserved region 3"
 FT 191..212
 FT /label= V3
 FT /note= "Variable region 3"
 FT 213..231
 FT /label= C4
 FT /note= "Conserved region 4"
 FT 232..238
 FT /label= V4
 FT /note= "Variable region 4"
 FT 239..594
 FT /label= C5
 FT /note= "Conserved region 5"
 FN WO200155182-A1.
 XX 02-AUG-2001.
 PD

Db 301 TDEGGLVTAKEVIDAVNKAQMRKTTTANGOTGQADKFEVTVSGTNVTFASGKGTATV 360
QY 203 SKDDGNTITWYDVVNGDALNVNOLQNSGWNLDKAVAGSSGKVTISGWNVSPSKGMDETV 262
Db 361 SKDDGNTITWYDVVNGDALNVNOLQNSGWNLDKAVAGSSGKVTISGWNVSPSKGMDETV 420
QY 263 NINAGNNIETIRNKGNDIATISMTPOFSSVSLGAGADAPTLISVGDALNVGSKDKNRPVR 322
Db 421 NINAGNNIETIRNKGNDIATISMTPOFSSVSLGAGADAPTLISVGDALNVGSKDKNRPVR 480
QY 323 ITNVAPEGEDDVTNVAOLKGYAQNLRINDVGNARAGIAQAATATAGLVAQATLPKGS 382
Db 481 ITNVAPEGEDDVTNVAOLKGYAQNLRINDVGNARAGIAQAATATAGLVAQATLPKGS 540
QY 383 MAIGGTYRGEAGYAGYSSISDGGNWIITKGTASGNSRHFASASVGYOW 433
Db 541 MAIGGTYRGEAGYAGYSSISDGGNWIITKGTASGNSRHFASASVGYOW 591

RESULT 2
US-09-669-974-21
; Sequence 21, Application US/09669974
; Patent No. 6333173

GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-21

Query Match 95.9%; Score 2108; DB 4; Length 591;
Best Local Similarity 73.3%; Pred. No. 3.7e-165;
Matches 433; Conservative 0; Mismatches 0; Indels 158; Gaps 1;

QY 1 MNKIYRIITWNSALNAAVWVSELTRNHTKRASATVKTAVLATLILFATVOASAN----- 52
Db 1 MNKIYRIITWNSALNAAVWVSELTRNHTKRASATVKTAVLATLILFATVOASANNEBQEDL 60
QY 53 ----- 52
Db 61 YLDPVQRTVAVLIVNSDKEGTGEKEKEEENSMDAVYENKGVLTAREITLKAGDNLKIKQ 120
QY 53 ----- 52
Db 121 NGTNFTYSLKDLTDLTISVGTETKLSFSANGKNKVNITSDTKGLNFAKETAGTNGDTTVHLN 180
QY 53 -----RAASVKVILNAGWNINIKGVKPGTTASDNVD 82
Db 181 GIGSTLFDTLINTGATTNVTNDNVTDEKRRASVKKDVLNAGWNINIKGVKPGTTASDNVD 240
QY 83 VRTDYVEFLSADTKTTTVNVEESKDNKKTETVIGAKTSYIKEDGKLYTGKDGENGSS 142
Db 241 VRTDYVEFLSADTKTTTVNVEESKDNKKTETVIGAKTSYIKEDGKLYTGKDGENGSS 300
QY 143 TDEGGLVTAKEVIDAVNKAQMRKTTTANGOTGQADKFEVTVSGTNVTFASGKGTATV 202
Db 301 TDEGGLVTAKEVIDAVNKAQMRKTTTANGOTGQADKFEVTVSGTNVTFASGKGTATV 360

QY 203 SKDDGNTITWYDVVNGDALNVNOLQNSGWNLDKAVAGSSGKVTISGWNVSPSKGMDETV 262
Db 361 SKDDGNTITWYDVVNGDALNVNOLQNSGWNLDKAVAGSSGKVTISGWNVSPSKGMDETV 420
QY 263 NINAGNNIETIRNKGNDIATISMTPOFSSVSLGAGADAPTLISVGDALNVGSKDKNRPVR 322
Db 421 NINAGNNIETIRNKGNDIATISMTPOFSSVSLGAGADAPTLISVGDALNVGSKDKNRPVR 480
QY 323 ITNVAPEGEDDVTNVAOLKGYAQNLRINDVGNARAGIAQAATATAGLVAQATLPKGS 382
Db 481 ITNVAPEGEDDVTNVAOLKGYAQNLRINDVGNARAGIAQAATATAGLVAQATLPKGS 540
QY 383 MAIGGTYRGEAGYAGYSSISDGGNWIITKGTASGNSRHFASASVGYOW 433
Db 541 MAIGGTYRGEAGYAGYSSISDGGNWIITKGTASGNSRHFASASVGYOW 591

RESULT 3
US-09-377-155-2
; Sequence 2, Application US/09377155
; Patent No. 6197312

GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-2

Query Match 95.7%; Score 2103.5; DB 3; Length 592;
Best Local Similarity 73.0%; Pred. No. 8.7e-165;
Matches 432; Conservative 0; Mismatches 1; Indels 159; Gaps 1;

QY 1 MNKIYRIITWNSALNAAVWVSELTRNHTKRASATVKTAVLATLILFATVOASAN----- 52
Db 1 MNKIYRIITWNSALNAAVWVSELTRNHTKRASATVKTAVLATLILFATVOASANNEBPRKKD 60
QY 53 ----- 52
Db 61 YLDPVQRTVAVLIVNSDKEGTGEKEKEEENSMDAVYENKGVLTAREITLKAGDNLKIK 120
QY 53 ----- 52
Db 121 QNGTNFTYSLKDLTDLTISVGTETKLSFSANGKNKVNITSDTKGLNFAKETAGTNGDTTVHL 180
QY 53 -----RAASVKVILNAGWNINIKGVKPGTTASDNVD 81
Db 181 NGISTLFDTLINTGATTNVTNDNVTDEKRRASVKKDVLNAGWNINIKGVKPGTTASDNVD 240
QY 82 FVRTDYVEFLSADTKTTTVNVEESKDNKKTETVIGAKTSYIKEDGKLYTGKDGENGSS 141
Db 241 FVRTDYVEFLSADTKTTTVNVEESKDNKKTETVIGAKTSYIKEDGKLYTGKDGENGSS 300
QY 142 STDEGGLVTAKEVIDAVNKAQMRKTTTANGOTGQADKFEVTVSGTNVTFASGKGTATV 201
Db 301 STDEGGLVTAKEVIDAVNKAQMRKTTTANGOTGQADKFEVTVSGTNVTFASGKGTATV 360
QY 202 VSKDDGNTITWYDVVNGDALNVNOLQNSGWNLDKAVAGSSGKVTISGWNVSPSKGMDETV 261
Db 361 VSKDDGNTITWYDVVNGDALNVNOLQNSGWNLDKAVAGSSGKVTISGWNVSPSKGMDETV 420

Db 481 ITNAPGVKEGDTVVAOLKGYAONLNRRIDVNDGNARAGIAQAATATAGLVOAYLPKSM 540
QY 383 MAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 433
|||||
Db 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 591

RESULT 6
US-09-669-974-11
; Sequence 11, Application US/09669974
; Patent No. 6333173

GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-11

Query Match 95.4%; Score 2096; DB 4; Length 591;
Best Local Similarity 72.9%; Pred. No. 3,6e-164;
Matches 431; Conservative 1; Mismatches 1; Indels 158; Gaps 1;

QY 1 MNKIRIITWNSALNMAVVVSELTNRHTRKASATVTAVALTLFFATVOASA----- 52
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Db 1 MNEILRIITWNSALNMAVVVSELTNRHTRKASATVTAVALTLFFATVOASANEBOEDL 60
|||||
QY 53 ----- 52
Db 61 YLDPVLRVAVLIYNSKEGEGEKEVEBNSDMAVYFNEKGVLTAREITLAKAGDNLIKQ 120
|||||
QY 53 ----- 52
Db 121 NCTNFTYSLKKDLTDLTJVSCTEKLFSFANGKNKVNITSDTKGLNFAKETAGTNGDTTVHLN 180
|||||
QY 53 -----RAASVYKDVNLNAGWNIGVYKPGTTASDNVDF 82
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Db 181 GIGSTLTDLTNTGATTNVTNDNVTYDDEKKRAASVYKDVNLNAGWNIGVYKPGTTASDNVDF 240
|||||
QY 83 VRTYVTEFLSADPTTTTVNVEKDKNGKTEYKIGAKTSVYKEKDKLVTGDKGENSS 142
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Db 241 VRTYVTEFLSADPTTTTVNVEKDKNGKTEYKIGAKTSVYKEKDKLVTGDKGENSS 300
|||||
QY 143 TDEGEGLTAKAEVIDAVKAGRMKTTTANGOTGADCFEYVTSCTNTTFFASGKGTATV 202
|||||
Db 301 TDEGEGLTAKAEVIDAVKAGRMKTTTANGOTGADCFEYVTSCTNTTFFASGKGTATV 360
|||||
QY 203 SKDDOGNITVYDVNVGDLNVLNOLNSGWNLDKSAVAGSSGKVISGNVSPSKGMDET 262
|||||
Db 361 SKDDOGNITVYDVNVGDLNVLNOLNSGWNLDKSAVAGSSGKVISGNVSPSKGMDET 420
|||||
QY 263 NINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDALNVSGKKNKVR 322
|||||
Db 421 NINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDALNVSGKKNKVR 480
|||||
QY 323 ITNAPGVKEGDTVVAOLKGYAONLNRRIDVNDGNARAGIAQAATATAGLVOAYLPKSM 382
|||||
Db 481 ITNAPGVKEGDTVVAOLKGYAONLNRRIDVNDGNARAGIAQAATATAGLVOAYLPKSM 540

QY 383 MAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 433
|||||
Db 541 MAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 591

RESULT 7
US-09-377-155-9
; Sequence 9, Application US/09377155
; Patent No. 6197312

GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-9

Query Match 92.5%; Score 2032.5; DB 3; Length 594;
Best Local Similarity 70.9%; Pred. No. 6,1e-159;
Matches 421; Conservative 3; Mismatches 9; Indels 161; Gaps 2;

QY 1 MNKIRIITWNSALNMAVVVSELTNRHTRKASATVTAVALTLFFATVOASA----- 51
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Db 1 MNKIRIITWNSALNMAVVVSELTNRHTRKASATVTAVALTLFFATVOASTDDDDLYLE 60
|||||
QY 52 ----- 51
Db 61 PVQRTAVVLSFRSDEKTEGEKEVEDSDNMGVYFDKGVLTAGTTLKAGDNLIKQNTNE 120
|||||
QY 52 ----- 51
Db 121 NTNASSFTYSLKKDLTDLTJVSCTEKLFSFANSNKNVNITSDTKGLNFAKETAGTNGDTTVH 180
|||||
QY 52 -----RAASVYKDVNLNAGWNIGVYKPGTTASDNV 80
|||||
Db 181 LNGIGSTLTDLTNTGATTNVTNDNVTYDDEKKRAASVYKDVNLNAGWNIGVYKPGTTASDNV 240
|||||
QY 81 DFVRTYDTEFLSADPTTTTVNVEKDKNGKTEYKIGAKTSVYKEKDKLVTGDKGENG 140
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Db 241 DFVRTYDTEFLSADPTTTTVNVEKDKNGKTEYKIGAKTSVYKEKDKLVTGDKGENG 300
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QY 141 SSTDEGELVTAKEVIDAVNAGRMKTTTANGOTGADCFEYVTSCTNTTFFASGKGT 200
|||||
Db 301 SSTDEGELVTAKEVIDAVNAGRMKTTTANGOTGADCFEYVTSCTNTTFFASGKGT 360
|||||
QY 201 TVSKDDOGNITVYDVNVGDLNVLNOLNSGWNLDKSAVAGSSGKVISGNVSPSKGMDE 260
|||||
Db 361 TVSKDDOGNITVYDVNVGDLNVLNOLNSGWNLDKSAVAGSSGKVISGNVSPSKGMDE 420
|||||
QY 261 TVNINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDALNVSGKKNK 319
|||||
Db 421 TVNINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDALNVSGKKNK 480
|||||
QY 320 PVRTITNAPGVKEGDTVVAOLKGYAONLNRRIDVNDGNARAGIAQAATATAGLVOAYLP 379
|||||
Db 481 PVRTITNAPGVKEGDTVVAOLKGYAONLNRRIDVNDGNARAGIAQAATATAGLVOAYLP 540
|||||
QY 380 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 433
|||||
Db 541 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 594

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, RESULT 8
, US-09-669-974-9
, Sequence 9, Application US/09669974
, Patent No. 6333173
, GENERAL INFORMATION:
, APPLICANT: PEAK, Ian Richard Anselm
, APPLICANT: JENNINGS, Michael Paul
, APPLICANT: MOXON, E. Richard
, TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
, FILE REFERENCE: 065064/0128
, CURRENT APPLICATION NUMBER: US/09/669,974
, CURRENT FILING DATE: 2000-09-26
, PRIOR APPLICATION NUMBER: US 09/377,155
, PRIOR FILING DATE: 1999-08-19
, PRIOR APPLICATION NUMBER: PCT/AU98/01031
, PRIOR FILING DATE: 1998-12-14
, PRIOR APPLICATION NUMBER: GB 9726398.2
, PRIOR FILING DATE: 1997-12-12
, NUMBER OF SEQ ID NOS: 33
, SOFTWARE: PatentIn Ver. 2.0
, SEQ ID NO 9
, LENGTH: 594
, TYPE: prt
, ORGANISM: Neisseria meningitidis
, US-09-669-974-9

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RESULT 11
US-09-377-155-7
; Sequence 7, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul

RESULT 12
US-09-669-974-7
Sequence 7, Application US/09669974
Patent No. 633173
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669, 974

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: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 17
: LENGTH: 592
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-377-155-17

Best Match          91.7%; Score 2015.5; DB 3; Length 592;
Query Local Similarity 70.8%; Pred. No. 1.5e-157;
Matches 419; Conservative 3; Mismatches 11; Indels 159; Gaps 2

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QY	1	MNKYIRIIMNSALNAAVYVSELTRNNHRRASATYKTAVALATLLEPTQASA-----	51
Db	1	MNKYIRIIMNSALNAAVSELTRNNHRRASATYKTAVALATLLEPTQANAATDEDEEBL	60
QY	52	-----	51
Db	61	ESVGRSVVGSIQAMESGVELETTISLMTNDNSKEFVDPIYVTLKAGDNLKIKONTNENT	120
QY	52	-----	51
Db	121	NASSFTYSLKKDLTGLINVENTEKLFGANGKRVNIISDTKGLNFAKETAGTNGDPTVHLN	180
QY	52	-----NRAASVQDVNLNGMNTKGVKPGTTASDNDVF	82
Db	181	GIGSTLTDMNLNTGATTNTVTDNNTDDEKKRRAASVQDVNLNGMNTKGVKPGTTASDNDVF	240
QY	83	VRYTDPVEFLSADPTKRTTVTVNESKDNKRTTEVKIGAKTSVIREKDGKLVTKDKNGENSS	142
Db	241	VRYTDPVEFLSADPTKRTTVTVNESKDNKRTTEVKIGAKTSVIREKDGKLVTKDKNGENSS	300
QY	143	TDEEGGLVTAKEVIDAIVKAKGRMKTTTANQOTQADKFEVYTSGTNTFPASGKTTATV	202
Db	301	TDEEGGLVTAKEVIDAIVKAKGRMKTTTANQOTQADKFEVYTSGTNTFPASGKTTATV	360
QY	203	SKDDOGNTIYVYDVNVGDALNVNQLONGSMILDSKAVVSGSKVTSGNVSPSKGMDFTV	262
Db	361	SKDDOGNTIYVYDVNVGDALNVNQLONGSMILDSKAVVSGSKVTSGNVSPSKGMDFTV	420
QY	263	NINAGNNIETIRNGKNIDIATSMTPQESSVSLGAGADAPTLUSDGD-ALNVGSKRDNKPV	321
Db	421	NINAGNNIETIRNGKNIDIATSMTPQESSVSLGAGADAPTLUSDDEGALNVGSKRDNKPV	480
QY	322	RITVVAQGVKRGDVTNVAOLKGVAKONLNRRIDYDGNARAGIAQAIAATAGLQVATLPKGS	381
Db	481	RITVVAQGVKRGDVTNVAOLKGVAKONLNRRIDYDGNARAGIAQAIAATAGLQVATLPKGS	540
QY	382	MMALGGGTYREAGYGAIGYSSISPOGNNIIRKGTASGNSRGHPGASASVGYOW	433
Db	541	MMALGGGTYREAGYGAIGYSSISAGGNNIIRKGTASGNSRGHPGASASVGYOW	592
RESULT 14			
US-09-669-974-17.			
Sequence 17, Application US/0966974			
Patent No. 6333173			
GENERAL INFORMATION:			
APPLICANT: PEAK, Ian Richard Anselm			
APPLICANT: JENNINGS, Michael Paul			
APPLICANT: MOXON, E. Richard			
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN			
FILE REFERENCE: 065064/0128			
CURRENT APPLICATION NUMBER: US/09/669, 974			
CURRENT FILING DATE: 2000-09-26			
PRIOR APPLICATION NUMBER: US 09/377,155			
PRIOR FILING DATE: 1999-08-19			
PRIOR APPLICATION NUMBER: PCT/09/01031			
PRIOR FILING DATE: 1998-12-14			
PRIOR APPLICATION NUMBER: GB 9726398.2			

; PRIOR FILING DATE: 1997-12-12
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: Patentl Ver. 2.0
 ; SEQ ID NO 17
 ; LENGTH: 592
 ; TYPE: PRT
 ; ORGANISM: Neisseria meningitidis
 US-09-669-974-17

Query Match 91.7%; Score 2015.5; DB 4; Length 592;
 Best Local Similarity 70.8%; Pred. No. 1.5e-157;
 Matches 419; Conservative 3; Mismatches 11; Indels 159; Gaps 2;

```

QY 1 MNKIYRIIWSALNMAVVSSELTNRNHTKRASATVAVATLTLFATVOASA----- 51
    |||||||
DB 1 MNKIYRIIWSALNMAVVSSELTNRNHTKRASATVAVATLTLFATVOANATDEDEEEL 60
    |||||||
QY 52 ----- 51
DB 61 ESVORSVVSIOASMEGSELETTISLSMTNDSKEFVDEYIVVTLKAGDNLKIKONTNE 120
QY 52 ----- 51
DB 121 NASSFTYSLKLDLGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN 180
QY 52 ----- 82
DB 181 GIGSTLTMDLNTGATNTVNDNTVDDEKKRAASVYKDVLMNAGWNIKGVKPGTTASDNVDF 240
QY 83 VRTYTVTEFLSADFTTTVNVESKNGKTEVKIGAKTSVIREKDGKLVTKGKEENSS 142
DB 241 VRTYTVTEFLSADFTTTVNVESKNGKTEVKIGAKTSVIREKDGKLVTKGKEENSS 300
QY 143 TDEGGLVTAKEVIDAVNKAQWRMKTITANGOTGADKEFTVSGTNTYFASGKGTATV 202
DB 301 TDEGGLVTAKEVIDAVNKAQWRMKTITANGOTGADKEFTVSGTNTYFASGKGTATV 360
QY 203 SKDDGNTTVMDVNVGDLNVLNQLNSGWNLSKAVAGSSGKVISGNVSPSKGMDTV 262
DB 361 SKDDGNTTVMDVNVGDLNVLNQLNSGWNLSKAVAGSSGKVISGNVSPSKGMDTV 420
QY 263 NINNGNNIEITRNGKNIDITATSMTPQFSSVSLGAGADAPTLSDVDD -ALNVGSKDNV 321
DB 421 NINNGNNIEITRNGKNIDITATSMTPQFSSVSLGAGADAPTLSDVDDGALNVGSKDNV 480
QY 322 RITNVAPGVKESGDVTNVNQLKGVANLNNRIDNVGNARAGIAQAIATAGLVAATLPKGS 381
DB 481 RITNVAPGVKESGDVTNVNQLKGVANLNNRIDNVGNARAGIAQAIATAGLVAATLPKGS 540
QY 382 MMAITGGTYRGAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 433
DB 541 MMAITGGTYRGAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 592
  
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RESULT 15
 US-09-377-155-13
 ; Sequence 13, Application US/09377155
 ; Patent No. 6197312

; GENERAL INFORMATION:
 ; APPLICANT: PEAK, Ian Richard Anselm
 ; APPLICANT: JENNINGS, Michael Paul
 ; APPLICANT: MOXON, E. Richard
 ; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
 ; FILE REFERENCE: 065064/0128
 ; CURRENT APPLICATION NUMBER: US/09/377, 155
 ; PRIOR FILING DATE: 1999-08-19
 ; PRIOR APPLICATION NUMBER: PCT/AU98/01031
 ; PRIOR FILING DATE: 1998-12-14
 ; PRIOR APPLICATION NUMBER: GB 9726398.2
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: Patentl Ver. 2.0
 ; SEQ ID NO 13

; LENGTH: 598
 ; TYPE: PRT
 ; ORGANISM: Neisseria meningitidis
 US-09-377-155-13

Query Match 91.5%; Score 2010.5; DB 3; Length 598;
 Best Local Similarity 69.9%; Pred. No. 3.9e-157;
 Matches 418; Conservative 3; Mismatches 12; Indels 165; Gaps 2;

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QY 1 MNKIYRIIWSALNMAVVSSELTNRNHTKRASATVAVATLTLFATVOASA----- 51
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DB 1 MNKIYRIIWSALNMAVVSSELTNRNHTKRASATVAVATLTLFATVOANATDDDDLYLE 60
    |||||||
QY 52 ----- 51
DB 61 PVQRTAVVLSFRSDEKTEGKEGTEDSNMAYVFDEKRVLKAGAITLAKAGDNLKIKONTNE 120
QY 52 ----- 51
DB 121 NTNENTNDSFTYSLKDLTDLTSVETKLSFGANGKNVNIISDTKGLNFAKETAGTNGD 180
QY 52 ----- 76
DB 181 PTVHLNGIGSTLTDLTLNTGATNTVNDNTVDDEKKRAASVYKDVLMNAGWNIKGVKPGTTA 240
QY 77 SDNVDFVRTYDTEFLSADFTTTVNVESKNGKTEVKIGAKTSVIREKDGKLVTKGDK 136
DB 241 SDNVDFVRTYDTEFLSADFTTTVNVESKNGKTEVKIGAKTSVIREKDGKLVTKGDK 300
QY 137 GENGSTDEGGLVTAKEVIDAVNKAQWRMKTITANGOTGADKEFTVSGTNTYFASGK 196
DB 301 GENGSTDEGGLVTAKEVIDAVNKAQWRMKTITANGOTGADKEFTVSGTNTYFASGK 360
QY 197 GTTATVSKDDGNTTVMDVNVGDLNVLNQLNSGWNLSKAVAGSSGKVISGNVSPSKG 256
DB 361 GTTATVSKDDGNTTVMDVNVGDLNVLNQLNSGWNLSKAVAGSSGKVISGNVSPSKG 420
QY 257 KMDETVNIAGNNIEITRNGKNIDITATSMTPQFSSVSLGAGADAPTLSDVDD -ALNVGSK 315
DB 421 KMDETVNIAGNNIEITRNGKNIDITATSMTPQFSSVSLGAGADAPTLSDVDDGALNVGSK 480
QY 316 KDNKRVRTTNAAPGVKESGDVTNVNQLKGVANLNNRIDNVGNARAGIAQAIATAGLVOA 375
DB 481 DANKRVRTTNAAPGVKESGDVTNVNQLKGVANLNNRIDNVGNARAGIAQAIATAGLVOA 540
QY 376 YLPKSMMAIGGTYRGAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 433
DB 541 YLPKSMMAIGGTYRGAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 598
  
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Search completed: October 6, 2003, 09:35:49
 Job time : 15.5793 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:35 ; Search time 12.3947 Seconds
(Without alignments)
3359.577 Million cell updates/sec

Title: US-09-771-382-26

Perfect score: 2197

Sequence: 1 MNKIYRIIWSALNANWVVS.....TASGNSRGHGASASVGYQW 433

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

PIR 76:*
1: pirl:*
2: pirl:*
3: pirl:*
4: pirl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2108	95.9	591	2	G81133
2	2009.5	91.5	592	2	A81888
3	345	15.7	298	2	I64138
4	340.5	15.5	2059	2	D82671
5	335	15.2	1190	2	A82615
6	329.5	15.0	1588	2	A86036
7	329.5	15.0	1588	2	H91188
8	326	14.8	1107	2	AC0976
9	315.5	14.4	658	2	AOH010
10	214	9.7	1004	2	C82672
11	189	8.6	1286	2	S28634
12	186.5	8.5	1018	2	H83135
13	186.5	8.5	1091	2	G64964
14	186	8.5	364	2	A81019
15	185	8.4	365	2	AB3486
16	182	8.3	1325	2	A64305
17	178	8.1	385	2	F90961
18	178	8.1	585	2	F85809
19	177.5	8.1	3705	2	AD0123
20	175	8.0	1910	2	AF0394
21	167.5	7.6	584	2	CA8658
22	167	7.6	1477	2	B43855
23	165.5	7.5	949	2	D90803
24	165.5	7.5	1005	2	H85611
25	165.5	7.5	1536	2	A43855
26	165.5	7.5	2249	2	A41477
27	165	7.5	1343	2	E90893
28	165	7.5	1388	2	B85547
29	165	7.5	5291	2	F90696

30	164.5	7.5	936	2	I40711	sapB protein - Cam
31	164	7.5	4919	2	T31105	hypothetical prote
32	163.5	7.4	338	2	D90697	adhesin/Invasin-11
33	163.5	7.4	338	2	G85347	adhesin/Invasin-11
34	162.5	7.4	1635	2	A10452	hemolysin [importe
35	162	7.4	1335	2	T17508	glycoprotein Vp260
36	162	7.4	1343	2	D85724	hypothetical prote
37	160.5	7.3	2015	2	B81989	hypothetical prote
38	160	7.3	1655	2	E97835	hypothetical prote
39	159	7.2	1417	2	A83080	hypothetical prote
40	158.5	7.2	595	2	A48658	flagellin - Escher
41	158	7.2	2020	2	C48399	ABC-type transport
42	157.5	7.2	1461	2	E90696	hypothetical prote
43	157	7.1	3013	2	AB0480	probable invasin y
44	156.5	7.1	920	2	S41539	fibrinogen-binding
45	156	7.1	920	2	I40614	surface array prot

ALIGNMENTS

RESULT 1

G81133
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: G81133
R:Retelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappoli, R. A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: A81000; MUID:20175753; PMID:10710307
A:Accession: G81133
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-591 <TEXT>
A:Cross-references: GB:AE002450; GB:AE002098; NID:97226229; PIDN:AAE41395.1; PID:9722
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0992

Query Match	Score	2108	DB 2	Length	591
Best Local Similarity	73.3%				
Matches	433	Conservative	0	Mismatches	0
				Indels	158
				Gaps	1
QY	1	MNKIYRIIWSALNANWVVS	ELTRNHTKRASATVKTAVLATLLFATVQASAN	-----	52
DB	1	MNKIYRIIWSALNANWVVS	ELTRNHTKRASATVKTAVLATLLFATVQASANNEDEEDL	60	
QY	53	-----	-----	-----	52
DB	61	YLDYVORTAVAVLIYNSDKEGTGEKEVENSMAVYFNEKGVLTAREITLKAGDNLKIQ	120		
QY	53	-----	-----	-----	52
DB	121	NGNFTYSLKKDLTDLTLSVTEKLSFSAKNGKNITSDTGLNFAKTAAGTNGDTTVYHLN	180		
QY	53	-----	-----	-----	82
DB	181	GIGSTLTDLLTGATNTVNDVTDDEKRRASVSKVLAAGNNIKGVKPGTTASDVDF	240		
QY	83	VRIYDVEEFSADTKTTTAVVESKDKGKTEVIGAKTSYIKEDGLVYVGKDGKENGSS	142		
DB	241	VRIYDVEEFSADTKTTTAVVESKDKGKTEVIGAKTSYIKEDGLVYVGKDGKENGSS	300		
QY	143	TDEGEGLVTAKEVYIDAVNKRAGMKTTTANGOTGOADKFEYVSGTVTFASGKGTATV	202		
DB	301	TDEGEGLVTAKEVYIDAVNKRAGMKTTTANGOTGOADKFEYVSGTVTFASGKGTATV	360		
QY	203	SKDDGNTIYVYVNVGDALNVQNLONGSNLDSKAVAGSSGIVSGNVSFSGKMDETV	262		

Db 361 SKDDGNTVAVDVNVDGALNVNOLNDSGNMLDSKAVAGSSGKVIYSGNVSPSKGMDTV 420
Qy 263 NINAGNNETIRNKNIDIASMTPOFSSVSLGAGADPTLSVGDALNVNOSKKNKVR 322
Db 421 NINAGNNETIRNKNIDIASMTPOFSSVSLGAGADPTLSVGDALNVNOSKKNKVR 480
Qy 323 ITNVAPEGKEDVTNNVQALKGVAONLNLRIDNVGNARAGIAQAIATAGLVAQVAYLPCKSM 382
Db 481 ITNVAPEGKEDVTNNVQALKGVAONLNLRIDNVGNARAGIAQAIATAGLVAQVAYLPCKSM 540
Qy 383 MAIGGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASGYOM 433
Db 541 MAIGGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASGYOM 591

RESULT 2
A:1888
Probable surface fibril protein NMA1200 [Imported] - Neisseria meningitidis (strain Z249)
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: A81888
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel,
; Holroyd, S.; Jørgels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajadream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: A81888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-592 <PAR>
A:Cross-references: GB:A1162755; GB:A1157959; NID:g7379742; PIDN:CAB84461.1; PID:g737989
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1200

Query Match 91.5%; Score 2009.5; DB 2; Length 592;
Best Local Similarity 70.4%; Pred. No. 3.6e-105;
Matches 417; Conservative 7; Mismatches 9; Indels 159; Gaps 3;

Qy 1 MNKIRIIRIWSALNMAVYVSELTRNHRKASATYKTAVALATLFTVOASA----- 51
Db 1 MNKIRIIRIWSALNMAVYVSELTRNHRKASATYKTAVALATLFTVOANATDEDEBEL 60
Qy 52 ----- 51
Db 61 ESVQSVVGSIQASMEGSELETISLSMTNDSKEFVDPIYVTLKAGNLKIKONTNENT 120
Qy 52 ----- 51
Db 121 NASSFTYSLKKDLTGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN 180
Qy 52 -----NRAASVKQVLANGNWIKGVKPGPTA--SDNVDF 82
Db 181 GIGSLTTLTLAGSSASHVDAGNQSTHYTRASIKYVLNAGNRIKVGKSTTGQSENVDF 240
Qy 83 VRTYDVEFLSADTKTTTVNVESKDNKGRKTEVIGAKTSVYKEKDKGLVTKDKGNGSS 142
Db 241 VRTYDVEFLSADTKTTTVNVESKDNKGRKTEVIGAKTSVYKEKDKGLVTKDKGNGSS 300
Qy 143 TDEGGGLVTAKEVIDAVKAKGRMKTITANGOTGADKFEYVTSSTNTVTFASGKGTATV 202
Db 301 TDEGGGLVTAKEVIDAVKAKGRMKTITANGOTGADKFEYVTSSTNTVTFASGKGTATV 360
Qy 203 SKDDGNTVAVDVNVDGALNVNOLNDSGNMLDSKAVAGSSGKVIYSGNVSPSKGMDTV 262
Db 361 SKDDGNTVAVDVNVDGALNVNOLNDSGNMLDSKAVAGSSGKVIYSGNVSPSKGMDTV 420
Qy 263 NINAGNNETIRNKNIDIASMTPOFSSVSLGAGADPTLSVGDALNVNOSKKNKVR 321
Db 421 NINAGNNETIRNKNIDIASMTPOFSSVSLGAGADPTLSVGDALNVNOSKKNKVR 480
Qy 322 RTTNVAPGVKEDVTNNVQALKGVAONLNLRIDNVGNARAGIAQAIATAGLVAQVAYLPCKS 381

Db 481 RTTNVAPGVKEDVTNNVQALKGVAONLNLRIDNVGNARAGIAQAIATAGLVAQVAYLPCKS 540
Qy 382 MAIGGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASGYOM 433
Db 541 MAIGGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASGYOM 592

RESULT 3
A:16138
adhesin homolog HI1732 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997
C:Accession: U00188
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kiehl,
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: U00188
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-298 <TIGR>
A:Cross-references: GB:U32846; GB:L42023; NID:g1574588; PID:g1574589; TIGR:HI1732

Query Match 15.7%; Score 345; DB 2; Length 298;
Best Local Similarity 29.9%; Pred. No. 1.9e-12;
Matches 87; Conservative 19; Mismatches 41; Indels 144; Gaps 2;

Qy 1 MNKIRIIRIWSALNMAVYVSELTRNHRKASATYKTAVALATLFTVOA----- 49
Db 1 MNKIRIIRIWSALNMAVYVSELTRNHRKASATYKTAVALATLFTVOAINDACTFVKVQ 60
Qy 50 ----- 49
Db 61 STEDDIEDSAATKDDNKQALKAGDTLTKAGKNLAKLDDGSGSVTFALAKDDVYTKA 120
Qy 50 ----- 49
Db 121 VSDTLTIGNTPPAAGGATPKVSTSTADGLAKTNGDTVAHLNGLASTLPDYTTNTGA 180
Qy 50 -----SANRAASVKQVLANGNWIKGVKPGPTA--SDNVDF 98
Db 181 STSVTFSPDIEKFAATIKDVLNAGWNKAKVAGTFENVVDIYAGDNEFTTGDKNT 240
Qy 99 TTVNVESKDNKGRKTEVIGAKTSVYKEKDKGLVTKD--KGENSSSTDEGE 147
Db 241 LDVYLTAKENGKTEVTKFTPKTSYKDNNGKLLTGKQLKDANTGTATNATE 291

RESULT 4
A:82671
surface protein xfr1529 [Imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: D82671
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: D82671
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2059 <SIM>
A:Cross-references: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAE84338.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carraro, D.M.; Carrier
as-Neto, E.; Docena, C.; El-Poriry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.: Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramee, E.E.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, E
 A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
 ; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savasak
 A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
 M.; Tsubako, M.H.; Valida, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Veltore, A.L.; Z
 A; Reference number: A59328
 A; Contents: annotation
 C; Genetics:
 A; Gene: XF1529

Query Match 15.5%; Score 340.5; DB 2; Length 2059;
 Best Local Similarity 24.6%; Pred. No. 3.6e-11;
 Matches 137; Conservative 70; Mismatches 177; Indels 173; Gaps 20;

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QY 17 VVVSELRNHTKRASVAVTATLFAVQASA-----NRASVADVLMAGNNT- 67
D 1536 VVVDLGLSLVGGSLTSLGIMSGHKITVTACTEDPTDAVNFSLKSVSEADVKGWTLT 1595
QY 68 -----KGVPCTTASDND-----FVRTYDVEFLSADFK-----TTTVNESK 106
D 1596 ASGANGSKVYSGGVLDKNTDGNLAISKSDSNVYENLSKDFVDEVTAAGNTVYVNTDGV 1655
QY 107 DNEKTEVKIGAKTSVKEKDKGLVTKDKGEN-----GSSTDEGEGLVTAKEVIDAV 159
D 1656 KVG--SDVSLGAMGLFANGPSPVTA SGFNAGDKYISHVAVGMAPTDAVNTVSLQAQVOSV 1713
QY 160 NKAGWRKRTT-----ANGOTGO---ADKFEVTVSGTNV-----TFASGKRTTA 200
D 1714 TVKATRYSTNDGCTGGNVDGATSGKAIAGVGTQASGEAAVSGAAAGSKGSTA 1773
QY 201 -----TVS-----KDDGNTITVM 213
D 1774 IGRNAISAGGSVALGPGADGKGASGYTKYSGVQNNVTGYTVSDAKAGFRTSISNV 1833
QY 214 YDVNVG-DALNVNQL-----QNSGWNLS-----RAVA 240
D 1834 ADKAEAMDVAVLRDLDAVNAOKSNLQTDMEHINNIEDVEFKITKGSASSVKGWGVAMA 1893
QY 241 GSSGKVTSGNVSPKGMDEVTNNAGNNIEITRNKNIDTATSMTOFSSVSLGAGADA 300
D 1894 IGTAAASGTESVALGK---NTNVSADNAVAI-GNG-----SVADRANSVSGSG-- 1939
QY 301 PTLISVDGDAIIVGSKKKNKPVRTITNVA PGYEGEDVTNVAOLKGAQNLNNRIDVNDGNAR 360
D 1940 -----GSEK-----QVTNVAAGTADTDAVNVSQLNGLITAKQYTDGAVGNLR 1982
QY 361 ---AGIAQIATAGLVQAVLPGKSMMAIGGTYRGAGYAIGYSSISDGNMIIKTGTAS 416
D 1983 RETSGVAAAIATANLEPOAVITPGRGMTSVGSSYQGSALAVGVSAVSESGHWVFKFTSGS 2042
QY 417 GNSRGHFGASAVGYQW 433
D 2043 ANTRSHVGVAGVGYQW 2059

```

RESULT 5

A82615
 surface protein XF1981 [imported] - Xylella fastidiosa (strain 9a5c)
 C;Species: Xylella fastidiosa
 C;Date: 18-Aug-2000 #sequence-revision 20-Aug-2000 #text-change 20-Aug-2000
 C;Accession: A82615
 R;Anonymous: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A;Reference number: A82515; MUID:20365717; PMID:10910347
 A;Note: for a complete list of authors see reference number A59328 below
 A;Accession: A82615
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1190 <SIM>
 A;Cross-references: GB:AE004017; GB:AE003849; NID:g9107083; PIDN:AAF84783.1; GSPDB:GN001

A;Experimental source: strain 9a5c
 R;Simpson, A.J.G.; Reinach, F.C.; Artuda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre
 as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Fr
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramee, E.E.; La
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins
 A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
 ; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sava
 A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
 M.; Tsubako, M.H.; Valida, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Veltore, A.L.
 A; Reference number: A59328
 A; Contents: annotation
 C; Genetics:
 A; Gene: XF1981

Query Match 15.2%; Score 335; DB 2; Length 1190;
 Best Local Similarity 26.9%; Pred. No. 3.7e-11;
 Matches 116; Conservative 54; Mismatches 151; Indels 110; Gaps 16;

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QY 61 LNAQ-WNIKVPETITASD-----NVDEVRYDYVEFLSADPKRTTNN 102
D 812 INAGSOKITTNVAAGTADTDAVNLSQLNTAMAGSAGKSVHYSTYD-----GGTGGNNY 865
QY 103 VESKDNEKTEVKIGAKTSVKEKDKGLVTKDKGENG-SSTDEGEGLVTAKEVIDAVNK 161
D 866 GDGATGTRSLAVGVTLASA-----EGATVSGSAAAGSKGSTAIGRNAVASADSVAGLD 921
QY 162 AGWRBKTTTANGOTQADKREFTVSGTNVTFASGKTTATVSKDDGNITVYVDNVGDA 221
D 922 -GAKDARGAESYTGKXSGLQNNVTGTVSDASKGERTVVS-----NVADAKKAT--DA 973
QY 222 LNVNQL-----QNSGNLDSKRAVAGSSGKVTSGNVSPKGMDEVTNNAGNNIEITRNK 277
D 974 VNLQDLRVADARVYDKNTKESLSEGT--VKNLSLNN----- 1011
QY 278 NIDATSMTPQFSSVSGAGADAPTLV-----GDALNVGSK-----KDNKPV----- 321
D 1012 -----SATP-----IAAGDATALIGVATASGADSIAMKNTKASASADNVAIGNHSVA 1059
QY 322 -----RTTNVAPGVKEDVTNVAOLKGAQNLNNRIDVNDGNAR---AG 362
D 1060 DRANTVSVGSAGSERQVTNVAAGTADTDAVNVSQLNGLITAKQYTDGAVGSLRRDPDGC 1119
QY 363 IAOAIATAGLVQAVLPGKSMMAIGGTYRGAGYAIGYSSISDGNMIIKTGTASGNSRGH 422
D 1120 VAAAIATANLEPOAVITPGRGMTSVGSSYRGOSALAVGVSSVSESGRWVFKFTSGSANTRSQ 1179
QY 423 FGASASVGYQW 433
D 1180 VGIAGVGYQW 1190

```

RESULT 6

A86036
 probable adhesin Z5029 [imported] - Escherichia coli (strain O157:H7, substrain EDL93
 C;Species: Escherichia coli
 C;Date: 16-Feb-2001 #sequence-revision 16-Feb-2001 #text-change 14-Sep-2001
 C;Accession: A86036
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
 iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
 Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A;Reference number: A83480; MUID:21074935; PMID:11206551
 A;Accession: A86036
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1588 <STO>
 A;Cross-references: GB:AE005174; NID:g12518349; PIDN:AA658749.1; GSPDB:GN00145; OMGP:
 A;Experimental source: strain O157:H7, substrain EDL933
 C; Genetics:

A;Gene: Z5029

Query Match	15.0%;	Score 329.5;	DB 2;	Length 1588;
Best Local Similarity	26.1%;	Pred. No. 1.1e-10;		
Matches 118;	Conservative 63;	Mismatches 177;	Indels 94;	Gaps 177;

[illegible]

RESULT 7

H91188
probable adhesin ECS4480 [similarity] - Escherichia coli (strain O157:H7, substrain RIMM)
C.Species: Escherichia coli
C.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001
R:Hagashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasavara, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A.Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and
A.Reference number: A96929; MUID:21156231; PMID:11258796
A.Accession: H91188
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-1588 <NAV>
A.Cross-References: GB:BA000007; PIDN:BA837903.1; PID:91363955; GSPDB:GN00154
A.Experimental source: Strain O157:H7, substrain RIMD 0509952
C.Genetics:
A:Gene: ECS4480

	Query Match	15.0%;	Score 329.5;	DB 2;	Length 1568;	
	Best Local Similarity	26.1%;	Pred. No. 1.le-10;			
	Matches 118; Conservative	63;	Mismatches 177;	Indels 94;	Gaps 17;	
OY	49 ASANRASVKKVLNAGNNIKGVKPGTTASDWDVEVRITYDIYE-FLSADTKTITTVNVESKD	107	:	: :	:	:
Dd	1164 SEAHDAVTVALROLONA-----IGAVATPTPKTFHFHANSTFEEDSLAIVGDSLAMGAKEIIV	1215	:	: ::	:	:
OY	108 NGKR-----TEVKIGAKTSYLKQKDGKYLVTKDKGENSSSDIEDEGLVTA	152	:	:	:	:
Dd	1216 NKGDKIGIGYGAYVDANALNGIALGSNAOVIHV--NSTAIS----NSGTTRGGQTNYT	1268	:	:	:	:
OY	153 KEVIDAWNKAQGWRMKTITTANGQ-----TGQAQDFEIVYSCTINVFPSAGSGITAIVSKD	205	:	: ::	:	:

```

Db      1269  AYNNDAPQNSVGSEVSADSGORQTNTNAAAGSAD-----TDAVNV--GQLKTKTDQVQSQN 1322
QY      206  DQGNITVM-----YDVNVGDAL-----INVQLQNSGNNLDSKAVVAGS 242

```

[illegible]

RESULT 8

AC0976
probable autotransporter sabb [imported] - *Salmonella enterica* subsp. *enterica* serovar
C:Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
A:Note: this species has also been called *Salmonella typhi*
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AC0976
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
S., T.; Moule, S., O'Gaora, P.
Nature 413, 846-852, 2001
A:Authors: Parry, C.; Quill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A.
Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica*
Reference number: AB0502; MUID:21534947PMD:11677608

A:Accession:AC0976
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1107 <PAR>
A:Cross-references: GB:AL513382; PIDN:CADO3303.1; PID:q16504923; GSPDB:GN00176
C:Genetics:
A:Gene: sarp

Query Match 14.8%; Score 326; DB 2; Length 1107;
Best Local Similarity 20.5%; Pred. No. 1.e-10;
Matches 142; Conservative 89; Mismatches 184; Indels 278; Gaps 25

OY	7	IIMNSALMANYV-----VELTRINRTKRASATVTAKVALITLLEFATVQASANRAKSYKD-	59
Dd	427	LIMEDDTGAFSANHGSGTSKITNVAAGALSIEDSDTDAVNGSOLEYETNOKYDONTSLADIN	486
OY	60	--VLNA-----WN-----IKGVKPGTTASDANDPV---RTPYT---	88
Dd	487	TSTINMLGTDALSMWDEEGAFSASHGSGTNKITNVAAGEIASDSIDALINGSQLYEFTNMI	546
OY	89	-----VEFLSADTKTTTVN-----VESDKNGKTEVKIGATSVYKEODGLVYG	134
Dd	547	SQYNESISQLAGDPJSEFYITENGTVGYKIIRINDNGLEGO-----DAYATGNATAVXY	599
OY	135	DK-----GENGSSTDEG-----EGLV-----TAKE	154
Dd	600	DAVASGACCLAGOUNSSSIIEBSIALSGSGTISRRAITTGIRETSATSDDCVIIGYNTTDRE	659
OY	155	VIDAIVANKA-----GWMMKRTTTANGOGU-----ADKEFTVSGTNVF	192
Dd	660	LLGALSLTGDEBSRHQITNVADGSPAODAUVTRQLONAIGAATTPTPKYHANSTEEDSL	719
OY	193	ASGGKTA-----TYSKDQG-----NIYMYIVYVNGDALNV--	225
Dd	720	AVGDSTLMGAKTIVNADAGIGIGINTLYVMALAINGIAIGSNARANHANSIAMNGSOTT	779

Db 331 -----SVALGSSMASSEPNVSVSGDGLRGPVR-----RIYVNGDIGINNDAVYKS 378
Qy 340 QLKGVANLNLRINDV-----DGNARAGIAOATAGLVOAYLPGRKSMMAIG----- 386
Db 379 QLDGVATSNVNVYASKNIAIAIDITGSGVASVSGODSTAGASQAQAAGDSIALGARSR 438
Qy 387 ---GGTYRGEAGYAGYSSISDGMNIIKGT---SGNSRGH---FGASASVG 430
Db 439 ANAIGSALGVDGHALGANSTALG---OSTAISGEGTSLIGNSFVGSATNG 488

RESULT 11

S28634
adhesin AIDA-I precursor - Escherichia coli plasmid pIB6
C:Species: Escherichia coli
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 08-Oct-1999
C:Accession: S28634; S22680; S28881; S72657
R:Benz, I.
submitted to the EMBL Data Library, March 1992
A:Reference number: S28634
A:Accession: S28634
A:Molecule type: DNA
A:Residues: 1-1286 <BEN>
A:Cross-references: EMBL:X65022; NID:942254; PIDN:CAA6156.1; PID:942255
R:Benz, I.; Schmidt, M.A.
Mol. Microbiol. 6, 1539-1546, 1992
A:Title: AIDA-I, the adhesin involved in diffuse adherence of the diarrhoeagenic Escherichia coli O157:H7
A:Reference number: S22680; MUID:92326638; PMID:1625582
A:Accession: S22680
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 839-1286 <BE2>
A:Cross-references: EMBL:X65022
A:Experimental source: strain 2787
A:Accession: S28881
A:Molecule type: protein
A:Residues: 30-56 <BE3>
A:Experimental source: strain 2787
R:Subr, M.; Benz, I.; Schmidt, M.A.
Mol. Microbiol. 22, 31-42, 1996
A:Title: Processing of the AIDA-I precursor: removal of AIDA and evidence for the outer A:Reference number: S72657; MUID:97055419; PMID:8899706
A:Accession: S72657
A:Molecule type: protein
A:Residues: 847-856 <SUH>
A:Experimental source: DAEC strain 2787
C:Genetics:
A:Genome: plasmid pIB6
C:Keywords: membrane protein
F:1.49/Domain: signal sequence #status predicted <Sig>
F:50-1286/Product: adhesin AIDA-I #status predicted <MAT>

Query Match 8.6%; Score 189; DB 2; Length 1286;
Best Local Similarity 24.7%; Pred. No. 0.0059;
Matches 111; Conservative 57; Mismatches 189; Indels 92; Gaps 23;
Qy 1 MNKIYRIIWNLSALNAVYVSELTRNHRKRASATYKTAFLA---TLLEFATVQASANRAASVYK 58
Db 1 MNKAYSIIMSHSRQAWIYASLARGH-----GFYLAKNLTLLVLAVSTIGNAFAV- 50
Qy 59 DYLAAGNRIKV--KPGTASDNDVFRITYDYVEFLSADRTKTTVN--VESKNGKTE 113
Db 51 -----NISGTVSSGTVSSGTEYOIV-----YSGRGSNATVNSGCTQIVNNGKXT- 95
Qy 114 VKIGAKTSVIREKNGKLVTKGDKGNGSSTDEGGLVTAKEVIDAVKAGRMKTTTANG 173
Db 96 -----TATVYNSG-----SONVGTSGATT---STVYNSGIGQIVSSG---VASATN 137
Qy 174 QTCGADRFETVSTGNTVAFSGKGTATVSKDQGNITVMDVAVGALANN--QIONS 230
Db 138 LSGAQNITVNGHASNIVIPSG-----GNQTI-PSGGITSTNLSGGQQRVS 184
Qy 231 GWNLSKRAVAGSSGKVIISGVNPSKRMDETNTINAGNNIETTRNGKNIDIAIATSMTPQFS 290

Db 185 SGGAIVNTIINSQ---AONLTSEGAI---STHISSGNOYISA-GANAEITVNSGQFQ 238
Qy 291 SVSLGAGADAPTLSDVDDALNVGSKKDNKPRIRNVAPGVKEGVTVNAOLKVAOULNN 350
Db 239 RVNSGAAVATGTVLSGQTQNVSSGSAISTSVYNSGVQTVFAGATVITPTVYNSGNOIIS 298
Qy 351 RIDNVGNARAGIAO-AIATAGLVOAYLPGRKSMMA-IGGQTYRGEAGYAGYSSISDGG 407
Db 299 -----GGIYSEITVNVSGTQNIYSGGSALSNIKGSQIYNSGTAIIN-TLYSDG 347
Qy 408 NWITK--GTASG---NSRGHFGASASVGY 431
Db 348 YQHTNRNGIASGTVIVNSGYVNTS-SGGY 375

RESULT 12

H83135
Probable adhesin PA4082 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: H83135
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L. ; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: H83135
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <STO>
A:Cross-references: GB:AE004824; GB:AE004091; NID:99950277; PIDN:AA607469.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4082

Query Match 8.5%; Score 186.5; DB 2; Length 1018;
Best Local Similarity 21.1%; Pred. No. 0.0061;
Matches 118; Conservative 75; Mismatches 224; Indels 143; Gaps 23;

Qy 1 MNKIYRIIWNLSALNAVYVSELTRNHRKRASATYKTAFLA---TLLEFATVQASANRAASVYK 60
Db 1 MNKCYALVWNVSSQCMWNVSESGRRKPKAGAKAIALVLAIGATLAPALPALSCTV 60
Qy 61 LNAQWN-----IKGVKPGTASDN--VD-FVPTYDYVEFLSADRTTTVNVESKNGKTE 113
Db 61 VCGSANEIHLHG---GNSLSVNGKVDKLLANMDS--FVAAGRGVLEFNPSSSSIALNR 115
Qy 114 VKIGAKTSVIR--EKDGKLVTKDKG---ENGSTDEGBGLVTAKEVIDAV--NKAGW 164
Db 116 V-IGTKASDIOGRIDANGOVFLVNPNGVLFGRGAQVAVVGVVASTLDTDAEFNGNSRY 174
Qy 165 RMKTTANGTGQADKRETYTSGTNTVFAS-----GKGTATVNSKDDQ 207
Db 175 FTGPGSTNGVNLHGAIITAAEGGSIALIGAQVNDRGTVLAOMGVGVLGASDLTLNFDN 234
Qy 208 GNITVMDVAVGDAIN-----VNOIONGMNLDSKRAVAGSSG 244
Db 235 KLDIRVDAGVANAALASNGGLKADGGRVLAARTANALNTVYNSGCAIEARSLRKNG 294
Qy 245 KVISGVNPSKRMDETNTINA-----GNNIETTRNGKNIDIAIATSMTP----- 287
Db 295 RIVLDGPGDGKVVWVGALSNALNLPBGHGVVEVRGAVEVALCTQVNTLASNLNGTGW 354
Qy 288 -----QPSVSLGAGADAPTL-----VDGDALVGS 314
Db 355 IAADKIDVRPSASVDGTVTHADTLSRNIASTNIELVSTKDDLDLDSGVNMAASGRRLGGS 414
Qy 315 KKD---NKPVRTVAVGVK---EG--DYTNVAOLKVAOULNNRID-----NVGNA 361
Db 415 AADLTTLNGLNASAKAGLELKAEGAIDINDKIYLGAGSAL--AMDAGGRHRYNGTASV 472

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:06:20 ; Search time 6.68663 Seconds
(without alignments)

3045.266 Million cell updates/sec

File: US-09-771-382-26
Perfect score: 2197
Sequence: 1 MNKIRIINNSALNAMYVS.....TASGNSRGHFGASASGVQW 433

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	189	8.6	1286	1 AIDA_ECOLI	Q03155 escherichia
2	186.5	8.5	1039	1 AGA3_ECOLI	P39180 escherichia
3	182	8.3	1325	1 YDEK_ECOLI	P32051 escherichia
4	165.5	7.5	2249	1 OMPA_RICRI	P15921 rickettsia
5	160	7.3	1655	1 OMPB_RICCN	Q9K433 r outer mem
6	158	7.2	2003	1 YDBA_ECOLI	P33666 escherichia
7	150	6.8	1300	1 120K_RICRI	P14914 rickettsia
8	150	6.8	1654	1 OMPB_RICRI	Q53047 r outer mem
9	148	6.7	550	1 FLIC_SHIFL	Q08860 shigella fl
10	147.5	6.7	2021	1 OMPA_RICCN	Q52657 rickettsia
11	147	6.7	1025	1 SLAP_CAUCR	P35828 caulobacter
12	145.5	6.6	1861	1 APD1_THERU	P38536 t amylopull
13	145	6.6	497	1 FLIC_ECOLI	P04949 escherichia
14	142.5	6.5	1007	1 Y741_CHLMD	Q09156 chlamydia m
15	142	6.5	1608	1 HLVA_SERMA	P15320 serralia ma
16	142	6.5	1953	1 BIGA_SALTY	P25927 salmonella
17	141.5	6.4	737	1 A1YS_ENTFA	P37710 enterococu
18	141.5	6.4	1567	1 ICERX_XANCT	P18127 xanthomonas
19	140.5	6.4	930	1 PMPB_CHLPN	Q92993 chlamydia p
20	140	6.4	1577	1 HLVA_PROMI	P16466 proteus mir
21	138.5	6.3	365	1 FLIC1_PROMI	P42262 proteus mir
22	138.5	6.3	2660	1 YEEL1_ECOS7	Q08897 escherichia
23	138	6.3	507	1 FLIC_SALON	Q06974 salmonella
24	137.5	6.3	367	1 FLIC2_PROMI	P42273 proteus mir
25	137	6.2	933	1 SLAP_CAME	P33627 campylobact
26	136.5	6.2	1656	1 OMPB_RICJA	Q06653 r outer mem
27	136	6.2	507	1 FLIC_SALBE	Q06968 salmonella
28	136	6.2	1228	1 SLAP_BACST	P35825 bacillus st
29	134.5	6.1	444	1 SLAP_IACAC	P35829 lactobacilli
30	134.5	6.1	1148	1 ICERX_PSESX	Q30611 pseudomonas
31	134.5	6.1	1569	1 YPDA_ECOLI	P52143 escherichia
32	133.5	6.1	504	1 FLIC_SALRO	Q06982 salmonella
33	133	6.1	464	1 FLIC1_ECO57	P58297 escherichia

ALIGNMENTS

```

RESULT 1
AIDA_ECOLI
ID AIDA_ECOLI STANDARD: PRT: 1286 AA.
AC Q03155,
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adhesin aidA-I precursor.
GN AIDA-I.
OS Escherichia coli.
OG Plasmid pIB6.
OC Bacteria: Proteobacteria: Gammaproteobacteria: Enterobacteriales:
OC Enterobacteriaceae: Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 50-56.
RC STRAIN=0126:H27 / 2787;
RX MEDLINE=92326538; PubMed=1625582;
RA Benz I., Schmidt M.A.;
RT "AIDA-I, the adhesin involved in diffuse adherence of the
RT diarrhoeagenic Escherichia coli strain 2787 (O126:H27), is
RT synthesized via a precursor molecule.";
RL MOL. Microbiol. 6:1539-1546(1992).
CC -I- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE
CC ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI
CC TO EPITHELIAL CELLS.
CC -I- SUBCELLULAR LOCATION: Outer membrane.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X65022; CAA46156.1; -
CC PIR: S28634; S28634.
CC InterPro: IPR006315; Autotransport.
CC InterPro: IPR005546; Autotransporter.
CC InterPro: IPR004899; Pertactin.
CC Pfam: PF03797; Autotransporter; 1.
CC TIGRPFAMs: TIGR01414; autotrans_bar1; 2.
CC Cell adhesion; Signal; Outer membrane; Plasmid.
CC SIGNAL 1 49
CC CHAIN 50 1286 ADHESIN AIDA-I.
CC PROPEP ? 1286
CC SEQUENCE 1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;
Query Match 8.6%; Score 189; DB 1; Length 1286;
Best Local Similarity 24.7%; Pred. No. 0.0043;
Matches 111; Conservative 57; Mismatches 189; Indels 92; Gaps 23;
OY 1 MNKIRIINNSALNAMYVSELTNRNHTKRSATVKTAVLA--TLLEFAVQASANRAASYK 58
||| | ||| : ||:| ||| | ||| ||| : :|

```

```

Db      1 MNKAYSTIWSHROAMIVASELARGH-----GEVLAKNTLLVIAVSTIGNAPAV- 50
QY      59 DVLNAGNINIGV--KPGTASDNVDYFRTDVEFLSADFTTIVN--VESKDNKTE 113
Db      51 -----NISGTAVSGGTSGGTQIY-----YSGRGNMNAVNSGGTQIVANGCKT- 95
QY      114 VKIATKSVIKENDKLVTKDKKENGSSDDEGGLYTAKEVIDAVNKAQRMTTANG 173
Db      96 -----TATVNSSG-----SQNVGTSGATI-----STIVNSGIGORVSSG-----VASATN 137
QY      174 OTGQADFEIVTSGTNTVFPASGKTATVSKDDGNTVMDVAVGALVNN--OLONS 230
Db      138 LSGAQNIVNLGHSNIVIFSG-----GNQTI-FSGITDSTNSSGGQORVS 184
QY      231 GWNIDSKAVAGSGSKVIGSNVSPSKMDFTVINAGNNIETIRNGKNIDATSMPTQFS 290
Db      185 SGVAVSNMTTINSQ---AQNTLSEGAII--STHSSGNGVISA-GANATEETIVNSGQFQ 238
QY      291 SVSLGAGADAPTLSDVDALNVGSKKDNKPRITNVAPGVKEGIVTVAQLKVAQNUN 350
Db      239 RVNSGAVATGTVLSGTQNVSSGSAISTSVYNSGVGTVPAGATVTTVNSGNGONISS 298
QY      351 RIDNVDNARAGIQ--AIIAGLVQAYLPKSKMAA-IGGGTGEAGVATGYSISDGG 407
Db      299 -----GGIVSETTVNSGTQNTYSGGSAISANIKSQIYNSECTAIN-TLVSDG 347
QY      408 NMIIK--GTASG---NSRGHGASASVGY 431
Db      348 YOHIRNGIASGTIVNOSGYNIS-SGGY 375

RESULT 2
AG43_ECOLI STANDARD; PRT; 1039 AA.
AC P39180; P75614; P76360; P97241; Q46771;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 43 precursor (AG43) (Fluifling protein).
GN Flv OR B2000.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE-97426617; PubMed-9278503;
RA Blatter F.R., Plunkett G., Iii, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.E.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE-97251358; PubMed-9097040;
RA Itoh T., Aliba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
RA Sivasubramaniam S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horiiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 4.0-1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-ML 308-225;
RA Henderson I.R., Owen P.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

RP PRELIMINARY SEQUENCE OF 53-78.
RC STRAIN-ML 308-225;
RX MEDLINE-89291704; PubMed-2661530;
RA Caffrey P., Owen P.;
RT "Purification and N-terminal sequence of the alpha subunit of antigen
RT 43, a unique protein complex associated with the outer membrane of
RT Escherichia coli.";
RL J. Bacteriol. 171:3634-3640(1989).
RN [5]
RP SEQUENCE OF 53-63.
RC STRAIN-K12 / EMG2;
RX MEDLINE-97443975; PubMed-9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
RN [6]
RP GENE NAME.
RX MEDLINE-97257509; PubMed-9103983;
RA Henderson I.R., Meenan M., Owen P.;
RT "Antigen 43, a phase-variable bipartite outer membrane protein,
RT determines colony morphology and autoaggregation in Escherichia coli
RT K-12.";
RL FEMS Microbiol. Lett. 149:115-120(1997).
CC -1- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION. MAY
CC FUNCTION AS AN ADHESIN.
CC -1- SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA
CC CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA
CC CHAIN).
CC -1- SUBCELLULAR LOCATION: Outer membrane-associated.
CC -1- SIMILARITY: TO ADHESIN AID-I AND TO BORDETELLA PERTACTIN.
CC
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CC
DR EMBL: AE000291; MACT5061.1; ALT INIT.
DR EMBL: D90838; BAI15825.1; ALT INIT.
DR EMBL: D90839; BAI15832.1; ALT INIT.
DR EMBL: U24429; AAB47869.1; -.
DR HSSP: P07505; ISRND.
DR EcoGene; EG12686; flv.
DR InterPro: IPR006315; Autotransport.
DR InterPro: IPR005546; Autotransporter.
DR InterPro: IPR004899; Pertactin.
DR Pfam; PF03797; Autotransporter; 1.
DR TIGRFAMs; TIGR01414; autotrans_bar1; 1.
KW Outer membrane; Signal; Complete proteome.
FT SIGNAL 1 52
FT CHAIN 53 551
FT CHAIN 552 1039
FT VARIANT 2
FT VARIANT 41 42
FT VARIANT 46 46
FT VARIANT 157 157
FT VARIANT 188 188
FT VARIANT 303 305
FT VARIANT 320 320
FT VARIANT 372 372
FT VARIANT 493 493
FT VARIANT 497 497
FT VARIANT 585 585
FT VARIANT 709 709
FT VARIANT 721 721
FT VARIANT 751 753
FT VARIANT 803 803
FT VARIANT 815 815
FT VARIANT 824 824
FT ANTIGEN 43 ALPHA CHAIN.
FT ANTIGEN 43 BETA CHAIN.
FT K -> N (IN STRAIN ML 308-225).
FT SL -> FE (IN STRAIN ML 308-225).
FT T -> K (IN STRAIN ML 308-225).
FT W -> L (IN STRAIN ML 308-225).
FT V -> F (IN STRAIN ML 308-225).
FT ATN -> STI (IN STRAIN ML 308-225).
FT A -> T (IN STRAIN ML 308-225).
FT N -> Q (IN STRAIN ML 308-225).
FT E -> V (IN STRAIN ML 308-225).
FT S -> N (IN STRAIN ML 308-225).
FT H -> Y (IN STRAIN ML 308-225).
FT E -> K (IN STRAIN ML 308-225).
FT M -> T (IN STRAIN ML 308-225).
FT GHL -> SHF (IN STRAIN ML 308-225).
FT S -> P (IN STRAIN ML 308-225).
FT A -> V (IN STRAIN ML 308-225).
FT C -> S (IN STRAIN ML 308-225).

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FT VARIANT 829 835 LNLVHTS -> MNLTYNA (IN STRAIN ML 308-
FT 225).
FT VARIANT 845 847 OGN -> LGA (IN STRAIN ML 308-225).
FT VARIANT 855 855 S -> T (IN STRAIN ML 308-225).
FT VARIANT 888 888 Q -> L (IN STRAIN ML 308-225).
FT VARIANT 1025 1025 S -> I (IN STRAIN ML 308-225).
FT CONFLICT 61 63 ETV -> TTT (IN REF. 5).
SQ SEQUENCE 1039 AA; 106841 MW; 5170D647C8DEBE0 CRC64;

Query Match 8.5%; Score 186.5; DB 1; Length 1039;
Best Local Similarity 21.8%; Pred. No. 0.0046;
Matches 112; Conservative 56; Mismatches 201; Indels 145; Gaps 20;

OY 1 MNKIRIINNSALNANVAVVSELTRNHTKASATVKAVALATLLFATVOASNRASVKVY 60
DB 5 LNTICRLVNMHTGAFVVASSELARAGKGGVAV-----ALSLAATVLPVLAADI--V 56
OY 61 LNAGNNIKVKGKGTASDNVDFV-----RTYDVEFLSADTKTTTVNESKDNQ--KRT 112
DB 57 VHPGETVNG---GTLANHDNQIVFGTNGMTISTGLEYGPRDEANANGQWODGGTANKT 113
OY 113 EVKIG-----AKTSVKEKDKLVTKG--DKGENGSTDEBEGVLTAKVETDANV 160
DB 114 TVTSGLOLRVNPBGVSVDTVISAGGQSLOGRAVNTTLNGEQMHEGAIATGYI--N 170
OY 161 KAGWR-----MKTTTA-----NGOTGQADKFEFV-----TS 186
DB 171 DKGWQVVKPGYATVDVVTGTAEGGPDANGDTCGRVBDARTITNKGRQIVRAEGTA 230
OY 187 GTNVTFASGKGTATVAVSKDDGNITVMDVNVGDALNVNOLONGMNI--DSKAVAGSSGK 245
DB 231 NTFVYVAGGDDQTVHGHALDTTLNGGYQVYHNGGTASD--TVVNSDGMQIVKNGVAGNTIV 289
OY 246 VLSGNSPSKGMDEHVNINAG-----NNEIFTPNGCN 278
DB 290 NOKGRLOVDAGGTATNVLTKGQALVTSTAATVYTGINRLGAPSVYEGKADNV--VLENGR 348
OY 279 IDIATSMTPQFSSVSIGA-----GADAPPLISV-----DGDALNVSSKKDNKPVRTT 324
DB 349 LQVLGHTATNTRVDDGGLVDVRNGSTATTVMGNGCVLLASGAAVSSTRSGK----- 403
OY 325 NVAPEGVEGDTNVNAOLKQVANOINLRIDNVGNARAGIAQIATAGLVAVYLPCKSKMA 384
DB 404 --AFSIGGQADALMKEGSSFTLN-----AGDTATDIT 435
OY 385 IGGCTYRGAGYAIGSSISDSGNNIIRKGTASGN 418
DB 436 VNGGLFTARGTLAGTTTLNNGAIIITLTSKTYVNN 469

RESULT 3
YDEK_ECOLI STANDARD; PRT; 1325 AA.
AC P32051; P76140; P77168;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical lipoprotein ydek precursor (ORF1).
GN YDEK OR ORF1 OR B1510.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).

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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,
RA Sampei G., Seki Y., Sivasubaram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 595-1325 FROM N.A.
RX MEDLINE=94100243; PubMed=8274505;
RA Cartwright P.J., Timms M.W., Lithgow T., Hoef P.B., Hoogenraad N.J.;
RT "An Escherichia coli gene showing a potential ancestral relationship
RT to the genes for the mitochondrial import site proteins ISP42 and
RT MOM38.";
RL Biochim. Biophys. Acta 1153:345-347(1993).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential).
CC -1- SIMILARITY: TO E. COLI YEAL.
CC -1- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
CC ISP42 AND MOM38.
CC -1- CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 653.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE000248; AAC74583.1; -
DR EMBL: D90793; BAA15190.1; ALT_INIT.
DR EMBL: D90794; BAA15197.1; ALT_INIT.
DR EMBL: X73295; CAA51730.1; ALT_FRAME.
DR PIR: A64905; A64905.
DR Ecogene: EG11780; ydek.
DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
KW Hypothetical protein; Membrane; Lipoprotein; Signal.
KW Complete proteome.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 1325 HYPOTHEICAL LIPOPROTEIN YDEK.
FT LIPID 19 19 N-ACYL DIGLYCERIDE (POTENTIAL).
FT CONFLICT 884 884 N -> K (IN REF. 3).
FT CONFLICT 1317 1317 M -> S (IN REF. 3).
FT FT
SQ SEQUENCE 1325 AA; 136514 MW; 26A3A066FA19ADV CRC64;

Query Match 8.3%; Score 182; DB 1; Length 1325;
Best Local Similarity 21.8%; Pred. No. 0.011;
Matches 125; Conservative 60; Mismatches 216; Indels 172; Gaps 23;

OY 1 MNKIRIINNSALNANVAVVSELTR-----NHTRAATVTAVALATLLFATVOASAN 52
DB 1 MNRIYVNWCTLOVFOACSELTRRAGKSTVNLKSSGLTKFSRLTGVLALLASGSAS 60
OY 53 RAA-----SVKDVNLNAGW-----NIKGVFPGTASDNVDFVRYDVEFLSAD 95
DB 61 GASLEVDNDQIINIDVDVAVDAVGVGTGVNIIAGNAS-----LTTITTSVIGANE 115
OY 96 TKTTVNV-----ESKDNKRTVEV-RIGAKTSVIRK-----DGLKVTGDKGNGSS 142
DB 116 DSEGTAVNVAGTWRLTLDSSNNAPLVNGSGGTINIKKGHVDGGLRSGSTGCVTV 175
OY 143 TDEGELVYAKVEYID-----AVNKAG-WRM 166
DB 176 NVEGEDSVLTLEFEGSYGTGSLNITDKGYTSSIAVILGYQAGSNGGVYVEKGEWLI 235

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QY 167 KTTTA-----NGOTGADKFEVTVSGTNTVF-----ASGKTTATVSKDDGNT 211
DB 236 KNDSDSIEFOJIGNGTGEA-----TIRREGGLVTAENTLIGGNATIGLNMVODDSDVTVR 291
QY 212 VMVD-----VNVGDALN--VNOLONGSMWL----- 234
DB 292 RLIVNGYNGTGNVSNNGNLNNKEYSLVGVODGSHGVYVNTDKHMFNLGEGEFRIYI 351
QY 235 ----DSKAVAGSSGKVIISGVNPSKGMDEF-----VNINANNIEITRNKN 278
DB 352 GDADGDGLNVSSEKGVDSGITTAG--MKETGTGNITVYKOKNSVITNLGTLGVDGSHGM 408
QY 279 IDITSMTPPESSVSLGAGADAPLSDGALNNGSKD--NKPVRTINVAPGVKEGVDYTN 337
DB 409 NISNOGLVNSNGSSLSYG---ETGVNVSITTGGMVEVKNVYTTIGVAGVGNLINSID 464
QY 338 VAOLKGAONLNNRIDVNDGNARAGIAVITAGLVOAYLP--GSKMAIGGTYRFBAG 395
DB 465 GG--KEVSQNTFTFGDKASGIGTLNMDATSSFPVGLVNGNFGSGIVNNGATLNSTG 522
QY 396 YAI-----GYSSISDGGNMIKGTASGNSR 420
DB 523 YGFIGNAGSGKGIIVNISTDSLMLNK--TSSTNAQ 554

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RESULT 4

OMPA_RICRI STANDARD; PRT; 2249 AA.

```

AC P15921;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (rOmpA) (rOmp A).
GN OMPA.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RC SEQUENCE FROM N.A.
RA MEDLINE=90354033; PubMed=2117568;
RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;
RT "A protective protein antigen of Rickettsia rickettsii has tandemly repeated, near-identical sequences.";
RL Infect. Immun. 58:2760-2769(1990).
CC -I- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
CC -I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.
CC -I- PTM: GLYCOSYLATED (PROBABLE).
CC -I- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.
CC -----
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DR EMBL_M31227; AAA26380.1; -.
DR PIR_A41477; A41477.
DR InterPro: IPR006315; Autotransport.
DR InterPro: IPR005546; Autotransport.
DR Pfam: PF03797; Autotransporter, 1.
DR TIGRPFAMS_TIGR01414; autotrans_berl. 3.
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.
FT SIGNAL 1 28
FT CHAIN 29 2249 POTENTIAL.
FT DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 212 1180 A (TYPE I).
FT REPEAT 287 358 B (TYPE II).

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FT REPEAT 359 430 C (TYPE II).
FT REPEAT 431 505 D (TYPE I).
FT REPEAT 506 577 E (TYPE II).
FT REPEAT 578 652 F (TYPE I).
FT REPEAT 653 724 G (TYPE II).
FT REPEAT 725 799 H (TYPE I).
FT REPEAT 800 874 I (TYPE I).
FT REPEAT 875 949 J (TYPE I).
FT REPEAT 950 1021 K (TYPE II).
FT REPEAT 1022 1093 L (TYPE II).
FT REPEAT 1094 1165 M (TYPE II).
FT REPEAT 1166 1180 TYPE I (INCOMPLETE).
SQ SEQUENCE 2249 AA; 224333 MW; A9D6464C089D087 CRC64;

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Query Match 7.5%; Score 165.5; DB 1; Length 2249;
Best Local Similarity 25.1%; Pred. No. 0.15;
Matches 127; Conservative 46; Mismatches 180; Indels 153; Gaps 27;

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QY 32 ATVAT-AVLATLLEFATVQASANR---AASYVDVLAGMNIKGVKPGTTASDNDVFRTYD 87
DB 807 ATISVGAGTATLGAVIKATTTKLTNAAAVLTITNAAVILGAVDNTGGDNVGLNLNG 866
QY 88 TVEFLSADTKTTTVNVESKNGKTEVIGAKT---SVIKERDGL----- 130
DB 867 ALSQVTDIGNT-----NSLAT-ISVGAGTATLGAVIKATTTKLTNAAVILITLNA 917
QY 131 -----VTGKDKENGSSST-DEGEGLVT---AKEVI 156
DB 918 NAVLTGAIIDNTGGDNVGLNLNGALISQVTDIGNTNSLATISVGAGTATLGAVIKAT 977
QY 157 DAVKAGRKAKTTTANQOTGADKFEVTVSGTNTFPASGKTITVYSKDDGNTTWAYDV 216
DB 978 TKLTDASAVKFTTPVYVGTGIDNTGNANNQI-VTFGNSTVTVGNV---GNTNALATV 1031
QY 217 NVGDALNVNOLONGSMWLDSKAVAGSSGKVIISGVNPSKGMDEFVNIING-----NNIE 271
DB 1032 NVGAGL--LQYQGVVAVANTINLTDNASAYFTTPVYVGTGIDNTGNANNQIYFTGNST 1089
QY 272 ITRNGKNIDATSMTPPESSVSLGAGADAPLSDVGDAL--NVGSKRDN-KPVRTINVAP 328
DB 1090 VTGNVGN-----TNLATVAVNGAG---LLQYQGVVAVKANTINLTDNASAVKFTN--P 1136
QY 329 CVKCGDVATNVAQLKGVQONLNNRIDVNDGNARA---GIAQAIAT---AGL-VQAYLPG 379
DB 1137 VVVYGAIDNNG-----NANNGIVTFEGNSTVGTGIDNTNALATVWVAGITLQAA--G 1186
QY 380 KSWMA-----IGGTYRKEAGVYAIY---SSISDGGNMIK----- 412
DB 1187 GSLAANNIDGARGTLEFNGPLDGG-----GKAIPYFKGALANGNNAIILNVTKILTA 1240
QY 413 -----GTASGNSRGH---FGASASVG 430
DB 1241 SHLTITGVAEINIGAGMLFTIDASVG 1266

```

RESULT 5

OMPB_RICCN STANDARD; PRT; 1655 AA.

```

AC O9KKA3; O9KK98; O9XC45;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scab) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompb); 32 kDa beta peptide].
GN OMPB OR RC1085.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RC SEQUENCE FROM N.A.

```


RT Escherichia coli K-12.
RL Blochmle 73:1361-1374(1991).
CC -1- SIMILARITY: TO S. TYPHIMURUM ORF NEAR CYS6 (AC P25928).
CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION: THE GENE CODING FOR
CC THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT
CC BETWEEN AMINO ACIDS 839 AND 840.
CC -----
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CC -----
DR EMBL: AE000237; AAC74483.1; ALT_SEQ.
DR EMBL: AE000237; AAC74487.1; ALT_SEQ.
DR EMBL: D90778; BAA15009.1; ALT_SEQ.
DR EMBL: D90778; BAA18880.1; ALT_SEQ.
DR EMBL: D90779; BAA18881.1; ALT_SEQ.
DR EMBL: X62680; -; NOT_ANNOTATED_CDS.
DR EcoGene: EG11307; ydbA.
KM Hypothetical protein: Complete proteome.
FT CONFLICT 489 489 I -> V (IN REF. 2).
FT CONFLICT 495 495 I -> V (IN REF. 2).
SQ SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220EE CRC64;

Query Match 7.2%; Score 158; DB 1; Length 2003;
Best Local Similarity 23.2%; Pred. No. 0.34;
Matches 112; Conservative 61; Mismatches 111; Indels 138; Gaps 26;

OY 33 TVKTAVIATLLEFATQVANSANRPAASVKVNLNAGNINIKVCKGTASDN--VDEVRVYDV 89
DB 151 TEKLTITRDSVF--TYTENADGTTSLD-----SNCRKATIMLMQIDEANTVAL 198
OY 90 EPLSADIKT-----TVNVESKDNKKTEVKIAGKTV---IEMKDKIYTKG 134
DB 199 EGVASADATIKWQYHNSELVITGNATVNNNGKTT--VDEKSTGEIINGNNKRVIODG 255
OY 135 DKENG-----SSTDEGECLVYAKE-----VIDA-----VNRAGWEMKTTTANQ 174
DB 256 DLVYSGGHHGIDITGDSATVNDKGTMTVTDPESGIDIDGKALVNNBG--ESTIINGG 312
OY 175 TGADAKREYV-----SGTNVTFASGK-----GTTAT 201
DB 313 TGQINDGDDATANNNGKTVYDGKDSGTETNGNNGKYIODGDLVSGGHHGIDITGDSAT 372
OY 202 VSKDGNITVMDVNVGDLNVO--LQNSGMNLDKAVAGSSGKVISGN--VSPSKG 257
DB 373 V--DNKGTMTVTDPESIGIOVDGDAVNNNG--ESAITNGGTQINGDDATANNNG 427
OY 258 -----MDETVINAGNN-----IEITRNKNIDI--ATSMPTQFSSVSLGAGADAPTL 303
DB 428 TVYDGKSTGTEIAGNNGKYIODGDLVSGGHHGIDITGDSATVNDKGTMTVTDPESIGI 487
OY 304 SVGDALNVSGKDNKRVYITINAVPKVEGDVYNAOLKVAQNLNR-IDNVGDNARAG 362
DB 488 QIDDDQALVNNES--TTINGCTG-----TQINGDDATANNNGKTVYDGKSTG 535
OY 363 IAOAIATAGLVQAVLPKSMMAIGGTYRGAAGVATIGSSYISOGNNIINGTAGNRSRGH 422
DB 536 -TKIAGNIGIVN--LDG-SLVTGG-----AHGEVNTGIDNGTVNNKGDIVVDTGS 582
OY 423 FG 424
DB 583 IG 584

DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 120 kDa surface-exposed protein.
GN P120.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-R:
RA MEDLINE-90136087; PubMed-2515418;
RT Gilmore R.D. Jr., Joste N., McDonald G.A.;
RT "Cloning, expression and sequence analysis of the gene encoding the
RT 120 kD surface-exposed protein of Rickettsia rickettsii.";
RL Mol. Microbiol. 3:1579-1586(1989).
CC -1- FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS
CC RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -1- MISCELLANEOUS: ITS C-TERMINUS POTENTIALLY MAY BEAR THE EPITOPES
CC CONFERRING ANTIGENICITY TO THE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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CC -----
DR EMBL: X16353; CAA34402.1; -.
DR PIR: S07575; S07575.
DR InterPro: IPR006315; Autotransport.
DR InterPro: IPR005546; Autotransporter.
DR Pfam: PF03797; Autotransporter; 1.
DR TIGRFAMs: TIGR01414; autotrans_1; 2.
KW Antigen; Glycoprotein; Cell wall; S-layer.
FT CARBOHYD 7
FT CARBOHYD 66
FT CARBOHYD 86
FT CARBOHYD 103
FT CARBOHYD 147
FT CARBOHYD 268
FT CARBOHYD 330
FT CARBOHYD 375
FT CARBOHYD 415
FT CARBOHYD 424
FT CARBOHYD 430
FT CARBOHYD 436
FT CARBOHYD 444
FT CARBOHYD 515
FT CARBOHYD 547
FT CARBOHYD 593
FT CARBOHYD 653
FT CARBOHYD 698
FT CARBOHYD 710
FT CARBOHYD 799
FT CARBOHYD 800
FT CARBOHYD 826
FT CARBOHYD 844
FT CARBOHYD 861
FT CARBOHYD 879
FT CARBOHYD 920
FT CARBOHYD 926
FT CARBOHYD 926
FT CARBOHYD 1116
FT CARBOHYD 1128
FT CARBOHYD 1140
FT CARBOHYD 1146
FT CARBOHYD 1211
FT CARBOHYD 1211
SQ SEQUENCE 1300 AA; 132801 MW; E09E52C3F647243D CRC64;

OX NCBL_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IID642;
RX MEDLINE=94335647; PubMed=8057852;
RA Tominga A., Mahmoud M.A.-H., Mukaihara T., Enomoto M.;
RT "Molecular characterization of intact, but cryptic, flagellin genes
in the genus Shigella";
RL Mol. Microbiol. 12:277-285(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
through comparison with genomes of Escherichia coli K12 and O157";
RL Nucleic Acids Res. 30:4432-4441(2002).
CC -1- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
CC FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
CC -----
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CC -----
DR EMBL; D16819; BAA04093.1; -
DR EMBL; AE015215; AAN43516.1; -
DR PIR; S44980; S44980.
DR InterPro: IPR001029; Flagellin_C.
DR InterPro: IPR001492; Flagellin_C.
DR Pfam; PF00700; Flagellin_C.1.
DR Pfam; PF00669; Flagellin_N.1.
DR PRINTS; PR00207; FLAGELLIN.
KW Flagella.
SQ SEQUENCE 550 AA; 56636 MW; C921C9A8EF200B6 CRC64;
Query Match 6.7%; Score 148; DB 1; Length 550;
Best Local Similarity 20.2%; Pred. No. 0.27;
Matches 92; Conservative 68; Mismatches 183; Indels 112; Gaps 18;
OY 19 VSELTFRHTRKASATVKTAV--LATLL-----FAIVQASANRAASYKDYLANGMNKG 69
DB 10 LSLITONNINKNOSALSSSIRLSGLRINSAKDDAQAATANRFTS-----NITKG 60
OY 70 V-----KPGTASDNVDFVR-----TY 86
DB 61 LTOAARRANDGISVAQTTEGALSETNNNNLQRIRELTYOASTGINSDDSLDIQELISRL 120
OY 87 DTVEFLSADPTKTTTVNVEKNGKRTVEKIGAKTSVIREKDGKLVTKGKNGESSNDEG 146
DB 121 DEIDRVSGQGFQFNCVNVTLAKDGSKM--IQVGANDGQTTTIDLKIDSDTGLNFPNVG 178
OY 147 EGL--VTAKEDVAVKAKGRMKTTPANGQTG--QADKFTVYSGTNV--TFASGKGT 199
DB 179 GAVVNTASAKADLVAAANATVGNKRYTSAGYDAKASDLAVGSDGPTVQATINNFGTA 238
OY 200 ATVS--KDDGNTVMDVNVGDALVNOQNSGMNDSKAVASSCK--VISGNVSPS 254
DB 239 ASATNRYTDSASKSYSDPTTASADAVOKYITPG-----VDDTAAGTTTIDGSAOV 290
OY 255 KKKADETVNINAGNNI-----ETTRNGKNIDATSMTPQPSVSLGAGADAPTLVSDGD 308
DB 291 QISSDGKTTASNGSKLVIDTGRILTKNGS-----GASLFEASLSTLANNTFATITIDIGT 346
OY 309 ALNVGSKDKNKPVRITNVAPGVKGGDYTVNAQLKGAONLNN-----RIDNVGDNAR 360

DB 347 SISE-TGNSTPRTDITITSVTGAK--VDQAADFRAVSTSGNNVDFTTAGSVNCTGAVT 402
OY 361 AGI-----AOATATGALVOAYLPGRKSMMAIGGG 388
DB 403 KGVDSVYVDNNNEALTTSDTVDFYIADDDGSVYNGSG 437
RESULT 10
OMPA_RICCN
ID OMPA_RICCN STANDARD: PRT: 2021 AA.
AC Q52657; P95591; P95592; P95593; P95594; Q52667; Q52668; Q52669;
AC Q52670; Q52674;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface
DE antigen) (OMP A).
GN OMPA OR RC1273.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
CC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBL_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=94171067; PubMed=8125327;
RA Crocquet-Vaides P.A., Weiss K., Walker D.H.;
RT "Sequence analysis of the 190-kDa antigen-encoding gene of Rickettsia
RT conorii (Malish 7 strain).";
RL Gene 140:115-119(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renseto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii";
RL Science 293:2093-2098(2001).
RN [3]
RP SEQUENCE OF 8-204 FROM N.A.
RC STRAIN=Indian tick typhus; ML, Malish 7, and Moroccan;
RX MEDLINE=97015921; PubMed=8862558;
RA Roux V., Fournier P.E., Raoult D.;
RT "Differentiation of spotted fever group rickettsiae by sequencing and
RT analysis of restriction fragment length polymorphism of PCR-amplified
RT DNA of the gene encoding the protein ompA";
RL J. Clin. Microbiol. 34:2058-2065(1996).
RN [4]
RP SEQUENCE OF 953-2012 FROM N.A.
RC STRAIN=Indian tick typhus, ML, Malish 7, and Moroccan;
RA Raoult D., Fournier P.E., Roux V.;
RT "Phylogenetic analysis of spotted fever group rickettsiae by study
RT of the outer surface protein ompA";
RL Submitted (Dec-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -1- PMW: GLYCOSYLATED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP B FAMILY.
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CC -----
DR EMBL; U01028; AAA17405.1; -
DR EMBL; AE008674; AAD03811.1; -
DR EMBL; U43794; AAB49549.1; -


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DR EMBL: U43798; AAB49550.1; -
DR EMBL: U43806; AAB49551.1; -
DR EMBL: U45244; AAB49566.1; -
DR EMBL: U46918; AAB49566.1; -
DR EMBL: U83440; AAC35176.1; -
DR EMBL: U83443; AAC35179.1; -
DR EMBL: U83448; AAC35184.1; -
DR EMBL: U83453; AAC35189.1; -
DR InterPro: IPR006315; Autotransport.
DR Pfam: PF03797; Autotransporter; 1.
DR TIGRfams: TIGR01414; autotrans_bar1; 1.
KW Autigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein;
KW Complete proteome.
FT CHAIN 1 38
FT DOMAIN 238 946
FT DOMAIN 1424 1528
FT VARIANT 60 60
FT VARIANT 76 76
FT VARIANT 86 137
FT VARIANT 126 133
FT VARIANT 953 954
FT VARIANT 1243 1245
FT VARIANT 1308 1308
FT VARIANT 1877 1877
FT CONFLICT 10 10
FT CONFLICT 92 92
FT CONFLICT 126 126
FT CONFLICT 137 137
FT CONFLICT 157 157
FT CONFLICT 368 369
FT CONFLICT 374 388
FT CONFLICT 640 640
FT CONFLICT 669 669
FT CONFLICT 793 793
FT CONFLICT 803 804
FT CONFLICT 809 823
FT CONFLICT 898 898
FT CONFLICT 908 908
FT CONFLICT 985 985
FT CONFLICT 1009 1009
FT CONFLICT 1013 1013
FT CONFLICT 1182 1182
FT CONFLICT 1314 1314
FT CONFLICT 1451 1451
FT CONFLICT 1624 1624
FT CONFLICT 1628 1628
FT CONFLICT 1872 1872
FT CONFLICT 1875 1875
FT CONFLICT 1878 1879
FT CONFLICT 1936 1936
FT CONFLICT 1965 1970
FT CONFLICT 1997 1997
SO SEQUENCE 2021 AA; 203328 MM; 327FC42D7CB24668 CXC64;

Query Match 6.78; Score 147.5; DB 1; Length 2021;
Best Local Similarity 21.04; Pred. No. 1.3;
Matches 125; Conservative 70; Mismatches 192; Indels 207; Gaps 29;

QY 10 NSALNMVYSELTRN-HIKRASATYKT-AVLATLEFATQASANR---AASVKDVIINAG 64
DB 631 NNCIVFTFGNSVTGNTGNATLAVVAGCIIATLBGAVIKATTTKLTNNAASVLTITNVN 650
QY 65 WNIKGVKPGTTASDNVDFRTYDVEFLSADTKTT---TVN---ESKDNQ---KKEV 114
DB 691 AVLTAIDNTGVDNGLVNLNGALSGVTGNIGNTNATLISVAGAKATIGAVIKATTT 750
QY 115 KIKAKSVIKERKCGKLVTC---KKKGNGSSTDEGGLVTAK---EVIDAVNKA--- 162
DB 751 KLTDNMSAVYFTNPVVTGAIDNTGNANNNGIATFTGDSVTGNTGNATLAVVAGGL 810

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QY 163 ---GWRKKTTLAN-----GOTGOADK-----FETV---SGTN 189
DB 811 RVGGGVKSVTITLTDNASNVTTPNPVVTGALDNTGNANNNGIYTTGGSTVGNIGNTN 870
QY 190 ---VTFASGKT-----TATVSKDDGDNITVAVDVVAGDNLVNOLONSGWNLSK 237
DB 871 ALATISVAGKATLIGAILIKATTTKLTNNAASVATFPNPVVTGALD-----NNG-NANN 924
QY 238 AVAGSGKATISGVNSVSKGMDFTVINAG-----NNIEI----- 272
DB 925 IYVTFDSTVTGNTGNATL--ATVWVGAGVTLQAGSILDANNIDGARSTLEFNGPLDG 982
QY 273 -----TRNKN--IDTATSMTPQF-----SSVSGAGDAPTLSDGDLN 311
DB 983 GGNATPYRKGAITANGNAILNVNTHKLTARHLITGTVAETINIGAG--NLAIDASAGD 1039
QY 312 V-----GSKDNKPYRTNVAPVGEQV-----T 336
DB 1040 VTLLNMODIFRALDSALVLSNLTGVGVNNILLAADLVAGVDEGVTFDGVNGNLIGS 1099
QY 337 NVAQLKGVQNLNN-----RIDVNDGNARAGIAQAIATAG 371
DB 1100 NVA---GAAMNIDGVGNKFNFTLLIYNAVYITPDVNLGEGIONVLINNADFTSTAFNAG 1156
QY 372 LVQAYLPKSKMAIGGTY-----REBAGYALIGYSSISDGNMIIIGTASGNSR 420
DB 1157 TIO-----INDATYITDANNGNMLIPAGNIKFAHADQOLIIONSGNDR 1200

RESULT 11
SLAP_CAUCR STANDARD; PRT; 1025 AA.
AC P35828; Q46015; Q9RF12;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE S-layer protein (Paracrystalline surface layer protein).
GN RSAA OR CCL1007.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21; 646-660 AND 1021-1025.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=93007489; PubMed=1393820;
RA Gilchrist A., Fisher J.A., Smit J.K.;
RT "Nucleotide sequence analysis of the gene encoding the Caulobacter
RT crescentus paracrystalline surface layer protein.";
RL Can. J. Microbiol. 38:193-202(1992).
RN [2]
RP REVISIONS TO 376; 636 AND 842-843.
RA Awram P.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J53001;
RX MEDLINE=21173698; PubMed=11259647;
RA Niernan W.C., Feldblyum T.V., Laub M.R., Ohta N., Maddock J.R.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.O., Durkin A.S., Gwin M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Osterback T., Tran K., Wolf A., Vamathevan J., Emsolava M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

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DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF02922; Isomylase_N; 1.
 DR Pfam; PF00395; SLH; 3.
 DR SMART; SM00642; Amy; 1.
 DR SMART; SM00632; Amy_C; 1.
 DR SMART; SM00600; FN3; 2.
 DR PROSITE; PS01072; SLH_DOMAIN; 3.
 KM Hydrolase; Glycosidase; Carbohydrate metabolism; Signal; Repeat;
 KM Multifunctional enzyme; Glycoprotein.
 FT SIGNAL 1 35
 FT CHAIN 36 1861
 FT DOMAIN 928 1018
 FT DOMAIN 1157 1248
 FT ACT_SITE 628 628
 FT ACT_SITE 657 657
 FT ACT_SITE 734 734
 FT ACT_SITE 1681 1739
 FT DOMAIN 1740 1803
 FT DOMAIN 1804 1861
 FT CONFLICT 1734 1734
 SQ SEQUENCE 1861 AA; 206104 MW; 06C23070E453B574 CRC64;
 D -> E (IN REF. 1; AAB00841).
 Query Match 6.68; Score 145.5; DB 1; Length 1861;
 Best Local Similarly 19.94; Pred. No. 1.5;
 Matches 103; Conservative 76; Mismatches 210; Indels 129; Gaps 24;
 QY 2 NKIYRIWNSALNA-----WVYVSELRHRTKRASATVKTAVLATILFATVQASANAAS 56
 Db 1208 NEVYNTIDSVINGVYNYKVVAVDUSFNRTESNVYIKDPVPIKIFNV-----T 1259
 QY 57 VKDVLNAGNKKGVKPGTASDNDVFEVRYDVEFLSADPKTTTVNESKNGKEVKI 116
 Db 1260 VPDYTPDAVNLACGFPAATMDPSAQ-----QMTIDNNTSITL-TLDEGQIEYKY 1310
 QY 117 --GAKSVIEKKG-----KLVTKGKNGSGSTDE-----GELVTAKE 154
 Db 1311 ARGSMKVEKDEGENEFASNRKYTYVQGNNEMTINDTVYRMDIPFIYSPSSNMTVDS 1370
 QY 155 VIDAIVNAG--WIRKTTTANGOTQADKFEVTSCTVTFPASGK-----GTTATVSKD 206
 Db 1371 NISMVEKGYTKGAKTYTIDSDVODKNGVFTKDSLVNGVYKIKIHVEPNDGSYVGN 1430
 QY 207 QGNIT-----VWYDVNVGDALVNVOLNLSGWNLDKAVAGSSGKV-ISCNVSPSK 255
 Db 1431 QGRTELTKDIEIDVHQENNSGSGGTNNMTSTSGSN-SSSTGSGSGTSTISNTS-NT 1488
 QY 256 GKADDEVNT--NAGNNIEITRN-GKNDITATSMTPQ---FSSVSLGADAPILSDGDA 309
 Db 1489 SMTSNTIGVITKNGNVITLTDAGKADKLIVNSKDKKVPFDITTTIGEG--QOKVVOISKDI 1547
 QY 310 LNVGS-----KKOKKPYRIT-----NVA PGYKEGDVTNVQALKGVAQNLNN 350
 Db 1548 LDTSAANGKDIIVIKSDNASIALTKRDALNOMONONGVAVSTIKDNGKPVNTVYSLNVVDI 1607
 QY 351 RIDNVQDN-----ARAGIAQAIATAGLVQAYLPKGSMAIGCGTGEAG-- 395
 Db 1608 TIGISGCVTLAKPVEVTLNISKANDPRKVA---VYYNPTNQMEYVGKQVADASSGTI 1663
 QY 396 -----YALGYSISDGNW---IITGNAS 416
 Db 1664 TFNATHPSOYAAFEYDFTNDIKD--NMARDVIEVLAS 1699
 RESULT 13
 FLIC_ECOLI STANDARD; PRT; 497 AA.
 AC P04949;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Flagellin.
 GN FLIC OR FLAF OR HAG OR B1923.
 OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=87057066; PubMed=3536885;
 RA Kuwajima G., Asaka J.-I., Fujiwara T., Fujiwara T., Node K., Kondo E.;
 RT "Nucleotide sequence of the hag gene encoding flagellin of
 RT Escherichia coli.";
 RL J. Bacteriol. 168:1479-1483(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=89281489; PubMed=2659972;
 RA Hanafusa T., Sakai A., Tomlinaga A., Enomoto M.;
 RT "Isolation and characterization of Escherichia coli hag operator
 RT mutants whose hag48 expression has become repressible by a Salmonella
 RT H1 repressor.";
 RL Mol. Gen. Genet. 216:44-50(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=97251358; PubMed=9097040;
 RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T.,
 RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
 RA Saito N., Sampei G., Seki Y., Sivasubram S., Tagami H.,
 RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiiuchi T.;
 RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 40.1-50.0 min region on the linkage map.";
 RL DNA Res. 3:379-392(1996).
 RN [5]
 RP SEQUENCE OF 1-19 FROM N.A.
 RX MEDLINE=83238225; PubMed=6305924;
 RA Ssekely E., Simon M.;
 RT "DNA sequence adjacent to flagellar genes and evolution of flagellar-
 RT phase variation.";
 RL J. Bacteriol. 155:74-81(1983).
 RN [6]
 RP SEQUENCE OF 1-12.
 RC STRAIN-K12 / EWG2;
 RX MEDLINE=97443975; PubMed=9298646;
 RA Link A.J., Robison K., Church G.M.;
 RT "Comparing the predicted and observed properties of proteins encoded
 RT in the genome of Escherichia coli K-12.";
 RL Electrophoresis 18:1259-1313(1997).
 RN [7]
 RP SEQUENCE OF 1-4.
 RC STRAIN-K12 / W3110;
 RX MEDLINE=98263247; PubMed=9600841;
 RA Walkins M.R., Gasteliger E., Tonella L., Ou K., Tyler M.,
 RA Sanchez J.-C., Gooley A.A., Walsh B.J., Bairoch A., Appel R.D.,
 RA Williams K.L., Hochstrasser D.F.;
 RT "Protein identification with N and C-terminal sequence tags in
 RT proteome projects.";
 RL J. Mol. Biol. 278:599-608(1998).
 CC -1- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
 CC FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
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DR EMBL; M14358; AAA23950.1; -
 DR EMBL; X17440; CA35488.1; -
 DR EMBL; AE000285; AAC74990.1; -
 DR EMBL; D90832; BA15744.1; -
 DR EMBL; D90833; BA15751.1; -
 DR EMBL; J01607; AA92491.1; -
 DR PIR; A57249; FLEC.
 DR SWISS-2DPAGE; P04949; COLI.
 DR Ecogene; EG10321; FLIC.
 DR Interpro; IPR001029; Flagellin_C.
 DR Interpro; IPR001492; Flagellin_N.
 DR Pfam; PF00700; Flagellin_C.1.
 DR Pfam; PF00669; Flagellin_N.1.
 DR PRINTS; PR00207; FLAGELLIN.
 DR Flagella; Complete proteome.
 FT INIT.MET 0
 FT CONFLICT 284 284 P -> L (IN REF. 2).
 SQ SEQUENCE 497 AA; 51163 MW; 24B5419C21C7B4E8 CRC64;

Query Match 6.6%; Score 145; DB 1; Length 497;
 Best Local Similarity 19.8%; Pred. No. 0.35;
 Matches 97; Conservative 83; Mismatches 170; Indels 140; Gaps 20;

OY 19 VSELRNHTKASATVTKAV--LATL-----FATYQASANRAASKYDLNMGWNIK 69
 DB 9 LSLTQNNININQSLSSISIERLSSGLRINSAKDDAQAALANRRTS-----NIKG 59
 OY 70 V-KGTTASDVNDFVRI-----Y 86
 DB 60 LTOARARNANDGISAQTEGALSELNNLQRYRELTYVATTTGNSDSLSTODEIKRRL 119
 OY 87 DTVEFLSADTKTTTVNVESSKDNKTEYKIGAKTSVIEKDKLVTKGDKENGSSDDEG 146
 DB 120 DEIDRVSGQTFQNGNVLAKNGSMK--IQVGANDNQTTIDLKQIDAKTLGIDGFSVKN 177
 OY 147 EGLVTAKYV-----IDAVKACGRMKT--TTANGOTGA-----DKFEYVS 186
 DB 178 DTVTTSAPVTAFGATTNNIKLGTITLSTEATDTGGTNPASIEGVYTDNGNDYAKITG 237
 OY 187 GTN-----VTFASGKGTATVSKD-----QGNITVYVNVGDD--- 220
 DB 238 GDNDGKYAVVANDGYTMTATGATANATVTDANTTKATTTTSGCTPVQIDNTAGSATAN 297
 OY 221 --ALNVNQLQNS-GWNLDSKAVAGSGKVISGNVSPSKGM-----DETVINAGNN 269
 DB 298 LGAVSLVYKLDQSKGNDTDTYALKDPTNGNLVADVNETTGAVSKITTYTDSGAASPTA 357
 OY 270 IETTRNGNIDIAISMTFQSSVSLGAGADAPLTSVGDALN-VGSKDNKPVRTTNVAP 328
 DB 358 VKLGDDDEKTEVVIDGKTYSDIADNGNLQTLGALGEALTAVANGETTLPKRLDAI 417
 OY 329 GVKR-----GDVTNVQALKGVAQNLNRINDVDCNARAGIAQA-----IATAGLV 374
 DB 418 ASVDKFRSLGAVON--RLDSAVTNLNTTNTNL-SEAOSRIQDADYATEVSNMSAQIIO 474
 OY 375 AYLPGRKSMMA 384
 DB 475 Q--AGNSVLA 482

RESULT 14
 Y741_CHLMU STANDARD: PRF; 1007 AA.
 ID Y741_CHLMU
 AC O9PJTG;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein TC0741 precursor.
 GN TC0741.
 OS Chlamydia muridarum.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxId=83560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MOPn / N19g;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linner K., Weidman J., Knouri H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., Deboy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RA "Genome sequences of Chlamydia trachomatis MOPn and Chlamydia
 RT pneumoniae AR39 ";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 CC -I SIMILARITY: BELONGS TO THE CHLAMYDIAL CPN0572/CT456/TC0741
 CC FAMILY.

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DR EMBL; AE002342; AAF39550.1; -
 DR PIR; H81670; H81670.
 DR TIGR; TC0741; -
 KW Hypothetical protein; Signal; Complete proteome.
 FT SIGNAL 1 51
 FT CHAIN 52 1007 POTENTIAL.
 FT SEQUENCE 1007 AA; 104006 MW; 842800C0871B1518 CRC64;

Query Match 6.5%; Score 142.5; DB 1; Length 1007;
 Best Local Similarity 22.0%; Pred. No. 1.1;
 Matches 113; Conservative 55; Mismatches 170; Indels 175; Gaps 27;

OY 44 FATYQASANRAASKYDLNMGWNIKGV-----PQT-TASQVNDVRYRTDYEF 91
 DB 411 FATPPSPSQ-----PVINNVNNGGTNVNIGDTNWSGSGTPTSSQSDM--STDYSDL 464
 OY 92 LSADTKT--TVNVESSKDNKTEYKIGAKTSVIEKDG--KLVYTKDK----- 136
 DB 465 DTSDDTNNQNTNGDINTNDSNNVNGSLSDVDSRDEDDGVSDPESTNGNSGKTSREE 524
 OY 137 -----GENGSSTDEBGLVTAKE---VIDAVNRKAGMRMKT 170
 DB 525 NGDPSGPDILAAVRKHLDTVYRGENGSGT---EGPLPANQMLGNVHIDVEONGSAKETII 581
 OY 171 ANGOTGQADKFEYTSNGTYTFASGKTATVNSDDQCNITVMDVNVGDALANVQLONS 230
 DB 582 TPGDGTDPDSSSVADADVEDTS--DTDSIGDD-----GVSDESTNGNSGKNT 628
 OY 221 GWNLDSKAVAGSGKVI-----SGNVSPSKGKDETVNINAGNNI-EITRNG 276
 DB 629 GKTISTEENGPSGPDILAAVRKHLDTVYRGENGSGTGPL--PANQMLGNVHIDVEONG 686
 OY 277 KNIDIAISMT-----QFSSVSLGAGADAPLS-----VGDALNVGSKKDK 319
 DB 687 AAGE--TLTPGDTRESTDTSSSVANADLEVDSDSGFGDDGISTDESTNGNSGKNT 744
 OY 320 PV-----RITNVAAGYKEDGYTNVAQALKGVAQNLNRINDVDCNARAGIAQA--- 359
 DB 745 PVGCGGTPSGPDILAAVRKHLDTVYRGENGSGTERPLPAN--QNLGDIHIDVEONGSAK 801
 OY 360 -----FAGIAQALATAGLVQAVLP-----GK-----SMAATGGGTGRTGEA 394
 DB 802 ETIVSPRYKGGGNGNSSPIGLA-SLLPATPTPLMTPTPTNCKAASLSIMINGGETGA--- 857

QY 395 GYAIGYSSISDGNMIIKGTAS-----GNSRGH 422
 DB 858 -----KLKNGGN--IPGETTIAELLPLRIGH 882

RESULT 15

HLA-SERMA STANDARD; PRT; 1608 AA.
 ID HLVA-SERMA
 AC P15320;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-NOV-1990 (Rel. 16, Last annotation update)
 DE Hemolysin precursor.
 GN SHLA.
 OS Serratia marcescens.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Serratia.
 OX NCBI_TaxID=615;
 RN (1)
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
 RC STRAIN=SN8;
 RX MEDLINE=88257037; PubMed=3290200;
 RA Poole K., Schiebel E., Braun V.;
 RT "Molecular characterization of the hemolysin determinant of Serratia
 marcescens.";
 RL J. Bacteriol. 170:3177-3188(1988).
 CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
 CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
 DEFINED.
 CC -1- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM
 ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA
 REQUIRES SHLB FUNCTION.
 CC -1- SUBCELLULAR LOCATION: Outer membrane.
 CC -1- SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M22618; AAA50323.1; -
 DR PIR: A28182; A28182.
 KM Hemolysis; Toxin; Outer membrane; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 1608 HEMOLYSIN.
 SQ SEQUENCE 1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;

Query Match 6.5%; Score 142; DB 1; Length 1608;
 Best Local Similarity 21.9%; Pred. No. 2;
 Matches 98; Conservative 53; Mismatches 156; Indels 140; Gaps 20;

QY 26 HTRKASATVKTAVLATLFAVYQASANRAASVYDLNAGMNIKVPRGTTASDNVDFVRT 85
 DB 717 HTRDSEKTRTEMSA-----SLSGGSVKLKAEDVTFSSSKLYADKGDASVSGN----- 766
 QY 86 YDVEFLSADITTYVNVESKDKNGKTEVKGAKTSVIEKDGKLVTKGDKGENGSSTDE 145
 DB 767 --KVSFLAADDKTAS--NTE-----QTKIGG-----GFYYTG----- 794
 QY 146 GEGLVYAKEVDAVNKAGWRMTTANGOTGQADKFEVYSGTVTFASGKGTATVSKD 205
 DB 795 -----GIDKLGSGVEAGYENKNT-QHOSKAITSGSDV----- 826
 QY 206 DQGNITVMYDVNVGALNVNOLNSGMNLSKAVAGSSGKVIISGNVSPSKMKMDETVIN 265
 DB 827 -KGNLT-----INARDKLTQGAQHVSAGVQENAAQVDHLLAADTASTTTTKTDVGVT- 880
 QY 266 AGNNITITRNGKNIDTATSMTPQFSSVSLGA-----GADAPTLSDVDGALNVG 313
 DB 881 -----GANVDYSAVTREYRAVGAAKADATGVIINDIGIGAPNVGIDIGAGGS 930

QY 314 SKK--DNKEPVRTTNVAPGV-----KEGDV-----TNVAQLKGVQNLN-----NRID 353
 DB 931 SEKRSSSQAVYSSVQAGSIDINAKGEVNDQGTQYQASKG-AVNLTADSHRSEAANRQD 989
 QY 354 NVQGNARAGIAAIAATAGLVQAVLPGKSMMAIG---GGTYRGEAGYAIQYSSISDGNM 409
 DB 990 EOSRDTT-----GSAG-VRYVTTGSDLTVDAKGEGGTQSRNSSSAQAVTGSIDAANG 1041
 QY 410 -----IIGTASGNSRGHFGASA 427
 DB 1042 INVNVKKAIDYOGTALNGRGKTAANA 1068

Search completed: October 6, 2003, 09:24:03
 Job time : 9.68663 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:10 : Search time 31.8023 Seconds
(without alignments)
3513.465 Million cell updates/sec

Title: US-09-771-382-26
Perfect score: 2197
Sequence: 1 MNKXRIINSLNMAWVVS.....FASGNRGHFGASASVGYQW 433

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.unclassified:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriaph:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2108	95.9	591	09JRI8	09JRI8 neisseria m
2	2104	95.8	591	09JPS7	09JPS7 neisseria m
3	2103.5	95.7	592	09AQF0	09AQF0 neisseria m
4	2096	95.4	591	093QY3	093QY3 neisseria m
5	2056.5	93.6	600	09JPS6	09JPS6 neisseria m
6	2049.5	93.3	592	09JPS9	09JPS9 neisseria m
7	2036.5	92.7	590	09JPS3	09JPS3 neisseria m
8	2033.5	92.6	594	09JPS2	09JPS2 neisseria m
9	2032.5	92.5	599	09JPS4	09JPS4 neisseria m
10	2032	92.4	594	09JPS8	09JPS8 neisseria m
11	2029.5	92.2	594	09JPS1	09JPS1 neisseria m
12	2025.5	92.1	594	09JPS7	09JPS7 neisseria m
13	2023.5	92.1	598	09JPS9	09JPS9 neisseria m
14	2015.5	91.7	592	09JPS2	09JPS2 neisseria m
15	2010.5	91.5	598	09JPS0	09JPS0 neisseria m
16	2010.5	91.5	598	09JPS0	09JPS0 neisseria m

17	2009.5	91.5	592	16	09JQW4	09JQW4 neisseria m
18	2006	91.3	595	2	09JPH0	09JPH0 neisseria m
19	2005.5	91.3	598	2	09JPS7	09JPS7 neisseria m
20	2001.5	91.1	598	2	09JQY5	09JQY5 neisseria m
21	1998	90.9	599	2	09JPS8	09JPS8 neisseria m
22	1981.5	90.2	600	2	09JPS5	09JPS5 neisseria m
23	1976	89.9	589	2	09JPS10	09JPS10 neisseria m
24	1964	89.4	589	2	09JQY1	09JQY1 neisseria m
25	1920	87.4	526	2	09JPS4	09JPS4 neisseria m
26	1920	87.4	530	2	09JPS1	09JPS1 neisseria m
27	776.5	35.3	1098	2	048152	048152 haemophilus
28	775.5	35.3	1096	2	08GM79	08GM79 haemophilus
29	734	33.4	2353	2	P71401	P71401 haemophilus
30	687.5	31.3	1204	2	08GM76	08GM76 haemophilus
31	664.5	30.2	1210	2	08GM74	08GM74 haemophilus
32	655.5	29.8	1210	2	08GM75	08GM75 haemophilus
33	509.5	23.2	1004	2	08GM77	08GM77 haemophilus
34	489.5	22.3	1002	2	08GM78	08GM78 haemophilus
35	382	17.4	1299	16	09F3X6	09F3X6 pasteurella
36	355.5	16.2	2314	2	08KOM8	08KOM8 moraxella c
37	340.5	15.5	2059	16	09PD50	09PD50 xyella fas
38	335	15.2	1190	16	09PC04	09PC04 xyella fas
39	329.5	15.0	1588	16	08XDG4	08XDG4 escherichia
40	328	14.9	1461	16	08ZL64	08ZL64 salmonella
41	326	14.8	1107	16	09F2D8	09F2D8 salmonella
42	326	14.8	1778	16	08FCB2	08FCB2 escherichia
43	315.5	14.4	641	16	08CKM1	08CKM1 yersinia pe
44	315.5	14.4	658	16	08ZHU0	08ZHU0 yersinia pe
45	301.5	13.7	2712	16	09F3X5	09F3X5 pasteurella

ALIGNMENTS

RESULT 1				
ID	09JRI8	PRELIMINARY;	PRT;	591 AA.
AC	09JRI8:			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 22, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 15, Last annotation update)			
DE	Outer membrane protein GNA92 (Adhesin) (Nha outer membrane protein).			
GN	GNA92 OR NMB0992 OR NHA.			
OS	Neisseria meningitidis, and			
OS	Neisseria meningitidis (serogroup B).			
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;			
OC	Neisseriaceae; Neisseria.			
OX	NCBI_TaxID=487, 491;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MC58 / Serogroup B, B2169, B283, and H447/6;			
RC	MEDLINE=20175756; PubMed=10710308;			
RX	Pizza M., Scariato V., Maignan V., Giuliani M.M., Arico' B.,			
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,			
RA	Galeotti C.L., Iuzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,			
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,			
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,			
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,			
RT	Moxon E.R., Grandi G., Rappuoli R.,			
RT	Identification of Vaccine Candidates Against Serogroup B			
RT	Meningococcus by Whole-Genome Sequencing. *;			
RL	Science 287.1816-1820(2000).			
RN	[2]			
RC	SEQUENCE FROM N.A.			
RC	STRAIN=MC58 / Serogroup B;			
RC	MEDLINE=20175755; PubMed=10710307;			
RA	Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,			
RA	Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,			
RA	Nelson W.C., Gwinn M.L., Deboy R., Peterson J.D., Hickey E.K.,			
RA	Hait D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,			
RA	Mason T., Clecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,			
RA	Cotton M.D., Uitterlind T.R., Khouri H., Qin H., Vamathevan J.,			

RA Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
 RT "Complete genome sequence of *Neisseria meningitidis* serogroup B strain
 RT MC58";
 RL Science 287:1809-1815(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=*N.meningitidis*; STRAIN=PMC21;
 RA Peak I.R., Srikanta V., Dieckelman M., Moxon R., Jennings M.P.;
 RT "Identification and characterization of a gene encoding a novel outer
 RT membrane protein of *Neisseria meningitidis*";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF226375; AAF42524.1; -
 DR EMBL: AF002450; AAF41395.1; -
 DR EMBL: AF226367; AAF42516.1; -
 DR EMBL: AF226370; AAF42519.1; -
 DR EMBL: AF226374; AAF42523.1; -
 DR EMBL: AF157611; AAK68872.1; -
 DR TIGR: MMB0992; -
 DR InterPro: IPR005594; Yada.
 DR Pfam: PF03895; Yada; 1.
 DR Complete Proteome.
 SQ SEQUENCE 591 AA; 62112 MW; 7C22F3CAE7F73EC6 CRC64;

Query Match 95.9%; Score 2108; DB 16; Length 591;
 Best Local Similarity 73.3%; Pred. No. 5.9e-90;
 Matches 433; Conservative 0; Mismatches 0; Indels 158; Gaps 1;
 Oy 1 MNKIYRIIWSALNAAVVSSELTNRNHTKRASATVKTAVLATLLEFATVOASAN----- 52
 Db 1 MNKIYRIIWSALNAAVVSSELTNRNHTKRASATVKTAVLATLLEFATVOASANNEOEEDL 60
 Oy 53 ----- 52
 Db 61 YLDPVORTVAVLIVNSDEKTEGKEKVEENSDMAVYFNEKGVLTAAREITLAKGNLKIQ 120
 Oy 53 ----- 52
 Db 121 NGTFNYSLKDLTDLISVTEKLSFSAANGKVNITSDTKLNFARAKETAGNGDTTVALN 180
 Oy 53 -----RAASVQDVNLNAGWNIKGVPPTTASDNVDF 82
 Db 181 GIGSLTDLTNTGATTTVNDNTDDEKKRAASVKDVLNAGWNIKGVPPTTASDNVDF 240
 Oy 83 VRTDYVEFLSADTKTTTVNVEESKDNKKEKTEVKGAKTSVYKEDGKLVTGKDGENGSS 142
 Db 241 VRTDYVEFLSADTKTTTVNVEESKDNKKEKTEVKGAKTSVYKEDGKLVTGKDGENGSS 300
 Oy 143 TDEEGGLVTAKEVIDAVNKAAGRMKTTTANGOTGADKFEVTVSGTNTVFASGKTATV 202
 Db 301 TDEEGGLVTAKEVIDAVNKAAGRMKTTTANGOTGADKFEVTVSGTNTVFASGKTATV 360
 Oy 203 SKDOGNITTVWYDVNAGDALNVNOLONGSNWLDKRAVAGSSGKVIISGNVSPSKKMDPTV 262
 Db 361 SKDOGNITTVWYDVNAGDALNVNOLONGSNWLDKRAVAGSSGKVIISGNVSPSKKMDPTV 420
 Oy 263 NINAGNNIETIRNKNIDIASMTPOFSSVSLGAGADAPTLISVGDALNVSSKKDNKDPVR 322
 Db 421 NINAGNNIETIRNKNIDIASMTPOFSSVSLGAGADAPTLISVGDALNVSSKKDNKDPVR 480
 Oy 323 ITTNAAPGKBEVDVNVNOLKGAONLNRRIDNVGNARAAGIAQAATATAGLVQAVLPKGS 382
 Db 481 ITTNAAPGKBEVDVNVNOLKGAONLNRRIDNVGNARAAGIAQAATATAGLVQAVLPKGS 540
 Oy 383 MAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 433
 Db 541 MAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 591

DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Outer membrane protein GNA992.
 GN GNA992.
 OS *Neisseria meningitidis*.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B2147;
 RX MEDLINE=20175756; PubMed=10710308;
 RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico B.,
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
 RA Ratti G., Santilli L., Savino S., Scarselli M., Storni E., Zuo P.,
 RA Broeker M., Hunt E., Knapp B., Blair E., Mason T., Tettelin H.,
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
 RA Moxon E.R., Grandi G., Rappuoli R.;
 RT "Identification of Vaccine Candidates Against Serogroup B
 RT Meningococcus by Whole-Genome Sequencing";
 RL Science 287:1816-1820(2000).
 DR EMBL: AF226366; AAF42515.1; -
 DR InterPro: IPR005594; Yada.
 DR Pfam: PF03895; Yada; 1.
 DR Complete Proteome.
 SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;

Query Match 95.8%; Score 2104; DB 2; Length 591;
 Best Local Similarity 73.1%; Pred. No. 9e-90;
 Matches 432; Conservative 1; Mismatches 0; Indels 158; Gaps 1;
 Oy 1 MNKIYRIIWSALNAAVVSSELTNRNHTKRASATVKTAVLATLLEFATVOASAN----- 52
 Db 1 MNKIYRIIWSALNAAVVSSELTNRNHTKRASATVKTAVLATLLEFATVOASANNEOEEDL 60
 Oy 53 ----- 52
 Db 61 YLDPVORTVAVLIVNSDEKTEGKEKVEENSDMAVYFNEKGVLTAAREITLAKGNLKIQ 120
 Oy 53 ----- 52
 Db 121 NGTFNYSLKDLTDLISVTEKLSFSAANGKVNITSDTKLNFARAKETAGNGDTTVALN 180
 Oy 53 -----RAASVQDVNLNAGWNIKGVPPTTASDNVDF 82
 Db 181 GIGSLTDLTNTGATTTVNDNTDDEKKRAASVKDVLNAGWNIKGVPPTTASDNVDF 240
 Oy 83 VRTDYVEFLSADTKTTTVNVEESKDNKKEKTEVKGAKTSVYKEDGKLVTGKDGENGSS 142
 Db 241 VRTDYVEFLSADTKTTTVNVEESKDNKKEKTEVKGAKTSVYKEDGKLVTGKDGENGSS 300
 Oy 143 TDEEGGLVTAKEVIDAVNKAAGRMKTTTANGOTGADKFEVTVSGTNTVFASGKTATV 202
 Db 301 TDEEGGLVTAKEVIDAVNKAAGRMKTTTANGOTGADKFEVTVSGTNTVFASGKTATV 360
 Oy 203 SKDOGNITTVWYDVNAGDALNVNOLONGSNWLDKRAVAGSSGKVIISGNVSPSKKMDPTV 262
 Db 361 SKDOGNITTVWYDVNAGDALNVNOLONGSNWLDKRAVAGSSGKVIISGNVSPSKKMDPTV 420
 Oy 263 NINAGNNIETIRNKNIDIASMTPOFSSVSLGAGADAPTLISVGDALNVSSKKDNKDPVR 322
 Db 421 NINAGNNIETIRNKNIDIASMTPOFSSVSLGAGADAPTLISVGDALNVSSKKDNKDPVR 480
 Oy 323 ITTNAAPGKBEVDVNVNOLKGAONLNRRIDNVGNARAAGIAQAATATAGLVQAVLPKGS 382
 Db 481 ITTNAAPGKBEVDVNVNOLKGAONLNRRIDNVGNARAAGIAQAATATAGLVQAVLPKGS 540
 Oy 383 MAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 433
 Db 541 MAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 591


```
RESULT 3
Q9AOF0 PRELIMINARY; PRT: 592 AA.
AC Q9AOF0;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Outer membrane protein.
GN NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon E.R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF125375; AAK09243.1;
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada.
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;

Query Match 95.7%; Score 2103.5; DB 2; Length 592;
Best Local Similarity 73.0%; Pred. No. 9.5e-90;
Matches 432; Conservative 0; Mismatches 1; Indels 159; Gaps 1;

QY 1 MNKIYRIINMSALNAMYVSELTRNHRKASATVKTAVLATLLFATVQASAN----- 52
DB 1 MNKIYRIINMSALNAMYVSELTRNHRKASATVKTAVLATLLFATVQASANNEPRKKD 60
QY 53 ----- 52
DB 61 LYDPVQRTAVLIYNSDKETGKEKEVEENSDMAVYENKGVLTAREITLKAGDNLIK 120
QY 53 ----- 52
DB 121 QNQTNPFTSLKQDLDTLSVGTSEKLSFANGKNVNTSDTKGLNFAKETAGTNGDTVHL 180
QY 53 ----- 52
DB 181 NGIGSTLTDLTLLNTGATTNTNDNVTDDEKRRASVADVLNAGNINIGVKGPTTASDND 240
QY 53 ----- 81
DB 181 NGIGSTLTDLTLLNTGATTNTNDNVTDDEKRRASVADVLNAGNINIGVKGPTTASDND 240
QY 82 FVRYTDFEFLSADTKTTTNNVESKDKGKTEVKIGAKTSYIKEDGKLVYTGKDGNGS 141
DB 241 FVRYTDFEFLSADTKTTTNNVESKDKGKTEVKIGAKTSYIKEDGKLVYTGKDGNGS 300
QY 142 STDEGEGLVTAKEVIDAVNKAQWRKTTTANGQTGOADKFETVSGTNVTFASGKTAT 201
DB 301 STDEGEGLVTAKEVIDAVNKAQWRKTTTANGQTGOADKFETVSGTNVTFASGKTAT 360
QY 202 VSKDQGNITVMDVNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGMD 261
DB 361 VSKDQGNITVMDVNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGMD 420
QY 361 VSKDQGNITVMDVNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGMD 420
QY 262 VNTNAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSDVGDALNVGSKDKP 321
DB 421 VNTNAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSDVGDALNVGSKDKP 480
QY 322 RITNVAAGVEGDVTNVAOLKGVAONLNRRIDNDVGNARAGIAQAIATAGLVQAYLP 381
DB 481 RITNVAAGVEGDVTNVAOLKGVAONLNRRIDNDVGNARAGIAQAIATAGLVQAYLP 540
QY 382 MAIGGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 433
DB 541 MAIGGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 592

RESULT 4
Q930Y3 PRELIMINARY; PRT: 591 AA.
ID Q930Y3
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AC Q930Y3;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE NHA outer membrane protein.
GN NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG329;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157606; AAK68867.1;
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada.
SQ SEQUENCE 591 AA; 62048 MW; C0DC600798859C65 CRC64;

Query Match 95.4%; Score 2096; DB 2; Length 591;
Best Local Similarity 72.9%; Pred. NO. 2.1e-89;
Matches 431; Conservative 1; Mismatches 1; Indels 158; Gaps 1;

QY 1 MNKIYRIINMSALNAMYVSELTRNHRKASATVKTAVLATLLFATVQASAN----- 52
DB 1 MNKIYRIINMSALNAMYVSELTRNHRKASATVKTAVLATLLFATVQASANNEQEEDL 60
QY 53 ----- 52
DB 61 LYDPVLTAVLIYNSDKETGKEKEVEENSDMAVYENKGVLTAREITLKAGDNLIK 120
QY 53 ----- 52
DB 121 NGTNPFTSLKQDLDTLSVGTSEKLSFANGKNVNTSDTKGLNFAKETAGTNGDTVHL 180
QY 53 ----- 82
DB 181 GIGSTLTDLTLLNTGATTNTNDNVTDDEKRRASVADVLNAGNINIGVKGPTTASDND 240
QY 83 VRYTDFEFLSADTKTTTNNVESKDKGKTEVKIGAKTSYIKEDGKLVYTGKDGNGS 142
DB 241 VRYTDFEFLSADTKTTTNNVESKDKGKTEVKIGAKTSYIKEDGKLVYTGKDGNGS 300
QY 143 TDEGEGLVTAKEVIDAVNKAQWRKTTTANGQTGOADKFETVSGTNVTFASGKTAT 202
DB 301 TDEGEGLVTAKEVIDAVNKAQWRKTTTANGQTGOADKFETVSGTNVTFASGKTAT 360
QY 203 SKDQGNITVMDVNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGMD 262
DB 361 SKDQGNITVMDVNVGDALNVNQLONGSNLDSKAVAGSSGKVISGNVSPSKGMD 420
QY 263 NINAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSDVGDALNVGSKDKN 322
DB 421 NINAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSDVGDALNVGSKDKN 480
QY 323 ITNVAAGVEGDVTNVAOLKGVAONLNRRIDNDVGNARAGIAQAIATAGLVQAYLP 382
DB 481 ITNVAAGVEGDVTNVAOLKGVAONLNRRIDNDVGNARAGIAQAIATAGLVQAYLP 540
QY 383 MAIGGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 433
DB 541 MAIGGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 591

RESULT 5
Q9JPS6 PRELIMINARY; PRT: 600 AA.
ID Q9JPS6
AC Q9JPS6;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
```

DT 01-OCT-2002 (TREMBLrel. 22, last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria: Proteobacteria: Betaproteobacteria: Neisseriales:
OC Neisseriaceae: Neisseria.
NCBI_TaxId=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E26;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Barcolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226371; AAF42520.1; --
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 600 AA; 62/62 MW; 36256963E0598CD1 CRC64;

Query Match 93.6%; Score 2056.5; DB 2; Length 600;
Best Local Similarity 70.8%; Pred. No. 1.4e-87;
Matches 425; Conservative 2; Mismatches 6; Indels 167; Gaps 1;

QY 1 MNKIRITWNSALNMAVYVSELTNRNHTKRASATVTAVALTLFPATVOASAN----- 52
DB 1 MNKIRITWNSALNMAVYVSELTNRNHTKRASATVTAVALTLFPATVOASADN 60
QY 53 ----- 52
DB 61 EEEETLEPVVTRAPVLSFYSDAEDTGEKEVTENTMGIYFKNGYIKAGTTLKAGDNLK 120
QY 53 ----- 52
DB 121 IKONTDENTNASSFTYSLKKELTDLTSVGTETKLSFGANGKNKVNITSDTKGLNFAKETAGT 180
QY 53 ----- 52
DB 181 NGDTTVHLNGISLTLDLTGATTNTNDNVTDDEKKRAASVSDVYLNAGNINIGVYKPG 240
QY 74 TTAADNVFVRTYDVEFLSADTKTTTVNVESSKDKGKTEYKIGAKTSYIKKDKLVTG 133
DB 241 TTAADNVFVRTYDVEFLSADTKTTTVNVESSKDKGKTEYKIGAKTSYIKKDKLVTG 300
QY 134 KDKGENGSTDEGEGLYTAKEVYDAVNKAGWRMKTTTTANGOTGADKFEYVTSNTNTPA 193
DB 301 KDKGENSGSTDEGEGLYTAKEVYDAVNKAGWRMKTTTTANGOTGADKFEYVTSNTNTPA 360
QY 194 SKGTATATVSKDDGNTTYMDVYNGDALNVQNLONGSNLDSKAVAGSSGKAVISGNVSP 253
DB 361 SKGTATATVSKDDGNTTYMDVYNGDALNVQNLONGSNLDSKAVAGSSGKAVISGNVSP 420
QY 254 SKGKDEPVNTNAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDGALNNG 313
DB 421 SKGKDEPVNTNAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDGALNNG 480
QY 314 SKDKKPVRTNVAAGVEGDTNVAOLKGVQNLNRRIDNDVGNARAGIAQAIAITAGLV 373
DB 481 SKDKKPVRTNVAAGVEGDTNVAOLKGVQNLNRRIDNDVGNARAGIAQAIAITAGLV 540
QY 374 QAYLPKSKMAIGGTYRGEAGYATGYSISDGGWIIKGTASGNSRGHFGASASVGYOM 433
DB 541 QAYLPKSKMAIGGTYRGEAGYATGYSISDGGWIIKGTASGNSRGHFGASASVGYOM 600

ID 09JPS9 PRELIMINARY; PRT: 592 AA.
AC 09JPS9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria: Proteobacteria: Betaproteobacteria: Neisseriales:
OC Neisseriaceae: Neisseria.
NCBI_TaxId=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=860800;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Barcolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226371; AAF42510.1; --
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 592 AA; 61/917 MW; 4A347151AFD3C879 CRC64;

Query Match 93.3%; Score 2049.5; DB 2; Length 592;
Best Local Similarity 71.8%; Pred. No. 3e-87;
Matches 425; Conservative 1; Mismatches 7; Indels 159; Gaps 2;

QY 1 MNKIRITWNSALNMAVYVSELTNRNHTKRASATVTAVALTLFPATVOASA----- 51
DB 1 MNKIRITWNSALNMAVYVSELTNRNHTKRASATVTAVALTLFPATVOANATDEDEEEL 60
QY 52 ----- 51
DB 61 ESVQSVYSGISQASMEGSELETISLSMTNDSKEFVPIYVYTLKAGDNLIKONTNENT 120
QY 52 ----- 51
DB 121 NASSFTYSLKKELTDLINVEETKLSFGANGKNKVNITSDTKGLNFAKETAGTNGDTTVHLN 180
QY 52 ----- 51
DB 181 GIGSTLTMLNTGATTNTNDNVTDDEKKRAASVSDVYLNAGNINIKYKPGTTASDNDVF 240
QY 83 VRTYDVEFLSADTKTTTVNVESSKDKGKTEYKIGAKTSYIKKDKLVTGKDKGENSS 142
DB 241 VRTYDVEFLSADTKTTTVNVESSKDKGKTEYKIGAKTSYIKKDKLVTGKDKGENSS 300
QY 143 TDEGEGLYTAKEVYDAVNKAGWRMKTTTTANGOTGADKFEYVTSNTNTPASGKTTATV 202
DB 301 TDEGEGLYTAKEVYDAVNKAGWRMKTTTTANGOTGADKFEYVTSNTNTPASGKTTATV 360
QY 203 SKDDGNTTYMDVYNGDALNVQNLONGSNLDSKAVAGSSGKAVISGNVSPSKGMDETV 262
DB 361 SKDDGNTTYMDVYNGDALNVQNLONGSNLDSKAVAGSSGKAVISGNVSPSKGMDETV 420
QY 263 NINAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDGALNNGSKDKNKPV 321
DB 421 NINAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDGALNNGSKDKNKPV 480
QY 322 RTTNVAPVKBSDVTNVAOLKGVQNLNRRIDNDVGNARAGIAQAIAITAGLVQAYLPKS 381
DB 481 RTTNVAPVKBSDVTNVAOLKGVQNLNRRIDNDVGNARAGIAQAIAITAGLVQAYLPKS 540
QY 382 MMAIGGTYRGEAGYATGYSISDGGWIIKGTASGNSRGHFGASASVGYOM 433
DB 541 MMAIGGTYRGEAGYATGYSISDGGWIIKGTASGNSRGHFGASASVGYOM 592

RESULT 7

09JPS3 PRELIMINARY: PRT: 590 AA.
AC 09JPS3: 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
DE Outer membrane protein GMA992.
CN GMA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE28;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing";
RL Science 287:1816-1820(2000).
DR EMBL: AF226378; AAF42527.1; -;
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC30D80C8 CRC64;

Query Match 92.7%; Score 2036.5; DB 2; Length 590;
Best Local Similarity 71.5%; Pred. No. 1.2e-86;
Matches 422; Conservative 3; Mismatches 8; Indels 157; Gaps 2;

QY 1 MNKYYRIIWNLSALNAAWVVSSELTNRNHRASATVATATLTLFATVOASA----- 51
DB 1 MNKYYRIIWNLSALNAAWVVSSELTNRNHRASATVATATLTLFATVOASATDEDEBDL 60
QY 52 ----- 51
DB 61 DPVQRTAVAVLVNSDKKESTGEKEVEENSDMAVYFNEKGVLTAGTITLKAGDNLIKIKNG 120
QY 52 ----- 51
DB 121 TNFTYSLEKKDLTDLTSVGETKLSFANGKNVITSDTKGLNFAKETAGTNGDTTVHLNGI 180
QY 52 ----- 84
DB 181 GSTLTDLTLTGATTTNTNDVTDDEKKRAASVADVLNAGWNIGKVGKGTASDVNDVR 240
QY 85 TYDVEFLSADTKTTTVNVESEKDKGKTEVIGAKTSVIREKDKGLVTGKDKGENSGSTD 144
DB 241 TYDVEFLSADTKTTTVNVESEKDKGKTEVIGAKTSVIREKDKGLVTGKDKGENSGSTD 300
QY 145 EGBELVTAKEVIDAVNKAAGRMRKTTTANGOTGQADKEFTVTSCTNVTFAASKGTATVSK 204
DB 301 EGBELVTAKEVIDAVNKAAGRMRKTTTANGOTGQADKEFTVTSCTNVTFAASKGTATVSK 360
QY 205 DDOGNTIYMYDVNVDALNVLNQLNSGMNLSKAVAGSSGKVISGNVSPSGKMDETVNI 264
DB 361 DDOGNTIYMYDVNVDALNVLNQLNSGMNLSKAVAGSSGKVISGNVSPSGKMDETVNI 420
QY 265 NAGNNIETTRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKKNKPVRI 323
DB 421 NAGNNIETTRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKNKPVRI 480
QY 324 TNVAPGVKEGVDYTNVAOLKGYAONLNRIIDVNDGNARAGIAQAIATAGLVQAYLPKGSMM 383
DB 481 TNVAPGVKEGVDYTNVAOLKGYAONLNRIIDVNDGNARAGIAQAIATAGLVQAYLPKGSMM 540

QY 384 AIGGTYRGEAGYAIAGYSSIDGGMWIKITAGSNGRCHFGASASVGYOM 433
DB 541 AIGGTYRGEAGYAIAGYSSIDGGMWIKITAGSNGRCHFGASASVGYOM 590

RESULT 8

09JPS2 PRELIMINARY: PRT: 594 AA.
AC 09JPS2: 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
DE Outer membrane protein GMA992.
CN GMA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE31;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing";
RL Science 287:1816-1820(2000).
DR EMBL: AF226379; AAF42528.1; -;
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 92.6%; Score 2033.5; DB 2; Length 594;
Best Local Similarity 71.0%; Pred. No. 1.6e-86;
Matches 422; Conservative 1; Mismatches 10; Indels 161; Gaps 2;

QY 1 MNKYYRIIWNLSALNAAWVVSSELTNRNHRASATVATATLTLFATVOASA----- 51
DB 1 MNKYYRIIWNLSALNAAWVVSSELTNRNHRASATVATATLTLFATVOASATDDDDLYLE 60
QY 52 ----- 51
DB 61 PVORTAPVLSFHADSEGTGEKEVTEEDSNMGVYFPDKGVLTAGTITLKAGDNLIKIKNTDE 120
QY 52 ----- 51
DB 121 NFNASSFTYSLEKKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGDTTVH 180
QY 52 ----- 80
DB 181 LINGGSTLTDLTLTGATTTNTNDVTDDEKKRAASVADVLNAGWNIGKVGKGTASDNV 240
QY 81 DFVRTYDVEFLSADTKTTTVNVESEKDKGKTEVIGAKTSVIREKDKGLVTGKDKGENG 140
DB 241 DFVRTYDVEFLSADTKTTTVNVESEKDKGKTEVIGAKTSVIREKDKGLVTGKDKGENG 300
QY 141 SSTDEGBELVTAKEVIDAVNKAAGRMRKTTTANGOTGQADKEFTVTSCTNVTFAASKGTAT 200
DB 301 SSTDEGBELVTAKEVIDAVNKAAGRMRKTTTANGOTGQADKEFTVTSCTNVTFAASKGTAT 360
QY 201 TVSKDDGNTIYMYDVNVDALNVLNQLNSGMNLSKAVAGSSGKVISGNVSPSGKMDKDE 260
DB 361 TVSKDDGNTIYMYDVNVDALNVLNQLNSGMNLSKAVAGSSGKVISGNVSPSGKMDKDE 420
QY 261 TVNINAGNNIETTRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKKNK 319
DB 421 TVNINAGNNIETTRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKNK 480

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OY 320 PVRITNVAPGVEGDVTNVAQLKGYAQNINRHIDVGNARAGIAQAIATAGLVQAYLPG 379
DB 481 PVRITNVAPGVEGDVTNVAQLKGYAQNINRHIDVGNARAGIAQAIATAGLVQAYLPG 540
OY 380 KSMMAIGGGTYRGEAGYAGTSSISDGNWIIKGTASGSRGHFGASASVGYOW 433
DB 541 KSMMAIGGGTYRGEAGYAGTSSISDGNWIIKGTASGSRGHFGASASVGYOW 594

RESULT 9
O93QY4 PRELIMINARY: PRT: 594 AA.
AC 093QY4: 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxId=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG327;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF157605; AAK68866.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada.
SQ SEQUENCE 594 AA: 62297 MW: 9DD48B04B3A8EA2 CRC64;

Query Match 92.5%; Score 2032.5; DB 2; Length 594;
Best Local Similarity 70.9%; Pred. No. 1.8e-86;
Matches 421; Conservative 3; Mismatches 9; Indels 161; Gaps 2;

OY 1 MKRIYRIINNSALNMVAVVSELTNRNHTKRASATVATATLLFATVQASA----- 51
DB 1 MKRIYRIINNSALNMVAVVSELTNRNHTKRASATVATATLLFATVQASTDDDDLYLE 60
OY 52 ----- 51
DB 61 PVQRTAVVLSFRSDEKGEKTEVEDSNMGVYFKKGVLTAGITILKAGDNLKIKONTNE 120
OY 52 ----- 51
DB 121 NNNASSFTYSLKKDLDTLTSVGTETKLSFSAANSKNVNTSDYGLNFAKTAETNGDTTVH 180
OY 52 ----- 51
DB 181 LMGISGLTDLTLNLTGATNTNDVNTDDEKRRASVKNVLAAGNNIKVKKGTASDNY 240
OY 81 DTVRTYDVEFLSADTKTTTVNESKDNKGTETKIGAKTSVIREKDGKLVTKDGKENG 140
DB 241 DTVRTYDVEFLSADTKTTTVNESKDNKGTETKIGAKTSVIREKDGKLVTKDGKENG 300
OY 141 SSTDGEGLVTAKEVIDAVNKAQWRKTTTANGQCGQADKEFTVNTSGTAVTPASGCTTA 200
DB 301 SSTDGEGLVTAKEVIDAVNKAQWRKTTTANGQCGQADKEFTVNTSGTAVTPASGCTTA 360
OY 201 TVSKDQDGNITVAVVNVGDALNVNQLQNSGNMLDSKAVAGSSGKVISGNTVPSKGMDE 260
DB 361 TVSKDQDGNITVAVVNVGDALNVNQLQNSGNMLDSKAVAGSSGKVISGNTVPSKGMDE 420
OY 261 TVNINAGNNIEITRNGKNIDATSMTPQFSVSLGAGADAPTLVSVDG-ALNVGSKDKK 319
DB 421 TVNINAGNNIEITRNGKNIDATSMTPQFSVSLGAGADAPTLVSVDGALNVGSKDKK 480
OY 320 PVRITNVAPGVEGDVTNVAQLKGYAQNINRHIDVGNARAGIAQAIATAGLVQAYLPG 379
DB 481 PVRITNVAPGVEGDVTNVAQLKGYAQNINRHIDVGNARAGIAQAIATAGLVQAYLPG 540
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DB 481 PVRITNVAPGVEGDVTNVAQLKGYAQNINRHIDVGNARAGIAQAIATAGLVQAYLPG 540
OY 380 KSMMAIGGGTYRGEAGYAGTSSISDGNWIIKGTASGSRGHFGASASVGYOW 433
DB 541 KSMMAIGGGTYRGEAGYAGTSSISDGNWIIKGTASGSRGHFGASASVGYOW 594

RESULT 10
O9JPR8 PRELIMINARY: PRT: 599 AA.
AC 09JPR8: 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992 (Nhba outer membrane protein).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxId=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH38;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarelli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappelli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H38;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF226383; AAF42532.1; -.
DR EMBL: AF157608; AAK68869.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada.
SQ SEQUENCE 599 AA: 62844 MW: BBA16EBF53C1970C CRC64;

Query Match 92.5%; Score 2032; DB 2; Length 599;
Best Local Similarity 70.5%; Pred. No. 1.9e-86;
Matches 422; Conservative 2; Mismatches 9; Indels 166; Gaps 2;

OY 1 MKRIYRIINNSALNMVAVVSELTNRNHTKRASATVATATLLFATVQASA----- 51
DB 1 MKRIYRIINNSALNMVAVVSELTNRNHTKRASATVATATLLFATVQANADEDEBEEL 60
OY 52 ----- 51
DB 61 EPPVASALVLAQFIDKEGNGENESTGNIGMSIYDNNHTLHGATVTLKAGDNLKIKONTN 120
OY 52 ----- 51
DB 121 KMTNENTDSSFTYSLKKDLDTLTSVETKLSFGANGKNVNTSDYGLNFAKTAETNGT 180
OY 52 ----- 51
DB 181 DTTVHLNGISGLTTLTTLNLTGATNTNDVNTDDEKRRASVKNVLAAGNNIKVKKGT 240
OY 76 ASDNVDFVATYDVEFLSADTKTTTVNESKDNKGTETKIGAKTSVIREKDGKLVTKGD 135
DB 241 ASDNVDFVATYDVEFLSADTKTTTVNESKDNKGTETKIGAKTSVIREKDGKLVTKGD 300
OY 136 KGEKSSSTDEGGLVTAKEVIDAVNKAQWRKTTTANGQCGQADKEFTVNTSGTAVTPASG 195
DB 136 KGEKSSSTDEGGLVTAKEVIDAVNKAQWRKTTTANGQCGQADKEFTVNTSGTAVTPASG 195
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Db 301 KGENSSSTDEGEGLVTAKEVIDAYNKAGWEMKTTTANGQTQADKEFTYVSGTNVTFASG 360
QY 196 KGTATVSKDDQGNITVMYDVNVDALNVNQLNSGWNLDKSKAVASSGKVISGNVSPSK 255
   |||||
Db 361 KGTATVSKDDQGNITVYKIDVNVGDALNVNQLNSGWNLDKSKAVASSGKVISGNVSPSK 420
QY 256 GKMEFTVNIAGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDG-DALNVGS 314
   |||||
Db 421 GKMEFTVNIAGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDGKALNVGS 480
QY 315 KKNKRVRTITNAPGKEGVTVAQOLKGVAQNLNNRIDVNDGNARAGIAQAIATAGLVQ 374
   |||||
Db 481 KKNKRVRTITNAPGKEGVTVAQOLKGVAQNLNNRIDVNDGNARAGIAQAIATAGLVQ 540
QY 375 AYPGKSMMAIGGCTTREGAGYAIIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 433
   |||||
Db 541 AYPGKSMMAIGGCTTREGAGYAIIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 599
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RESULT 11

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Q9JPT3 PRELIMINARY; PRT; 594 AA.
ID 09JPT3
AC 09JPT3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_Taxid=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88, and BZ232;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Iuzzini E., Manetti R., Marchetti E., Mora M., Ntli S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.D., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226376; AAF42525.1; -
DR EMBL; AF226369; AAF42518.1; -
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B9D04B46 CRC64;
```

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Query Match 92.4%; Score 2029.5; DB 2; Length 594;
Best Local Similarity 70.9%; Pred. No. 2,5e-86;
Matches 421; Conservative 1; Mismatches 11; Indels 161; Gaps 2;
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QY 1 MNKIYRIINNSALNANWVSELTRNHTKRASATVATLTLFAVVOASA----- 51
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Db 1 MNKIYRIINNSALNANWVSELTRNHTKRASATVATLTLFAVVOASTDDDDLYLE 60
QY 52 ----- 51
Db 61 PVORTAPVLSFHADSEGTGEKVEYEDSNMVGFDKGVLAGTTTLKAGDNLIKONTDE 120
QY 52 ----- 51
Db 121 NTNASSFTYSLKDLTDLFVETEKLSFGANGKRVNITSDTKGLNPAKETAGTNGDTYH 180
QY 52 -----NRAASVQDVNLNGWNIKGVKPGTTASDNV 80
Db 181 LINGIGSTLIDTLNTGATVNTDNTYDDEKKRAASVQDVNLNGWNIKGVKPGTTASDNV 240
QY 81 DFNRYVDVEFLSADTKTTTVNVESKDNCKRTEVIGAKTSVIREKDGKLVTKDGENG 140
```

```
Db 241 DFNRYVDVEFLSADTKTTTVNVESKDNCKRTEVIGAKTSVIREKDGKLVTKDGENG 300
QY 141 SSTDEGEGLVTAKEVIDAYNKAGWEMKTTTANGQTQADKEFTYVSGTNVTFASGTTA 200
   |||||
Db 301 SSTDEGEGLVTAKEVIDAYNKAGWEMKTTTANGQTQADKEFTYVSGTNVTFASGTTA 360
QY 201 TVSKDDQGNITVYKIDVNVGDALNVNQLNSGWNLDKSKAVASSGKVISGNVSPSKKME 260
   |||||
Db 361 TVSKDDQGNITVYKIDVNVGDALNVNQLNSGWNLDKSKAVASSGKVISGNVSPSKKME 420
QY 261 TVNINAGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKDNK 319
   |||||
Db 421 TVNINAGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDGKALNVGSKDNK 480
QY 320 PVRTITNAPGKEGVTVAQOLKGVAQNLNNRIDVNDGNARAGIAQAIATAGLVQATLP 379
   |||||
Db 481 PVRTITNAPGKEGVTVAQOLKGVAQNLNNRIDVNDGNARAGIAQAIATAGLVQATLP 540
QY 380 KSMMAIGGCTTREGAGYAIIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 433
   |||||
Db 541 KSMMAIGGCTTREGAGYAIIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 594
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RESULT 12

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Q9JPH7 PRELIMINARY; PRT; 594 AA.
ID 09JPH7
AC 09JPH7;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992 (Nhla outer membrane protein).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_Taxid=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BZ198, and 297-0;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Iuzzini E., Manetti R., Marchetti E., Mora M., Ntli S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.D., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226376; AAF42525.1; -
DR EMBL; AF226358; AAF42507.1; -
DR EMBL; AF157604; AAK68865.1; -
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62361 MW; 436BDDDE68263C5C CRC64;
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Query Match 92.2%; Score 2025.5; DB 2; Length 594;
Best Local Similarity 70.9%; Pred. No. 3,8e-86;
Matches 421; Conservative 2; Mismatches 10; Indels 161; Gaps 2;
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QY 1 MNKIYRIINNSALNANWVSELTRNHTKRASATVATLTLFAVVOASA----- 51
   |||||
Db 1 MNKIYRIINNSALNANWVSELTRNHTKRASATVATLTLFAVVOANATDDDDLYLE 60
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OY 52 ----- 51
Db 61 PVQRTAVVLSRSPDKEGTEGEDSDSNMAYVFDEKRVLKAGATILKAGDNLKIKONTNE 120
OY 52 ----- 51
Db 121 NTNDSFTYSLKDLTDLTSVETEKLSFGANGNKVNITSDPKGLNFAKETAGTNGDPTVH 180
OY 52 ----- 80
Db 181 INGISLTLDLTLNTGATTNTVNDNVTDDEKRRASVADVLNAGNNIKGVKPGTTASDNV 240
OY 81 DFNRYDVEFLSADPTKTTTVNVEESKDKKTEVKAITSYIKKDKGLVTGKKGNG 140
Db 241 DFNRYDVEFLSADPTKTTTVNVEESKDKKTEVKAITSYIKKDKGLVTGKKGNG 300
OY 141 SSTDGEGGLVTAKEVIDAVNKAQMRKTTTANGOTGADKFEVTSNTVTFASGKTGA 200
Db 301 SSTDGEGGLVTAKEVIDAVNKAQMRKTTTANGOTGADKFEVTSNTVTFASGKTGA 360
OY 201 TVSKDDGNTVMDVNVGDALNVNOLONGMNLDSKAVAGSSGKVISGNVSPSKGKMD 260
Db 361 TVSKDDGNTVMDVNVGDALNVNOLONGMNLDSKAVAGSSGKVISGNVSPSKGKMD 420
OY 261 TVNINAGNNIETTRNGKNIDTATSMTPPOFSSVSLGAGADAPTLSDGD-ALNVGSKDKN 319
Db 421 TVNINAGNNIETTRNGKNIDTATSMTPPOFSSVSLGAGADAPTLSDGDALNVGSKDKN 480
OY 320 PVRTINAVPVGKEDVTVNAQLKGYAQNLRNIDVNDNARAGIAQATATGLVQAYLP 379
Db 481 PVRTINAVPVGKEDVTVNAQLKGYAQNLRNIDVNDNARAGIAQATATGLVQAYLP 540
OY 380 KSMAAIGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 433
Db 541 KSMAAIGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 594
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RESULT 13

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OGJPR9 PRELIMINARY; PRT; 598 AA.
AC OGJPR9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NGH36;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizzia M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Kappun U.
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL: AF226382; AAF42531.1;
DR InterPro: IPR005594; YADA.
DR Pfam: PF03895; YADA.1.
SQ SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;
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Query Match 92.1%; Score 2023.5; DB 2; Length 598;
Best Local Similarity 70.4%; Pred. No. 4.8e-86;
Matches 421; Conservative 2; Mismatches 10; Indels 165; Gaps 2;

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OY 1 MNKIYRIIWSALNAAVYVSELTNRNHTKRASTYVTAVALTLLPATVQASA----- 51
Db 1 MNKIYRIIWSALNAAVYVSELTNRNHTKRASTYVTAVALTLLPATVQANATDDELDYLE 60
OY 52 ----- 51
Db 61 PVQRTAVVLSRSPDKEGTEGEDSDSNMAYVFDEKRVLKAGATILKAGDNLKIKONTNE 120
OY 52 ----- 51
Db 121 NTNENTDSFTYSLKDLTDLTSVETEKLSFGANGNKVNITSDPKGLNFAKETAGTNGD 180
OY 52 ----- 76
Db 181 PTVHLNGISLTLDLTLNTGATTNTVNDNVTDDEKRRASVADVLNAGNNIKGVKPGTTA 240
OY 77 SDNVDFVRYPTVEFLSADPTKTTTVNVEESKDKKTEVKAITSYIKKDKGLVTGKDK 136
Db 241 SDNVDFVRYPTVEFLSADPTKTTTVNVEESKDKKTEVKAITSYIKKDKGLVTGKDK 300
OY 137 GENGSSDDEGGLVTAKEVIDAVNKAQMRKTTTANGOTGADKFEVTSNTVTFASGK 196
Db 301 DENGSSTDGEGGLVTAKEVIDAVNKAQMRKTTTANGOTGADKFEVTSNTVTFASGK 360
OY 197 GTTATVSKDDGNTVMDVNVGDALNVNOLONGMNLDSKAVAGSSGKVISGNVSPSKG 256
Db 361 GTTATVSKDDGNTVMDVNVGDALNVNOLONGMNLDSKAVAGSSGKVISGNVSPSKG 420
OY 257 KMDEVNINAGNNIETTRNGKNIDTATSMTPPOFSSVSLGAGADAPTLSDGD-ALNVGSK 315
Db 421 KMDEVNINAGNNIETTRNGKNIDTATSMTPPOFSSVSLGAGADAPTLSDGDALNVGSK 480
OY 316 KDNKFEVRIITNAPGVKEDVTVNAQLKGYAQNLRNIDVNDNARAGIAQATATGLVQ 375
Db 481 DFNKFEVRIITNAPGVKEDVTVNAQLKGYAQNLRNIDVNDNARAGIAQATATGLVQ 540
OY 376 YLPKKSMAAIGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 433
Db 541 YLPKKSMAAIGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 598
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RESULT 14

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OG30Y2 PRELIMINARY; PRT; 592 AA.
AC OG30Y2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE Outer membrane protein.
GN NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H41;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis."
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF157609; AAK6870.1;
DR InterPro: IPR005594; YADA.
DR Pfam: PF03895; YADA.1.
SQ SEQUENCE 592 AA; 61869 MW; F9403A0BA18BEA7 CRC64;
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Query Match 91.7%; Score 2015.5; DB 2; Length 592;
Best Local Similarity 70.8%; Pred. No. 1.1e-85;
Matches 419; Conservative 3; Mismatches 11; Indels 159; Gaps 2;
1 MNKIYRIIWSALNAAVYVSELTNRNHTKRASTYVTAVALTLLPATVQASA----- 51
1 MNKIYRIIWSALNAAVYVSELTNRNHTKRASTYVTAVALTLLPATVQANATDDEDEBEL 60

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QY 52 ----- 51
DB 61 ESVORSVGSIQASMEGSVELETISLMTNDSKEFDPYIVTLKAGDNLKIKONTNENT 120
QY 52 ----- 51
DB 121 NASSFTYSLKDLTGLINVEETKLSFGANGKRYNISDTKGLNFAKETAGTNGDTTVHLN 180
QY 52 ----- 82
DB 181 GIGSTLTMLNTGATTNTNDVYDDEKRRASVADVLNAGNNINGVPGTTASDNVD 240
QY 83 VRTYDVEELSDPFTKTTTVNVEESKDNKTEVEKIGAKTSYKEKDKLVTGKDKGENGS 142
DB 241 VRTYDVEELSDPFTKTTTVNVEESKDNKTEVEKIGAKTSYKEKDKLVTGKDKGENGS 300
QY 143 TDEGELVTAKEVIDAVNKAQMRKTTTANGOTGQADKFEYVSGTNVTFASGKTATV 202
DB 301 TDEGELVTAKEVIDAVNKAQMRKTTTANGOTGQADKFEYVSGTNVTFASGKTATV 360
QY 203 SKDDOGNITVMDVNVGDLNVNOLNSGNNLDSKAVAGSSGKVIISGNVSPSKGKDEYV 262
DB 361 SKDDOGNITVMDVNVGDLNVNOLNSGNNLDSKAVAGSSGKVIISGNVSPSKGKDEYV 420
QY 263 NINAGNNIETTRNGKNIDATSMTPOFSSVSLGAGADAPTLVSVDG-ALNVGSKKDNKPY 321
DB 421 NINAGNNIETTRNGKNIDATSMTPOFSSVSLGAGADAPTLVSVDGALNVGSKKDNKPY 480
QY 322 RITTVNAPVKEGDVTVNAOLKGYAQNLNRRIDVNDGNARAGIAQAIAITAGLVQAYLPKGS 381
DB 481 RITTVNAPVKEGDVTVNAOLKGYAQNLNRRIDVNDGNARAGIAQAIAITAGLVQAYLPKGS 540
QY 382 MMAIGGTYRGEAGYALGYSISDGNMTIKGTASGNSRHFASASVGYQW 433
DB 541 MMAIGGTYRGEAGYALGYSISDGNMTIKGTASGNSRHFASASVGYQW 592

RESULT 15
Q9JPS0 PRELIMINARY: PRT: 598 AA.
AC Q9JPS0;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992 (Nhha outer membrane protein).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_Taxid=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NH15;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H15;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF226381; AAF42530.1; -

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DR EMBL: AF157607; AAK68868.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 598 AA; 62763 MW; E6C7AEF0BB8A63CB CRC64;

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Query Match 91.5%; Score 2010.5; DB 2; Length 598;
Best Local Similarity 69.9%; Pred. No. 1,9e-85;
Matches 418; Conservative 3; Mismatches 12; Indels 165; Gaps 2;

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QY 1 MNKIVRIINSSALNAVWVSELTRNHTKRASATVATLTLFATVOASA----- 51
DB 1 MNKIVRIINSSALNAVWVSELTRNHTKRASATVATLTLFATVOAADDDLYLE 60
QY 52 ----- 51
DB 61 PVQRTAVVLSFRSDKRGTEGEKTEDSNNAVYFDEKRYLKAGAITLKAGDNLKIKONTNE 120
QY 52 ----- 51
DB 121 NTNENTNDSFTYSLKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180
QY 52 ----- 76
DB 181 PTVHLNGISGTLTDLTLNTGATTNTNDVYDDEKRRASVADVLNAGNNIKGVKPGTFA 240
QY 77 SDNVDFVRYDYVEFLSADTKTTTVNVEESKDNKTEVEKIGAKTSYKEKDKLVTGKDK 136
DB 241 SDNVDFVRYDYVEFLSADTKTTTVNVEESKDNKTEVEKIGAKTSYKEKDKLVTGKDK 300
QY 137 GENGSSSTDEGELVTAKEVIDAVNKAQMRKTTTANGOTGQADKFEYVSGTNVTFASGK 196
DB 301 DENGSSSTDEGELVTAKEVIDAVNKAQMRKTTTANGOTGQADKFEYVSGTNVTFASGN 360
QY 197 GTTATVSKDDOGNITVMDVNVGDLNVNOLNSGNNLDSKAVAGSSGKVIISGNVSPSKG 256
DB 361 GTTATVSKDDOGNITVMDVNVGDLNVNOLNSGNNLDSKAVAGSSGKVIISGNVSPSKG 420
QY 257 KMDFTVINAGNNIETTRNGKNIDATSMTPOFSSVSLGAGADAPTLVSVDG-ALNVGSK 315
DB 421 KMDFTVINAGNNIETTRNGKNIDATSMTPOFSSVSLGAGADAPTLVSVDGALNVGSK 480
QY 316 KDNKPVRTTVNAPVKEGDVTVNAOLKGYAQNLNRRIDVNDGNARAGIAQAIAITAGLVQA 375
DB 481 DANKPVRTTVNAPVKEGDVTVNAOLKGYAQNLNRRIDVNDGNARAGIAQAIAITAGLVQA 540
QY 376 YLPGRKSMAAGGTYRGEAGYALGYSISDGNMTIKGTASGNSRHFASASVGYQW 433
DB 541 YLPGRKSMAAGGTYRGEAGYALGYSISDGNMTIKGTASGNSRHFASASVGYQW 598

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Search completed: October 6, 2003, 09:30:42
Job time : 34.8023 secs

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PA (UYOU) UNITV QUEENSLAND.
 XX
 PI Peak IRA, Jennings MP;
 XX
 DR WPI: 2001-488774/53.
 DR N-PSDB: AAS09176.
 XX
 PT New Nhha surface antigen polypeptides and polynucleotides from
 PT Neisseria meningitidis, useful in producing vaccines for treating or
 PT preventing broad spectrum of Neisseria meningitidis -
 XX
 PS Claim 12; Fig 9; 91pp; English.
 XX
 CC The present invention relates to the isolation of novel Neisseria
 CC meningitidis mutant polypeptides of the surface antigen Nhha
 CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
 CC characterised by deletions of non-conserved amino acids, particularly
 CC the deletion of variable regions. The deletion mutants are useful in
 CC diagnostics, therapeutic and prophylactic vaccines against a broader
 CC spectrum of N. meningitidis, and in designing and/or screening of
 CC medicaments. The mutant proteins when used as a vaccine can effectively
 CC immunise against a broader spectrum of N. meningitidis strains than
 CC would be expected from a corresponding wild-type surface antigen.
 CC The present sequence represents N. meningitidis strain PMC21 surface
 CC antigen Nhha deletion mutant #4.
 CC
 XX
 SQ Sequence 502 AA;
 Query Match 100.0%; Score 2544; DB 22; Length 502;
 Best Local Similarity 100.0%; Pred. No. 1.9e-152;
 Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC AAY27202;
 XX
 DT 24-SEP-1999 (first entry)
 XX
 DE Amino acid sequence of N. meningitidis protein ORF40-1.
 XX
 KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;
 KW bacterial infection; treatment.
 XX
 OS Neisseria meningitidis.
 XX
 PN WO936544-A2.
 XX
 PD 22-JUL-1999.
 XX
 PF 14-JAN-1999; 99MO-IB00103.
 XX
 PR 09-OCT-1998; 98GB-0022143.
 PR 14-JAN-1998; 98GB-0000760.
 PR 01-SEP-1998; 98GB-0019015.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Grandi G, Maignani V, Pizsa M, Rappuoli R, Scarlato V;
 XX
 DR WPI: 1999-444400/37.
 DR N-PSDB: AAX99124.
 XX
 PT New protein and its nucleotide sequence, useful in vaccines or
 PT diagnostic compositions for treating and/or preventing Neisseria
 PT meningitidis infections
 XX
 PS Claim 1; Page 62; 123pp; English.
 XX
 CC The invention provides proteins (AAY27201-245) from Neisseria
 CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)
 CC encoding the proteins. Compositions comprising the protein, nucleic acid
 CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a
 CC vaccine composition or a diagnostic composition. The composition is also
 CC useful for treating or preventing an infection due to Neisseria
 CC bacteria, especially Neisseria meningitidis.
 CC
 XX
 SQ Sequence 591 AA;
 Query Match 96.7%; Score 2459.5; DB 20; Length 591;
 Best Local Similarity 84.9%; Pred. No. 5e-147;
 Matches 502; Conservative 0; Mismatches 0; Indels 89; Gaps 4;

QY	Db	Sequence	Score	Length	Indels	Gaps
QY	361	SKDDQNGTWTAVYDVNWGDAALVNDLQNSGWLDSKFAVSSGSKVTSNGVSPSSKGMDETV	96.7%	591	0	0
QY	332	NINAGNNIETTRNGKNDIDATSMTPQSSVSLGAGADAPTLVSVDGALNVGSKDKNPFVR	84.9%	591	0	0
Db	421	NINAGNNIETTRNGKNDIDATSMTPQSSVSLGAGADAPTLVSVDGALNVGSKDKNPFVR				
QY	392	ITNVAAGVKEGDVNNVAOLKCAVQNLNRRIDNVGNNARAGTAQAATATAGLYQAATLPKSM				
Db	481	ITNVAAGVKEGDVNNVAOLKCAVQNLNRRIDNVGNNARAGTAQAATATAGLYQAATLPKSM				
QY	452	MAIGGTVRGAGYAIGYSSISDGSNMWIKGTASGNSRGHFGASASVGYOW				
Db	541	MAIGGTVRGAGYAIGYSSISDGSNMWIKGTASGNSRGHFGASASVGYOW				
QY	361	SKDDQNGTWTAVYDVNWGDAALVNDLQNSGWLDSKFAVSSGSKVTSNGVSPSSKGMDETV				
QY	332	NINAGNNIETTRNGKNDIDATSMTPQSSVSLGAGADAPTLVSVDGALNVGSKDKNPFVR				
Db	421	NINAGNNIETTRNGKNDIDATSMTPQSSVSLGAGADAPTLVSVDGALNVGSKDKNPFVR				
QY	392	ITNVAAGVKEGDVNNVAOLKCAVQNLNRRIDNVGNNARAGTAQAATATAGLYQAATLPKSM				
Db	481	ITNVAAGVKEGDVNNVAOLKCAVQNLNRRIDNVGNNARAGTAQAATATAGLYQAATLPKSM				
QY	452	MAIGGTVRGAGYAIGYSSISDGSNMWIKGTASGNSRGHFGASASVGYOW				
Db	541	MAIGGTVRGAGYAIGYSSISDGSNMWIKGTASGNSRGHFGASASVGYOW				
QY	361	SKDDQNGTWTAVYDVNWGDAALVNDLQNSGWLDSKFAVSSGSKVTSNGVSPSSKGMDETV				
QY	332	NINAGNNIETTRNGKNDIDATSMTPQSSVSLGAGADAPTLVSVDGALNVGSKDKNPFVR				
Db	421	NINAGNNIETTRNGKNDIDATSMTPQSSVSLGAGADAPTLVSVDGALNVGSKDKNPFVR				
QY	392	ITNVAAGVKEGDVNNVAOLKCAVQNLNRRIDNVGNNARAGTAQAATATAGLYQAATLPKSM				
Db	481	ITNVAAGVKEGDVNNVAOLKCAVQNLNRRIDNVGNNARAGTAQAATATAGLYQAATLPKSM				
QY	452	MAIGGTVRGAGYAIGYSSISDGSNMWIKGTASGNSRGHFGASASVGYOW				
Db	541	MAIGGTVRGAGYAIGYSSISDGSNMWIKGTASGNSRGHFGASASVGYOW				
QY	361	SKDDQNGTWTAVYDVNWGDAALVNDLQNSGWLDSKFAVSSGSKVTSNGVSPSSKGMDETV				
QY	332	NINAGNNIETTRNGKNDIDATSMTPQSSVSLGAGADAPTLVSVDGALNVGSKDKNPFVR				
Db	421	NINAGNNIETTRNGKNDIDATSMTPQSSVSLGAGADAPTLVSVDGALNVGSKDKNPFVR				
QY	392	ITNVAAGVKEGDVNNVAOLKCAVQNLNRRIDNVGNNARAGTAQAATATAGLYQAATLPKSM				
Db	481	ITNVAAGVKEGDVNNVAOLKCAVQNLNRRIDNVGNNARAGTAQAATATAGLYQAATLPKSM				
QY	452	MAIGGTVRGAGYAIGYSSISDGSNMWIKGTASGNSRGHFGASASVGYOW				
Db	541	MAIGGTVRGAGYAIGYSSISDGSNMWIKGTASGNSRGHFGASASVGYOW				
QY	361	SKDDQNGTWTAVYDVNWGDAALVNDLQNSGWLDSKFAVSSGSKVTSNGVSPSSKGMDETV				
QY	332	NINAGNNIETTRNGKNDIDATSMTPQSSVSLGAGADAPTLVSVDGALNVGSKDKNPFVR				
Db	421	NINAGNNIETTRNGKNDIDATSMTPQSSVSLGAGADAPTLVSVDGALNVGSKDKNPFVR				
QY	392	ITNVAAGVKEGDVNNVAOLKCAVQNLNRRIDNVGNNARAGTAQAATATAGLYQAATLPKSM				
Db	481	ITNVAAGVKEGDVNNVAOLKCAVQNLNRRIDNVGNNARAGTAQAATATAGLYQAATLPKSM				
QY	452	MAIGGTVRGAGYAIGYSSISDGSNMWIKGTASGNSRGHFGASASVGYOW				
Db	541	MAIGGTVRGAGYAIGYSSISDGSNMWIKGTASGNSRGHFGASASVGYOW				
QY	361	SKDDQNGTWTAVYDVNWGDAALVNDLQNSGWLDSKFAVSSGSKVTSNGVSPSSKGMDETV				
QY	332	NINAGNNIETTRNGKNDIDATSMTPQSSVSLGAGADAPTLVSVDGALNVGSKDKNPFVR				
Db	421	NINAGNNIETTRNGKNDIDATSMTPQSSVSLGAGADAPTLVSVDGALNVGSKDKNPFVR				
QY	392	ITNVAAGVKEGDVNNVAOLKCAVQNLNRRIDNVGNNARAGTAQAATATAGLYQAATLPKSM				
Db	481	ITNVAAGVKEGDVNNVAOLKCAVQNLNRRIDNVGNNARAGTAQAATATAGLYQAATLPKSM				
QY	452	MAIGGTVRGAGYAIGYSSISDGSNMWIKGTASGNSRGHFGASASVGYOW				
Db	541	MAIGGTVRGAGYAIGYSSISDGSNMWIKGTASGNSRGHFGASASVGYOW				
QY	361	SKDDQNGTWTAVYDVNWGDAALVNDLQNSGWLDSKFAVSSGSKVTSNGVSPSSKGMDETV				
QY	332	NINAGNNIETTRNGKNDIDATSMTPQSSVSLGAGADAPTLVSVDGALNVGSKDKNPFVR				
Db	421	NINAGNNIETTRNGKNDIDATSMTPQSSVSLGAGADAPTLVSVDGALNVGSKDKNPFVR				
QY	392	ITNVAAGVKEGDVNNVAOLKCAVQNLNRRIDNVGNNARAGTAQAATATAGLYQAATLPKSM				
Db	481	ITNVAAGVKEGDVNNVAOLKCAVQNLNRRIDNVGNNARAGTAQAATATAGLYQAATLPKSM				
QY	452	MAIGGTVRGAGYAIGYSSISDGSNMWIKGTASGNSRGHFGASASVGYOW				
Db	541	MAIGGTVRGAGYAIGYSSISDGSNMWIKGTASGNS				

Db	61	YLDPRQRTVAVLIVNSDKRGTEKEKEVEENSDMAVYFNENKGVLTAREITLLAKADNLKIKQ	120
QY	65	---FTYSLSKDLDLTSVGETEKLSPSANGKNVITSDTKGLNFAKETAGTNGDTTVHLN	120
Db	121	NCNTFTYSLSKDLDLTSVGETEKLSPSANGKNVITSDTKGLNFAKETAGTNGDTTVHLN	180
QY	121	GIGSLTD-----RAASYVDVLAAGNITGVK-----NVDF	151
Db	181	GIGSLTLDLTLMTGATTVTNDNVTTDDEKKRAASYVDVLAAGNITGVKPGTTASDNVDF	240
QY	152	VRTYDVFELSDTKTTTVNVEESKDNKTEVKIGAKTSVIREKDGKLVYTKDKGENGSS	211
Db	241	VRTYDVFELSDTKTTTVNVEESKDNKTEVKIGAKTSVIREKDGKLVYTKDKGENGSS	300
QY	212	TDEGGLVTAKEVIDAVNKAQRMKTTTANGOTGQADKEFTVTSGTNVTFASCGTTATV	271
Db	301	TDEGGLVTAKEVIDAVNKAQRMKTTTANGOTGQADKEFTVTSGTNVTFASCGTTATV	360
QY	272	SKDDOGNTVMYDVNVGALANVNOLONSGMNLDKSKVAASSGKVIISGNNVSPSKGKDETV	331
Db	361	SKDDOGNTVMYDVNVGALANVNOLONSGMNLDKSKVAASSGKVIISGNNVSPSKGKDETV	420
QY	332	NINAGNNIEITPENGKNIDATSMTPOFSSVSLGAGADAPTLISVDGALNVGSKKDKPVR	391
Db	421	NINAGNNIEITPENGKNIDATSMTPOFSSVSLGAGADAPTLISVDGALNVGSKKDKPVR	480
QY	392	ITNVAPGVKEGDVTNVVADLKGYAONLNRRIDNVGNARAGIAQAIATFAGLVQAYLRPKSM	451
Db	481	ITNVAPGVKEGDVTNVVADLKGYAONLNRRIDNVGNARAGIAQAIATFAGLVQAYLRPKSM	540
QY	452	MAIGGGTTRGEGGYAIGYSSISDGGWIIITKGASGSRGHFGASASVGYOW	502
Db	541	MAIGGGTTRGEGGYAIGYSSISDGGWIIITKGASGSRGHFGASASVGYOW	591

RESULT 4

AAU06171

ID AAU06171 standard; Protein: 591 AA.

XX AAU06171;

XX 24-OCT-2001 (first entry)

XX

DE N. meningitidis PMC21 surface antigen NhhA polypeptide sequence.

XX

KM Surface antigen NhhA; meningococcal disease; meningitis vaccine.

XX

OS Neisseria meningitidis strain PMC21.

XX

XX

XX Key

XX Location/Qualifiers

XX FH 1..51

XX FH Peptide

XX /label= signal_peptide

XX 1..50

XX FH Region

XX /label= C1

XX /note= "Conserved region 1"

XX 51..108

XX FH Region

XX /label= V1

XX /note= "Variable region 1"

XX 52..591

XX FH Protein

XX /label= Mature_NhhA

XX /note= "Predicted mature protein, specifically claimed in claim 12"

XX 109..120

XX FH Region

XX /label= C2

XX /note= "Conserved region 2"

XX 121..124

XX FH Region

XX /label= V2

XX /note= "Variable region 2"

XX 125..188

XX FH Region

XX /label= C3

XX /note= "Conserved region 3"

XX 189..210

XX Region

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FT      /label= V3
FT      /note= "Variable region 3"
FT      211...229
FT      /label= C4
FT      /note= "Conserved region 4"
FT      230..236
FT      /label= V4
FT      /note= "Variable region 4"
FT      237..591
FT      /label= C5
FT      /note= "Conserved region 5"
FT      WO20015182-A1.
PN      XX
PD      02-AUG-2001.
XX      XX
PF      25-JAN-2001; 2001WO-AU00069.
XX      XX
PK      25-JAN-2000; 2000US-0177917.
XX      XX
PA      (UYOU ) UNIV QUEENSLAND.
XX      XX
PI      Peak IRA, Jennings MP;
XX      XX
DR      WPI; 2001-488774/53.
XX      XX
DR      N-PSDB; AAS09161.
XX      XX
PT      New Nhha surface antigen polypeptides and polynucleotides from
PT      Neisseria meningitidis, useful in producing vaccines for treating or
PT      preventing broad spectrum of Neisseria meningitidis -
XX      XX
PS      Claim 9, Fig 1; 91pp; English.
XX      XX
CC      The present invention relates to the isolation of novel Neisseria
CC      meningitidis mutant polypeptides of the surface antigen Nhha
CC      (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC      characterised by deletions of non-conserved amino acids, particularly
CC      the deletion of variable regions. The deletion mutants are useful in
CC      diagnostics, therapeutic and prophylactic vaccines against a broader
CC      spectrum of N. meningitidis, and in designing and/or screening of
CC      medicaments. The mutant proteins when used as a vaccine can effectively
CC      immunise against a broader spectrum of N. meningitidis strains than
CC      would be expected from a corresponding wild-type surface antigen.
CC      The present sequence representing the wild type surface antigen Nhha
CC      from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences
CC      (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC      the present invention.
XX      XX
SQ      Sequence 591 AA:

Query Match      96.7%; Score 2459.5; DB 22; Length 591;
Best Local Similarity 84.9%; Pred. No. 5e-147;
Matches 502; Conservative 0; Mismatches 0; Indels 89; Gaps 4;

OY      1 MNKIRITWNSALNAAVYVSELRNHRKRASATYKTAVALTLRTVQASAN----- 52
      |||||||
DB      1 MNKIRITWNSALNAAVYVSELRNHRKRASATYKTAVALTLRTVQASANNEOEEDL 60
      |||||||

OY      53 -----TIAQONLKIKIO 64
      |||||||
DB      61 YLDPQRTVAVLVNSKEGTEGKEKEVEENSDMAVYFNEKGVLARRETLTLAAGDMLKIQ 120
      |||||||

OY      65 ----FTVSLKRDLDLTSVTEKLSFSANGKNVNTSDPTKGLNFAKETAGTNGDTTVAHN 120
      |||||||
DB      121 NGTNTYSLKKDLMDLTSVTEKLSFSANGKNVNTSDPTKGLNFAKETAGTNGDTTVAHN 180
      |||||||

OY      121 GIGSLTDP-----RAASYKDYLANGWNKGYK-----NWDF 151
      |||||||
DB      181 GIGSLTDLTLNTGATTNVTNDNVTDEKKRAASVKDVLNAGWNKGYKPGTTASDNVDF 240
      |||||||

OY      152 VRTDYVLEFSLADRTTTVNESKONGKKEVEKIGAKSVYKREKDGKLVTKDGENSS 211
      |||||||
DB      241 VRTDYVLEFSLADRTTTVNESKONGKKEVEKIGAKSVYKREKDGKLVTKDGENSS 300

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OY      212 TDEGGLVTAKEVIDAVNKAQMRMKTATTANGQTQADKFEYVTSNTTFFASGKGTATV 271
      |||||||
DB      301 TDEGGLVTAKEVIDAVNKAQMRMKTATTANGQTQADKFEYVTSNTTFFASGKGTATV 360
      |||||||

OY      272 SKDDOGNTTVAVDVAVGALVNLQNSGWNLDKAAVAGSSGKVTSGVSPSKGMDETV 331
      |||||||
DB      361 SKDDOGNTTVAVDVAVGALVNLQNSGWNLDKAAVAGSSGKVTSGVSPSKGMDETV 420
      |||||||

OY      332 NINAGNNETIRNGCNIDTATSMPPQFSSVSLGACADAPTLISVDDALNVSSKKDKPVR 391
      |||||||
DB      421 NINAGNNETIRNGCNIDTATSMPPQFSSVSLGACADAPTLISVDDALNVSSKKDKPVR 480
      |||||||

OY      392 ITNVAPEGVEDVTNVAQLKGYAQNLRIDNVGNAFAGIAQAIATAGLVQAYLPGKSM 451
      |||||||
DB      481 ITNVAPEGVEDVTNVAQLKGYAQNLRIDNVGNAFAGIAQAIATAGLVQAYLPGKSM 540
      |||||||

OY      452 MAIGGGYTRGEGVTAIGTSSISDGGNWLKGTASNSRGHFGASASVGYQW 502
      |||||||
DB      541 MAIGGGYTRGEGVTAIGTSSISDGGNWLKGTASNSRGHFGASASVGYQW 591
      |||||||

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RESULT 5

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AAV23737
ID      AAV23737 standard; Protein; 592 AA.
XX      XX
AC      AAV23737;
XX      XX
DT      08-SEP-1999 (first entry)
XX      XX
DE      A surface protein of Neisseria meningitidis.
XX      XX
KW      Surface protein; surface glycoprotein; infection; vaccine;
XX      XX
OS      Immunoreactive peptide.
XX      XX
OS      Neisseria meningitidis.
XX      XX
PN      WO9931132-A1.
XX      XX
PD      24-JUN-1999.
XX      XX
PF      14-DEC-1998; 98WO-AU01031.
XX      XX
PR      12-DEC-1997; 97GB-0026398.
XX      XX
PA      (ISIS-) ISIS INNOVATION LTD.
XX      XX
PA      (UYOU ) UNIV QUEENSLAND.
XX      XX
PI      Jennings MP, Moxon ER, Peak IRA;
XX      XX
DR      WPI; 1999-418754/35.
XX      XX
DR      N-PSDB; AAX85788.
XX      XX
PT      Neisseria meningitidis surface proteins useful for treating N.
PT      meningitidis infections
XX      XX
PS      Claim 1; Page 86-87; 132pp; English.
XX      XX
CC      The present sequence represents a surface protein of Neisseria
CC      meningitidis which is approximately 62 kDa. The N. meningitidis
CC      surface glycoproteins, nucleic acids, the primers and optionally
CC      a thermostable polymerase, or antibodies are useful in a kit for
CC      the detection or diagnosis of N. meningitidis infection in humans.
CC      The N. meningitidis surface glycoproteins can also be used to
CC      prevent or treat N. meningitidis infection in humans, especially
CC      in the form of vaccines. The proteins and antibodies can also
CC      be used to identify immunoreactive peptides.
XX      XX
SQ      Sequence 592 AA:

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```

Query Match      96.5%; Score 2455; DB 20; Length 592;
Best Local Similarity 84.6%; Pred. No. 9.7e-147;
Matches 501; Conservative 0; Mismatches 1; Indels 90; Gaps 4;

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```

QY 1 MNKIYRIIMNSALNAAWVSELTNRHTRKASATYKTAVALTLLEFATYOASAN-----52
DQ 1 MNKIYRIIMNSALNAAWVSELTNRHTRKASATYKTAVALTLLEFATYOASANNRPRKDD 60
QY 53 -----TLKADNLKIK 63
DQ 61 LYDPVORTVAVLIVNSDKEGTGEKEVEEDSNAAVYFNEKGVLTAREITLAKADNLKIK 120
QY 64 Q----FTYSLKKDLTDLTSVTEKLSFSAANGKRVNTSPDKGLNFAKETAGTNDPTVHL 119
DQ 121 QNGNFTYSLKKDLTDLTSVTEKLSFSAANGKRVNTSPDKGLNFAKETAGTNDPTVHL 180
QY 120 NGIGSTLTD-----RAASVCDVLANGNKIGVK-----NVD 150
DQ 181 NGIGSTLTDLTLLNGATNTVNDVYTDDEKKRAASVCDVLANGNKIGVKRGTASDNVD 240
QY 151 FVRTDYVEFLSADTKTTVNVESKDKNGKTEVKIGAKTSVYKEKDKLVTKDKGENGS 210
DQ 241 FVRTDYVEFLSADTKTTVNVESKDKNGKTEVKIGAKTSVYKEKDKLVTKDKGENGS 300
QY 211 STDEGELVTAKEVIDAVNKAAGMRKTTTANGOTGOADKPEVTYSGTNVTFASGKGTAT 270
DQ 301 STDEGELVTAKEVIDAVNKAAGMRKTTTANGOTGOADKPEVTYSGTNVTFASGKGTAT 360
QY 271 VSKDDGNITVMYDVNVDALNVNQLONGSNLDSKAVAGSSGKVIISGNVSPSKGMDT 330
DQ 361 VSKDDGNITVMYDVNVDALNVNQLONGSNLDSKAVAGSSGKVIISGNVSPSKGMDT 420
QY 331 VNINAGNNIETTRNGKNIDATSMTPQSSVSIGAGADAPTLVSDGALNVGSKKDKPV 390
DQ 421 VNINAGNNIETTRNGKNIDATSMTPQSSVSIGAGADAPTLVSDGALNVGSKKDKPV 480
QY 391 RITNVAGVGEVDVTNVAOLKGVAQNLRNDVNGARAGIAQATAGIYQAYLPGKS 450
DQ 481 RITNVAGVGEVDVTNVAOLKGVAQNLRNDVNGARAGIAQATAGIYQAYLPGKS 540
QY 451 MMAIGGTYGEGAGVYAGVYSGISDGNMIIKGTASGNSRGHFGASASVGYQM 502
DQ 541 MMAIGGTYGEGAGVYAGVYSGISDGNMIIKGTASGNSRGHFGASASVGYQM 592

RESULT 6
AAV57045
ID AAV57045 standard; Protein: 591 AA.
XX
AC AAV57045;
XX
DQ 21-FEB-2000 (first entry)
XX
DE BASB029 amino acid sequence from N. meningitidis strain H44/76.
XX
KW BASB029; Neisseria meningitidis; surface fibril protein; HSF; diagnosis;
infection; treatment; prevent; antibacterial drug.
XX
OS Neisseria meningitidis.
XX
FH Key Location/Qualifiers
FT Misc-difference 90 /note= "Encoded by AAT"
FT Misc-difference 92 /note= "Encoded by GAT"
FT Misc-difference 98 /note= "Encoded by AAC"
FT Misc-difference 108 /note= "Encoded by AATC"
FT Misc-difference 123 /note= "Encoded by ACA"
FT Misc-difference 269 /note= "Encoded by AAA"
FT Misc-difference 389 /note= "Encoded by CGT"
XX

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PN W0955683-A2.
 PD 18-NOV-1999.
 XX 07-MAY-1999; 99WO-EP03255.
 XX 13-MAY-1998; 98GB-0010276.
 PR (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 PA Ruelle J;
 XX WPI: 2000-053103/04.
 DR N-PSDB: AAZ39865.
 XX
 FT New polypeptide from neisseria meningitidis useful for diagnosis,
 treatment or prevention of bacterial infections in mammal
 Claim 4; Fig 2; 74pp; English.

This is the Neisseria meningitidis BASB029 amino acid sequence from serogroup B strain H44/76. The BASB029 protein is homologous to the Haemophilus influenzae surface fibril (HSF) protein. The invention relates to BASB029 polynucleotide sequences (AAZ39864-239865) and polypeptide sequences (AAV57044-Y57045) and their immunogenic fragments. BASB029 polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029 polynucleotides and polypeptides are useful for generating an immune response in an animal. A therapeutic composition comprising an antibody directed against BASB029 is useful in treating humans with Neisseria meningitidis disease. The polynucleotide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes. Particularly genetic immunisation. Antibodies against BASB029 polynucleotides and polypeptides are also useful for treating infections particularly bacterial infections. The protein is useful in the screening and development of antibacterial drugs. Fused recombinant protein is useful for the stimulation of the immune system of an organism receiving the protein.

Sequence 591 AA;

Query Match 96.4%; Score 2452.5; DB 21; Length 591;
 Best Local Similarity 84.6%; Pred. No. 1.4e-146;
 Matches 500; Conservative 1; Mismatches 1; Indels 89; Gaps 4;

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QY 1 MNKIYRIIMNSALNAAWVSELTNRHTRKASATYKTAVALTLLEFATYOASAN-----52
DQ 1 MNKIYRIIMNSALNAAWVSELTNRHTRKASATYKTAVALTLLEFATYOASANNRPRKDD 60
QY 53 -----TLKADNLKIK 64
DQ 61 LYDPVORTVAVLIVNSDKEGTGEKEVEEDSNAAVYFNEKGVLTAREITLAKADNLKIK 120
QY 65 ----FTYSLKKDLTDLTSVTEKLSFSAANGKRVNTSPDKGLNFAKETAGTNDPTVHL 120
DQ 121 NGNFTYSLKKDLTDLTSVTEKLSFSAANGKRVNTSPDKGLNFAKETAGTNDPTVHL 180
QY 121 GIGSTLTD-----RAASVCDVLANGNKIGVK-----NVD 151
DQ 181 GIGSTLTDLTLLNGATNTVNDVYTDDEKKRAASVCDVLANGNKIGVKRGTASDNVD 240
QY 152 VRTDYVEFLSADTKTTVNVESKDKNGKTEVKIGAKTSVYKEKDKLVTKDKGENGS 211
DQ 241 VRTDYVEFLSADTKTTVNVESKDKNGKTEVKIGAKTSVYKEKDKLVTKDKGENGS 300
QY 212 TDEGELVTAKEVIDAVNKAAGMRKTTTANGOTGOADKPEVTYSGTNVTFASGKGTATV 271
DQ 301 TDEGELVTAKEVIDAVNKAAGMRKTTTANGOTGOADKPEVTYSGTNVTFASGKGTATV 360
QY 272 SKDDGNITVMYDVNVDALNVNQLONGSNLDSKAVAGSSGKVIISGNVSPSKGMDT 331

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Db      361 SKDDGNTVMYDVNVGDLNVNQLQNSGWNIDSKAVAGSSGKVISGNVSPSKGMDTV 420
QY      332 NINAGNNEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDGDALNVGSKKNKPYR 391
      421 NINAGNNEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDGDALNVGSKKNKPYR 480
Db      332 ITNVA PGVEGDVTNVAQLKGVAQNLNRRIDVNDGNARAGIAQAIAATAGLVQAYLPKGS 451
      481 ITNVA PGVEGDVTNVAQLKGVAQNLNRRIDVNDGNARAGIAQAIAATAGLVQAYLPKGS 540
QY      452 MAIGGCTYRGAGYAIIGYSSISDGNWIIKGTASGNSRHFASASVGYOW 502
      541 MAIGGCTYRGAGYAIIGYSSISDGNWIIKGTASGNSRHFASASVGYOW 591
Db      591 MAIGGCTYRGAGYAIIGYSSISDGNWIIKGTASGNSRHFASASVGYOW 591

RESULT 7
AAU23741
ID      AAU23741 standard; Protein; 591 AA.
XX
AC      AAU23741;
XX
DE      08-SEP-1999 (first entry)
XX
DE      A surface protein of Neisseria meningitidis.
XX
KM      Surface protein; surface glycoprotein; infection; vaccine;
XX      immunoreactive peptide.
XX
OS      Neisseria meningitidis.
XX
PN      WO9931132-A1.
XX
PD      24-JUN-1999.
XX
PF      14-DEC-1998; 98MO-AU01031.
XX
PR      12-DEC-1997; 97GB-0026398.
XX
PA      (ISIS-) ISIS INNOVATION LTD.
XX      (UYGU) UNIV QUEENSLAND.
XX
PI      Jennings MP, Moxon ER, Peak IRA;
XX
DR      WPI: 1999-418754/35.
XX      N-PSDB: AAX85793.
XX
PT      Neisseria meningitidis surface proteins useful for treating N.
      meningitidis infections
XX
PS      Claim 1; Page 104-106; 132pp; English.
XX
CC      The present sequence represents a surface protein of Neisseria
      meningitidis which is approximately 62 kDa. The N. meningitidis
      surface glycoproteins, nucleic acids, the primers and optionally
      a thermostable polymerase, or antibodies are useful in a kit for
      the detection or diagnosis of N. meningitidis infection in humans.
      CC      The N. meningitidis surface glycoproteins can also be used to
      prevent or treat N. meningitidis infection in humans, especially
      in the form of vaccines. The proteins and antibodies can also
      be used to identify immunoreactive peptides.
XX
SQ      Sequence 591 AA;

Query Match      96.2%; Score 2447.5; DB 20; Length 591;
Best Local Similarity 84.6%; Pred No. 2.9e-146;
Matches 500; Conservative 1; Mismatches 1; Indels 89; Gaps 4;

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Db      61 YLDPVLRVAVAILVNSDEKGEKKEVEENSDMAVYFNEKGVLTAREITLAKGDNLIKQ 120
QY      65 ----FTYSLKRD/LD/LTSVGETEKLSEFANGKNVITSDTKGLNFAKETAGTNGDTTVHLN 120
      121 NGTNTFTSLKRLD/LTSVGETEKLSEFANGKNVITSDTKGLNFAKETAGTNGDTTVHLN 180
Db      121 GIGSTLFTD-----RAASYKDVILNAGWNITGVK-----NDVF 151
      181 GIGSTLFTD/LTNTGATTVNTNDNVYTDDEKKRAASYKDVILNAGWNITGVKPGTTASDNVDF 240
QY      152 VRTYPTVEFLSADRTTNTVNVESKNGKTEVKGAKTSVIEKDGKLVGTGDKGENSS 211
      241 VRTYPTVEFLSADRTTNTVNVESKNGKTEVKGAKTSVIEKDGKLVGTGDKGENSS 300
QY      212 TDEGEGLVTAKEVIDAVNKAQWRMKTITANGOTGADKFEVYTSNTYFASGKTATV 271
      301 TDEGEGLVTAKEVIDAVNKAQWRMKTITANGOTGADKFEVYTSNTYFASGKTATV 360
Db      272 SKDDGNTVMYDVNVGDLNVNQLQNSGWNIDSKAVAGSSGKVISGNVSPSKGMDTV 331
      361 SKDDGNTVMYDVNVGDLNVNQLQNSGWNIDSKAVAGSSGKVISGNVSPSKGMDTV 420
QY      332 NINAGNNEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDGDALNVGSKKNKPYR 391
      421 NINAGNNEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDGDALNVGSKKNKPYR 480
QY      392 ITNVA PGVEGDVTNVAQLKGVAQNLNRRIDVNDGNARAGIAQAIAATAGLVQAYLPKGS 451
      481 ITNVA PGVEGDVTNVAQLKGVAQNLNRRIDVNDGNARAGIAQAIAATAGLVQAYLPKGS 540
Db      452 MAIGGCTYRGAGYAIIGYSSISDGNWIIKGTASGNSRHFASASVGYOW 502
      541 MAIGGCTYRGAGYAIIGYSSISDGNWIIKGTASGNSRHFASASVGYOW 591

RESULT 8
AAU06175
ID      AAU06175 standard; Protein; 591 AA.
XX
AC      AAU06175;
XX
DE      24-OCT-2001 (first entry)
XX
DE      N. meningitidis EG329 surface antigen NhbA polypeptide sequence.
XX
KM      Surface antigen NhbA, meningococcal disease; meningitis vaccine.
XX
OS      Neisseria meningitidis strain EG329.
XX
XX      Location/Qualifiers
FH      1..50
FT      Region
      /label= C1
      /note= "Conserved region 1"
FT      51..108
      /label= V1
      /note= "Variable region 1"
FT      109..120
      /label= C2
      /note= "Conserved region 2"
FT      121..124
      /label= V2
      /note= "Variable region 2"
FT      125..188
      /label= C3
      /note= "Conserved region 3"
FT      189..210
      /label= V3
      /note= "Variable region 3"
FT      211..229
      /label= C4
      /note= "Conserved region 4"
FT      230..236
      /label= V4
FT      Region

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FT /note= "Variable region 4"
 FT 237..591
 FT /label= C5
 FT /note= "Conserved region 5"
 XX
 PN WO200155182-A1.
 XX
 XX 02-AUG-2001.
 PD
 PF 25-JAN-2001; 2001WO-AU00069.
 XX
 XX 25-JAN-2000; 2000US-0177917.
 PR
 XX (UYOU) UNIV QUEENSLAND.
 PA
 XX
 PI Peak IRA, Jennings MP;
 XX
 XX WPI; 2001-488774/53.
 DR N-PSDB; AAS09165.
 DR
 XX
 XX
 PT New Nhha surface antigen polypeptides and polynucleotides from
 PT Neisseria meningitidis, useful in producing vaccines for treating or
 PT preventing broad spectrum of Neisseria meningitidis -
 XX
 PS Claim 9; Fig 1; 91bp; English.
 XX
 XX The present invention relates to the isolation of novel Neisseria
 CC meningitidis mutant polypeptides of the surface antigen Nhha
 CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
 CC characterised by deletions of non-conserved amino acids, particularly
 CC the deletion of variable regions. The deletion mutants are useful in
 CC diagnostics, therapeutic and prophylactic vaccines against a broader
 CC spectrum of N. meningitidis, and in designing and/or screening of
 CC medicaments. The mutant proteins when used as a vaccine can effectively
 CC immunise against a broader spectrum of N. meningitidis strains than
 CC would be expected from a corresponding wild type surface antigen.
 CC The present sequence representing the wild type surface antigen Nhha
 CC from N. meningitidis strain EG329 is 1 of 10 Nhha polypeptide sequences
 CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
 CC the present invention.
 CC
 XX
 SQ Sequence 591 AA;
 Query Match 96.2%; Score 2447.5; DB 22; Length 591;
 Best Local Similarity 84.6%; Pred. No. 2,9e-146;
 Matches 500; Conservative 1; Mismatches 1; Indels 89; Gaps 4;

DB 361 SKDDQGITVWYDVNVDALNVNOLNSGMNLDKRAVAGSSGKVISGNVSPSKGMDETV 420
 QY 332 NINAGNNIETIRNKNIDIASMTPOFSSVSLGAGAPTLSTVGDALNWGSKDKNPKVR 391
 DB 421 NINAGNNIETIRNKNIDIASMTPOFSSVSLGAGAPTLSTVGDALNWGSKDKNPKVR 480
 QY 392 ITTVAPGVKESGDVTNVQNLKVAQNLNRRIDNVGNARAGIAQAIATAGLVQAVLPCKSM 451
 DB 481 ITTVAPGVKESGDVTNVQNLKVAQNLNRRIDNVGNARAGIAQAIATAGLVQAVLPCKSM 540
 QY 452 MAIGGTYRGEAGYAGYSSISDGNMIKGTASGSRGHEGASASVGYQW 502
 DB 541 MAIGGTYRGEAGYAGYSSISDGNMIKGTASGSRGHEGASASVGYQW 591
 RESULT 9
 AAU06182
 ID AAU06182 standard; Protein: 512 AA.
 XX
 AC AAU06182;
 XX
 XX 24-OCT-2001 (first entry)
 DE N. meningitidis PMC21 Nhha deletion mutant #1.
 XX
 KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;
 KM mutant; mutcin.
 XX
 OS Neisseria meningitidis strain PMC21.
 XX
 FH Key location/Qualifiers
 FT Peptide 1..51
 FT /label= Signal_peptide
 FT Protein 52..512
 FT /label= Mature_Nhha_deletion_mutant_#1
 FT /note= "Predicted mature protein, specifically
 claimed in claim 12"
 XX
 PN WO200155182-A1.
 XX
 XX 02-AUG-2001.
 PD
 PF 25-JAN-2001; 2001WO-AU00069.
 XX
 XX 25-JAN-2000; 2000US-0177917.
 PR
 XX (UYOU) UNIV QUEENSLAND.
 PA
 PI Peak IRA, Jennings MP;
 XX
 XX WPI; 2001-488774/53.
 DR N-PSDB; AAS09172.
 DR
 XX
 XX
 PT New Nhha surface antigen polypeptides and polynucleotides from
 PT Neisseria meningitidis, useful in producing vaccines for treating or
 PT preventing broad spectrum of Neisseria meningitidis -
 XX
 PS Claim 12; Fig 5; 91bp; English.
 XX
 XX The present invention relates to the isolation of novel Neisseria
 CC meningitidis mutant polypeptides of the surface antigen Nhha
 CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
 CC characterised by deletions of non-conserved amino acids, particularly
 CC the deletion of variable regions. The deletion mutants are useful in
 CC diagnostics, therapeutic and prophylactic vaccines against a broader
 CC spectrum of N. meningitidis, and in designing and/or screening of
 CC medicaments. The mutant proteins when used as a vaccine can effectively
 CC immunise against a broader spectrum of N. meningitidis strains than
 CC would be expected from a corresponding wild type surface antigen.
 CC The present sequence represents N. meningitidis strain PMC21 surface
 CC antigen Nhha deletion mutant #1.
 CC
 XX

SO Sequence 512 AA:
Query Match 93.7%; Score 2383; DB 22; Length 512;
Best Local Similarity 90.6%; Pred. No. 2,8e-142;
Matches 481; Conservative 1; Mismatches 1; Indels 48; Gaps 3;

QY 1 MKKIRIIMNSALNMAVAVSELTRNHTKRASATVKTAVLATLLEFATVOASANTLAKADNL 60
DB 1 MKKIRIIMNSALNMAVAVSELTRNHTKRASATVKTAVLATLLEFATVOASAN----- 52
QY 61 KIKOPTYSLKKDLMDLTVSGTEKLSFSSANGNKVNTISPTKGLNFAKETAAGTGGDTTVHLN 120
DB 53 -----NEDTLTVSGTEKLSFSSANGNKVNTISPTKGLNFAKETAAGTGGDTTVHLN 101
QY 121 GIGSTLTPD-----RAASYKDVNLNMGWNLKGVK-----NYDF 151
DB 102 GIGSTLTPDNLNTGATVNTDNTVTDDEKKRAASYKDVNLNMGWNLKGVKPGTTASDNDVF 161
QY 152 VRTYDTVEFLSADRTTTTVNVESSKNGKTEYKIGAKTSVKEKDGKLVTKDGKENGSS 211
DB 162 VRTYDTVEFLSADRTTTTVNVESSKNGKTEYKIGAKTSVKEKDGKLVTKDGKENGSS 221
QY 212 TDEGGLTAKEDVDAVNAKAGRMKTTTANGOTGADKFEYVTSCTNTFFASGKGTATV 271
DB 222 TDEGGLTAKEDVDAVNAKAGRMKTTTANGOTGADKFEYVTSCTNTFFASGKGTATV 281
QY 272 SKDDOGNTTVYDVNVGDALNVNOLONGSMNLSKAVAGSSGKVISGNVSPSKGMDET 331
DB 282 SKDDOGNTTVYDVNVGDALNVNOLONGSMNLSKAVAGSSGKVISGNVSPSKGMDET 341
QY 332 NINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLISVDGDLNVSCKKNKPYR 391
DB 342 NINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLISVDGDLNVSCKKNKPYR 401
QY 392 ITTNAVPGKEGVDTVNAOLKGYAONLNRRIDVNDGNARAQIAQIATATAGLVQAYLPGRSM 451
DB 402 ITTNAVPGKEGVDTVNAOLKGYAONLNRRIDVNDGNARAQIAQIATATAGLVQAYLPGRSM 461
QY 452 MAIGGGYRGAGYAIIGYSSISDGGNMTIKGTASGNSRGHFGASASVGYOW 502
DB 462 MAIGGGYRGAGYAIIGYSSISDGGNMTIKGTASGNSRGHFGASASVGYOW 512

RESULT 10
AAV23743
ID AAV23743 standard; Protein; 599 AA.
AC AAV23743;
XX
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
XX
XX immunoreactive peptide.
OS Neisseria meningitidis.
XX
XX
PN MO9931132-A1.
PD 24-JUN-1999.
XX
XX
PF 14-DEC-1998; 98WO-AU01031.
PR 12-DEC-1997; 97GB-0026398.
XX
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UYOU) UNIV QUEENSLAND.
XX
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX
XX WPI: 1999-418754/35.
DR N-PSDB; AAX85795.

XX
PT Neisseria meningitidis surface proteins useful for treating N.
XX meningitidis infections
PS Claim 1; Page 114-115; 132pp; English.

CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.

SO Sequence 599 AA:
Query Match 93.2%; Score 2371.5; DB 20; Length 599;
Best Local Similarity 81.6%; Pred. No. 1.8e-141;
Matches 489; Conservative 2; Mismatches 11; Indels 97; Gaps 5;

QY 1 MKKIRIIMNSALNMAVAVSELTRNHTKRASATVKTAVLATLLEFATVOASAN----- 52
DB 1 MKKIRIIMNSALNMAVAVSELTRNHTKRASATVKTAVLATLLEFATVOANNADEDEEBEL 60
QY 53 -----TLKAGNLIKIKO--- 64
DB 61 EPVVASALVLOFMDKEGNGENESTGNIGWSIYDNNHTLHGATVTLKAGDLKIKQMTN 120
QY 65 -----FTYSLKKDLTDLSVGTBKLSFSSANGNKVNTISPTKGLNFAKETAAGTNG 113
DB 121 KNTNENTNDSSFTYSLKKDLTDLSVGTBKLSFANGNKVNTISPTKGLNFAKETAAGTNG 180
QY 114 DTTVHLNIGSTLTPD-----RAASYKDVNLNMGWNLKGVK----- 147
DB 161 DTTVHLNIGSTLTPDNLNTGATVNTDNTVTDDEKKRAASYKDVNLNMGWNLKGVKPGTT 240
QY 148 ---NVDFTYDTVEFLSADRTTTTVNVESSKNGKTEYKIGAKTSVKEKDGKLVTKGD 204
DB 241 ASDNDVFYHTYDTVEFLSADRTTTTVNVESSKNGKTEYKIGAKTSVKEKDGKLVTKGD 300
QY 205 KGENGSSTDEGGLTAKEDVDAVNAKAGRMKTTTANGOTGADKFEYVTSCTNTFFASG 264
DB 301 KGENGSSTDEGGLTAKEDVDAVNAKAGRMKTTTANGOTGADKFEYVTSCTNTFFASG 360
QY 265 KGTATVSKDDOGNTTVYDVNVGDALNVNOLONGSMNLSKAVAGSSGKVISGNVSPSK 324
DB 361 KGTATVSKDDOGNTTVYDVNVGDALNVNOLONGSMNLSKAVAGSSGKVISGNVSPSK 420
QY 325 GKMDETVINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLISVDG-DALNVGS 383
DB 421 GKMDETVINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLISVDGKALNVGS 480
QY 384 KKDKNPVAITTVNAPGVKGDVTVNAOLKGYAONLNRRIDVNDGNARAQIAQIATAGLVQ 443
DB 481 KDANKPVAITTVNAPGVKGDVTVNAOLKGYAONLNRRIDVNDGNARAQIAQIATAGLVQ 540
QY 444 AYLPGKSMATGCGYRGAGYAIIGYSSISDGGNMTIKGTASGNSRGHFGASASVGYOW 502
DB 541 AYLPGKSMATGCGYRGAGYAIIGYSSISDGGNMTIKGTASGNSRGHFGASASVGYOW 599

RESULT 11
AAU06176
ID AAU06176 standard; Protein; 599 AA.
XX
XX
AC AAU06176;
XX
XX
DT 24-OCT-2001 (first entry)
XX
XX N. meningitidis H38 surface antigen NhbA polypeptide sequence.
DE

XX Neisseria meningitidis surface proteins useful for treating N.
 PT meningitidis infections
 PS
 XX Claim 1; Page 100-101; 132pp; English.
 XX
 CC The present sequence represents a surface protein of Neisseria
 CC meningitidis which is approximately 62 kDa. The N. meningitidis
 CC surface glycoproteins, nucleic acids, the primers and optionally
 CC a thermostable polymerase, or antibodies are useful in a kit for
 CC the detection or diagnosis of N. meningitidis infection in humans.
 CC The N. meningitidis surface glycoproteins can also be used to
 CC prevent or treat N. meningitidis infection in humans, especially
 CC in the form of vaccines. The proteins and antibodies can also
 CC be used to identify immunoreactive peptides.
 CC
 XX Sequence 594 AA:
 SQ
 Query Match 93.0%; Score 2366; DB 20; Length 594;
 Best Local Similarity 82.0%; Pred. No. 4e-141;
 Matches 487; Conservative 4; Mismatches 11; Indels 92; Gaps 5;

1 MNKIIRIIMNSALNMVAVVSELTNRHTRKASATVAVLATLLEFATVOASAN----- 52
 1 MNKIIRIIMNSALNMVAVVSELTNRHTRKASATVAVLATLLEFATVOASATDDDDLYLE 60
 53 -----TLKAGDNLIKIKO----- 64
 61 PVORTAVVLSFRSDEKTEGEVTEEDSNMVGFFDKGVLTAGTITLKGDNLIKIKONTNE 120
 65 -----FTYSLKKDLTDLTSTGTEKLSFSAANGKNVITSDTRKGLNFAKETAGTNGDTTVH 118
 121 NTNASSFTYSLKKDLTDLTSTGTEKLSFSAANGKNVITSDTRKGLNFAKETAGTNGDTTVH 180
 119 LKIGISLTLD-----RAASVADVNLNAGNINIGVK-----NV 149
 181 LKIGISLTLDLTDLNLTGATTNTNDNVTDDEKKRAASVADVNLNAGNINIGVKPGTTASDNV 240
 150 DVFRTYDVEELSDTKTTTVNVESEKDNKGKTEVKGATSVYKEKDKLVYTGKDKGENG 209
 241 DVFRTYDVEELSDTKTTTVNVESEKDNKGKTEVKGATSVYKEKDKLVYTGKDKGENG 300
 210 SSTDGEGELVTAKEVIDAVNKAAGRMKTTTANGTGQADKEPTVTSNTVPFASCKGTTA 269
 270 TVSKDDGQNTIVMYDVNVDALNVNQLONGNLDKRAVAGSSGKVIISGNVSPSKGKDE 329
 361 TVSKDDGQNTIVMYDVNVDALNVNQLONGNLDKRAVAGSSGKVIISGNVSPSKGKDE 420
 330 TVNINAGNIEITRNGKNIDATSMTPQSSVSLGAGADAPTLVSDGD-ALNVGSKKDNK 388
 421 TVNINAGNIEITRNGKNIDATSMTPQSSVSLGAGADAPTLVSDGDALNVGSKDANK 480
 369 PVRTTNVAPVYKEGVTVNAQLKGYAONLNRRIDVNDGNARAGIAQAIATAGLVAYLPG 448
 481 PVRTTNVAPVYKEGVTVNAQLKGYAONLNRRIDVNDGNARAGIAQAIATAGLVAYLPG 540
 449 KSMMAIGGCTYRGEAGVYALGYSSISDGNMIIKGTASGNSRCHFGASASVGVOM 502
 541 KSMMAIGGCTYRGEAGVYALGYSSISDGNMIIKGTASGNSRCHFGASASVGVOM 594

RESULT 13
 AAY57044
 ID AAY57044 standard; Protein; 594 AA.
 AC AAY57044;
 XX
 DT 21-FEB-2000 (first entry)
 XX
 DE BAB029 amino acid sequence from N. meningitidis strain ATCC13090.
 XX

KM BAB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis;
 KM infection; treatment; prevent; antibacterial drug.
 XX
 XX Neisseria meningitidis.
 OS
 FH Key location/Qualifiers
 FT Misc-difference 104 /note= "Encoded by AATC"
 XX
 XX WO958683-A2.
 XX
 XX 18-NOV-1999.
 XX
 XX 07-MAY-1999; 99WO-EP03255.
 XX
 XX 13-MAY-1998; 98GB-0010276.
 XX
 XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 XX Ruelle J;
 XX
 XX WPI: 2000-053103/04.
 XX
 XX N-PSDB; AA239864.
 XX
 PT New polypeptide from neisseria meningitidis useful for diagnosis,
 PT treatment or prevention of bacterial infections in mammal
 XX
 XX Claim 4; Fig 2; 74pp; English.
 XX
 CC This is the Nisseria meningitidis BAB029 amino acid sequence from
 CC serogroup B strain ATCC13090. The BAB029 protein is homologous to the
 CC Haemophilus influenzae surface fibril (HSF) protein. The invention
 CC relates to BAB029 polynucleotide sequences (AA239864-239865) and
 CC polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments.
 CC BAB029 polypeptides are useful in a method of diagnosing a Neisseria
 CC meningitidis infection in a mammal. Compositions containing BAB029
 CC polynucleotides and polypeptides are useful for generating an immune
 CC response in an animal. A therapeutic composition comprising an antibody
 CC directed against BAB029 is useful in treating humans with Neisseria
 CC meningitidis disease. The polynucleotide is useful in the diagnosis of
 CC the stage of infection, type of infection, susceptibility to an
 CC infection which results from increased or decreased expression of the
 CC polynucleotide, and for therapeutic or prophylactic purposes.
 CC particularly genetic immunisation. Antibodies against BAB029
 CC polynucleotides and polypeptides are also useful for treating infections
 CC particularly bacterial infections. The protein is useful in the
 CC screening and development of antibacterial drugs. Fused recombinant
 CC protein is useful for the stimulation of the immune system of an organism
 CC receiving the protein.
 CC
 XX
 XX Sequence 594 AA:
 SQ
 Query Match 93.0%; Score 2366; DB 21; Length 594;
 Best Local Similarity 82.0%; Pred. No. 4e-141;
 Matches 487; Conservative 4; Mismatches 11; Indels 92; Gaps 5;

1 MNKIIRIIMNSALNMVAVVSELTNRHTRKASATVAVLATLLEFATVOASAN----- 52
 1 MNKIIRIIMNSALNMVAVVSELTNRHTRKASATVAVLATLLEFATVOASATDDDDLYLE 60
 53 -----TLKAGDNLIKIKO----- 64
 61 PVORTAVVLSFRSDEKTEGEVTEEDSNMVGFFDKGVLTAGTITLKGDNLIKIKONTNE 120
 65 -----FTYSLKKDLTDLTSTGTEKLSFSAANGKNVITSDTRKGLNFAKETAGTNGDTTVH 118
 121 NTNASSFTYSLKKDLTDLTSTGTEKLSFSAANGKNVITSDTRKGLNFAKETAGTNGDTTVH 180
 119 LKIGISLTLD-----RAASVADVNLNAGNINIGVK-----NV 149
 181 LKIGISLTLDLTDLNLTGATTNTNDNVTDDEKKRAASVADVNLNAGNINIGVKPGTTASDNV 240
 150 DVFRTYDVEELSDTKTTTVNVESEKDNKGKTEVKGATSVYKEKDKLVYTGKDKGENG 209

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Db      241 DFWRTYDTVEFLADRTKTTVTNNVESKDKNGKRTVEKIGAKTSVIEKDKGLVTGDKEND 300
Qy      210 SSTDEGEGLVTAKEVIDAVNKAQRMKTTANGOTGOADKEFTVTSCTNTFPASGKGT 269
Db      301 SSTDKGEGLVTAKEVIDAVNKAQRMKTTANGOTGOADKEFTVTSCTNTFPASGKGT 360
Qy      270 TVSKDDGNTVMTDVNVGDLNVLNOLNSGWNLSKAVAGSSGKVTSGNVSPSKGKMD 329
Db      361 TVSKDDGNTVMTDVNVGDLNVLNOLNSGWNLSKAVAGSSGKVTSGNVSPSKGKMD 420
Qy      330 TVNINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLTSDGD-ALNVGSKDKN 388
Db      421 TVNINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLTSDGDALNVGSKDKN 480
Qy      389 PVRTTNVAPGVKESGDVNVNVAOLKGVNOLNLRIDNVGNARAGIAQAIATAGLVQAYLP 448
Db      481 PVRTTNVAPGVKESGDVNVNVAOLKGVNOLNLRIDNVGNARAGIAQAIATAGLVQAYLP 540
Qy      449 KSMMAIGGTYRGEGAGYAGYSSISDGNMIIKGTASGSRGHRGASASVGYOW 502
Db      541 KSMMAIGGTYRGEGAGYAGYSSISDGNMIIKGTASGSRGHRGASASVGYOW 594

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RESULT 14
AAU06174
ID AAU06174 standard; Protein: 594 AA.

XX AAU06174;

DT 24-OCT-2001 (first entry)

DE N. meningitidis EG327 surface antigen Noha polypeptide sequence.

KM Surface antigen Noha; meningococcal disease; meningitis vaccine.

OS Neisseria meningitidis strain EG327.

XX Location/Qualifiers

FT Key

FT Region

FT Region

FT Region

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PR 25-JAN-2000; 2000US-0177917.

XX (UYOU) UNIV QUEENSLAND.

PA Peak IRA, Jennings MP.

PI WPI; 2001-488774/53.

DR N-PSDB; AAS09164.

XX New Noha surface antigen polypeptides and polynucleotides from

PT Neisseria meningitidis, useful in producing vaccines for treating or

PT preventing broad spectrum of Neisseria meningitidis.

PS Claim 9; Fig 1; 91pp; English.

XX The present invention relates to the isolation of novel Neisseria

CC meningitidis mutant polypeptides of the surface antigen Noha

CC (AAU06182-AAU06186). The modified or mutant Noha polypeptides are

CC characterised by deletions of non-conserved amino acids, particularly

CC the deletion of variable regions. The deletion mutants are useful in

CC diagnostics, therapeutic and prophylactic vaccines against a broader

CC spectrum of N. meningitidis, and in designing and/or screening of

CC medicaments. The mutant proteins when used as a vaccine can effectively

CC immunise against a broader spectrum of N. meningitidis strains than

CC would be expected from a corresponding wild-type surface antigen.

CC The present sequence representing the wild type surface antigen Noha

CC from N. meningitidis strain EG327 is 1 of 10 Noha polypeptide sequences

CC (AAU06173-AAU06180) from 10 different N. meningitidis strains given in

CC the present invention.

XX Sequence 594 AA;

SO Query Match 93.0%; Score 2366; DB 22; Length 594;

Best Local Similarity 82.0%; Pred. No. 4e-141;

Matches 487; Conservative 4; Mismatches 11; Indels 92; Gaps 5;

Qy 1 MNKIYRITMNSALNAAVVSSELTNRNHRASATVATVATLLEFATVQASAN----- 52

Db 1 MNKIYRITMNSALNAAVVSSELTNRNHRASATVATVATLLEFATVQASATVQATDDEDDLYLE 60

Qy 53 -----TLKAGDNLTKQ----- 64

Db 61 PVORTAVLSPRSDEKSTGEKEVTEDESNMGVYFPDKGVLTAGITTLKAGDNLTKQNTNE 120

Qy 65 -----FTYSLKQDLDLTSGTEKLSFSAANGKVNITSDPKGTFPAKETAAGTGDPTVH 118

Db 121 NTNASFTYSLKQDLDLTSGTEKLSFSAANGKVNITSDPKGTFPAKETAAGTGDPTVH 180

Qy 119 LMGIGSTLTD-----RAASYKDYLNAGMNIKGVK-----NV 149

Db 181 LMGIGSTLTDLNTGATNTVNTNDVDEKRRASAKVDVLAAGMNIKGVKPGTTASDNV 240

Qy 150 DFWRTYDTVEFLADRTKTTVTNNVESKDKNGKRTVEKIGAKTSVIEKDKGLVTGDKENG 209

Db 241 DFWRTYDTVEFLADRTKTTVTNNVESKDKNGKRTVEKIGAKTSVIEKDKGLVTGDKEND 300

Qy 210 SSTDEGEGLVTAKEVIDAVNKAQRMKTTANGOTGOADKEFTVTSCTNTFPASGKGT 269

Db 301 SSTDKGEGLVTAKEVIDAVNKAQRMKTTANGOTGOADKEFTVTSCTNTFPASGKGT 360

Qy 270 TVSKDDGNTVMTDVNVGDLNVLNOLNSGWNLSKAVAGSSGKVTSGNVSPSKGKMD 329

Db 361 TVSKDDGNTVMTDVNVGDLNVLNOLNSGWNLSKAVAGSSGKVTSGNVSPSKGKMD 420

Qy 330 TVNINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLTSDGD-ALNVGSKDKN 388

Db 421 TVNINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLTSDGDALNVGSKDKN 480

Qy 389 PVRTTNVAPGVKESGDVNVNVAOLKGVNOLNLRIDNVGNARAGIAQAIATAGLVQAYLP 448

Db 481 PVRTTNVAPGVKESGDVNVNVAOLKGVNOLNLRIDNVGNARAGIAQAIATAGLVQAYLP 540

Qy 449 KSMMAIGGTYRGEGAGYAGYSSISDGNMIIKGTASGSRGHRGASASVGYOW 502

Db 301 TDEGGLVTAKEVIDAANKAGRMKTTTANGOTGADKFEYVTSCTNTVTFASGKGTATV 360
Qy 272 SKDDOGNITVMDVNVGDALNVNOLONGMNLDSKAVAGSSGKVTISGNVSPSKGMDET 331
Db 361 SKDDOGNITVMDVNVGDALNVNOLONGMNLDSKAVAGSSGKVTISGNVSPSKGMDET 420
Qy 332 NINAGNNIETFRNGKNIDIAITSMTPQFSSVSLGACADAPTSLVDDALVSGKKKPKVR 391
Db 421 NINAGNNIETFRNGKNIDIAITSMTPQFSSVSLGACADAPTSLVDDALVSGKKKPKVR 480
Qy 392 ITNVPAGYKESGDTVVAOLKGVQNLNRRIDVNDGNARAGIAQAATATAGLVQAYLPKSM 451
Db 481 ITNVPAGYKESGDTVVAOLKGVQNLNRRIDVNDGNARAGIAQAATATAGLVQAYLPKSM 540
Qy 452 MAIGGTYRGEAGYVAGYSSISDGGNWIITKGTASGNSRGHFGASASVGYW 502
Db 541 MAIGGTYRGEAGYVAGYSSISDGGNWIITKGTASGNSRGHFGASASVGYW 591

RESULT 2
US-09-669-974-21
; Sequence 21, Application US/09669974
; Patent No. 6333173

; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-21

Query Match 96.7%; Score 2459.5; DB 4; Length 591;
Best Local Similarity 84.9%; Pred. No. 1.5e-187;
Matches 502; Conservative 0; Mismatches 0; Indels 89; Gaps 4;

Qy 1 MNKIRIIRIWSALNMMVVVSELTNRHTRKASATVKTAVLATLLFATVOASAN----- 52
Db 1 MNKIRIIRIWSALNMMVVVSELTNRHTRKASATVKTAVLATLLFATVOASANNEOEEDL 60
Qy 53 -----TLKAGDNLKIK 64
Db 61 IYLDVQRTVAVLIVNSDEKGEKEKEVEENSDMAVYFNEKGVLTAAREITTLKAGDNLKIK 120
Qy 65 -----FTYSIKKDLDTLSVGTSEKLSFSANGKNVITSDPTGLNFAKETAGTGTTHLN 120
Db 121 NGTNTYELSKKDLDTLSVGTSEKLSFSANGKNVITSDPTGLNFAKETAGTGTTHLN 180
Qy 121 GIGSTLTD-----RAASVKDVLNAGNMIKGVK-----NVDE 151
Db 181 GIGSTLTDLTLNTGATVNTNDNTDDEKRAASVKDVLNAGNMIKGVKPGTTASDNVDE 240
Qy 152 VRTVTFVEFLSADTKTTTVNVESKDKGKTEVKIAKTSYIKERKGLVYTGKDKGENSS 211
Db 241 VRTVTFVEFLSADTKTTTVNVESKDKGKTEVKIAKTSYIKERKGLVYTGKDKGENSS 300
Qy 212 TDEGGLVTAKEVIDAANKAGRMKTTTANGOTGADKFEYVTSCTNTVTFASGKGTATV 271
Db 301 TDEGGLVTAKEVIDAANKAGRMKTTTANGOTGADKFEYVTSCTNTVTFASGKGTATV 360

Qy 272 SKDDOGNITVMDVNVGDALNVNOLONGMNLDSKAVAGSSGKVTISGNVSPSKGMDET 331
Db 361 SKDDOGNITVMDVNVGDALNVNOLONGMNLDSKAVAGSSGKVTISGNVSPSKGMDET 420
Qy 332 NINAGNNIETFRNGKNIDIAITSMTPQFSSVSLGACADAPTSLVDDALVSGKKKPKVR 391
Db 421 NINAGNNIETFRNGKNIDIAITSMTPQFSSVSLGACADAPTSLVDDALVSGKKKPKVR 480
Qy 392 ITNVPAGYKESGDTVVAOLKGVQNLNRRIDVNDGNARAGIAQAATATAGLVQAYLPKSM 451
Db 481 ITNVPAGYKESGDTVVAOLKGVQNLNRRIDVNDGNARAGIAQAATATAGLVQAYLPKSM 540
Qy 452 MAIGGTYRGEAGYVAGYSSISDGGNWIITKGTASGNSRGHFGASASVGYW 502
Db 541 MAIGGTYRGEAGYVAGYSSISDGGNWIITKGTASGNSRGHFGASASVGYW 591

RESULT 3
US-09-377-155-2
; Sequence 2, Application US/09377155
; Patent No. 6197312

; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-2

Query Match 96.5%; Score 2455; DB 3; Length 592;
Best Local Similarity 84.6%; Pred. No. 3.4e-187;
Matches 501; Conservative 0; Mismatches 1; Indels 90; Gaps 4;

Qy 1 MNKIRIIRIWSALNMMVVVSELTNRHTRKASATVKTAVLATLLFATVOASAN----- 52
Db 1 MNKIRIIRIWSALNMMVVVSELTNRHTRKASATVKTAVLATLLFATVOASANNEPRKKD 60
Qy 53 -----TLKAGDNLKIK 63
Db 61 IYLDVQRTVAVLIVNSDEKGEKEKEVEENSDMAVYFNEKGVLTAAREITTLKAGDNLKIK 120
Qy 64 Q-----FTYSIKKDLDTLSVGTSEKLSFSANGKNVITSDPTGLNFAKETAGTGTTHLN 119
Db 121 QNGTNTYELSKKDLDTLSVGTSEKLSFSANGKNVITSDPTGLNFAKETAGTGTTHLN 180
Qy 120 NGIGSTLTD-----RAASVKDVLNAGNMIKGVK-----NVDE 150
Db 181 NGIGSTLTDLTLNTGATVNTNDNTDDEKRAASVKDVLNAGNMIKGVKPGTTASDNVDE 240
Qy 151 FVRTVDFVEFLSADTKTTTVNVESKDKGKTEVKIGARTSYIKERKGLVYTGKDKGENSS 210
Db 241 FVRTVDFVEFLSADTKTTTVNVESKDKGKTEVKIGARTSYIKERKGLVYTGKDKGENSS 300
Qy 211 STDEGGLVTAKEVIDAANKAGRMKTTTANGOTGADKFEYVTSCTNTVTFASGKGTAT 270
Db 301 STDEGGLVTAKEVIDAANKAGRMKTTTANGOTGADKFEYVTSCTNTVTFASGKGTAT 360
Qy 271 VSKDDOGNITVMDVNVGDALNVNOLONGMNLDSKAVAGSSGKVTISGNVSPSKGMDET 330
Db 361 VSKDDOGNITVMDVNVGDALNVNOLONGMNLDSKAVAGSSGKVTISGNVSPSKGMDET 420

OY	331	NNNAGNNIETTRNCKNIDIASMTPOFSSVSLGAGAADPTLSVGDALNVSGKKONKRY	390
Dd	421	VVINAGNNIETTRNCKNIDIASMTPOFSSVSLGAGAADPTLSVGDALNVSGKKONKRY	480
OY	391	RITNAPPVCKEDDVNVAOLKGVAONLNNRIDNVGNARAGIAQAIATATGLVQAYLPGRS	450
Dd	481	RITNAPPVCKEDDVNVAOLKGVAONLNNRIDNVGNARAGIAQAIATATGLVQAYLPGRS	540
OY	451	MMAIIGGYRCGAGYAIGYSISDGGNMWIKGTASGNSRGHGASASVYQW	502
Dd	541	MMAIIGGYRCGAGYAIGYSISDGGNMWIKGTASGNSRGHGASASVYQW	592

RESULT 4
 US-09-669-974-2
 ; Sequence 2, Application US/09669974
 ; Patent No. 6333173
 ; GENERAL INFORMATION:
 ; APPLICANT: PEAK, Ian Richard Anselm
 ; APPLICANT: JENNINGS, Michael Paul
 ; APPLICANT: MOXON, E. Richard
 ; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
 ; FILE REFERENCE: 065064/0128
 ; CURRENT APPLICATION NUMBER: US/09/669, 974
 ; CURRENT FILING DATE: 2000-09-26
 ; PRIOR APPLICATION NUMBER: US 09/377, 155
 ; PRIOR FILING DATE: 1999-08-19
 ; PRIOR APPLICATION NUMBER: PCT/AU98/01031
 ; PRIOR FILING DATE: 1998-12-14
 ; PRIOR APPLICATION NUMBER: GB 9726398.2
 ; PRIOR FILING DATE: 1997-12-12
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 592
 ; TYPE: PRT
 ; ORGANISM: Neisseria meningitidis
 US-09-669-974-2

Query Match	96.5%	Score 2455	DB 4	Length 592
Best Local Similarity	84.6%	Pred. No. 3.4e-187		
Matches 501	Conservative 0	Mismatches 1	Indels 90	Gaps 4
QY	1	MNKIYRIIWSALNAMYVSEITRNHTRRASATVKTAVLATLLEATVQASAN-----	52	
Db	1	MNKIYRIIWSALNAMYVSEITRNHTRRASATVKTAVLATLLEATVQASANNEPRKKD	60	
QY	53	-----TLKAGDNLIK	63	
Db	61	LYLDPVORTVAVLIYNSDEKSTGEKEKVENSDMAVYFNEKGVLAREITLTKAGDNLIK	120	
QY	64	Q-----FPTSLKKDLDTLTSVGETEKSEFSANGKNVITSDTGLNFAKETAGNGTPTVHL	119	
Db	121	QNGIRFTYSLKKDLDTLTSVGETEKSEFSANGKNVITSDTGLNFAKETAGNGTPTVHL	180	
QY	120	NGISGTLD-----RAASVKVVLNAGWIRIKGVK-----NVD	150	
Db	181	NGISGTLDLTLNGATLNTNDVNTDDEKKRAASVKVVLNAGWIRIKGVKGTASDND	240	
QY	151	FVRITDIYEFISADTKITTTVANVESKDNGKRTIEVIGACTSVIKEKDKLVTGDKGNGS	210	
Db	241	FVRITDIYEFISADTKITTTVANVESKDNGKRTIEVIGACTSVIKEKDKLVTGDKGNGS	300	
QY	211	STDEGEGLVTPAKEVIDAVNKKAGMRKTTTANGOTGOAKPEFVNSGTVWTFASGKGTAT	270	
Db	301	STDBEGGLVTPAKEVIDAVNKKAGMRKTTTANGOTGOAKPEFVNSGTVWTFASGKGTAT	360	
QY	271	VSKDDQGNITWYDVNVGDALNVNQLQSGNWLJSKAAVSSGKVIISGNVSPSKKMDET	330	
Db	361	VSKDDQGNITWYDVNVGDALNVNQLQSGNWLJSKAAVSSGKVIISGNVSPSKKMDET	420	
QY	331	VWNAAGNIEITRNKNTDIATSMTPQFSSVSLGADAPTLSDGDALNVSCKDNKPV	390	

Db 421 VNINANGNNIEITRNRCKNIDIAIATSMTPQFSVSVALGADAPLTVSDGADALNVGSKKONKPEY 480

Qy 391 RITNPAPEVKEDDPTNVAOLKGVADLNNLRINDVGNARAGTAAATATAGIYQATYLPGRS 450

Db 481 RITNPAPEVKEDDPTNVAOLKGVADLNNLRINDVGNARAGTAAATATAGIYQATYLPGRS 540

Qy 451 MMAIGGGYKGEAGYALIGSSISDGGNWTIKCTAGSNGKGFHGAASVGYQW 502

Db 541 MMAIGGGYKGEAGYALIGSSISDGGNWTIKCTAGSNGSKGHFGAASVGYQW 592

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RESULT 5
US-09-377-155-11
: Sequence 11, Application US/09377155
: Patent No. 6197312
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/377, 155
: CURRENT FILING DATE: 1995-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 11
:
: LENGTH: 591
:
: TYPE: PRT
:
: ORGANISM: Neisseria meningitidis
:
: US-09-377-155-11

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Query	Match	Similarity	Score	24.47-51	DB: 3	Length	591
Best Local	Similarity	84.6%	Pred. 1.3e-186				
Matches	500	Conservative	1	Mismatches	1	Indels	89
							Gaps
							4
Qy	1	MNKIYRIIWNLSALNAAVVVSELTNRNHRKASATYKTAVALATLTFATVOASAN-----	52				
Db	1	MNEILRIIWNLSALNAAVVVSELTNRNHRKASATYKTAVALATLTFATVOASANEQEDL	60				
Qy	53	-----TLRAGDLKIKIQ 64					
Db	61	YLDPLRTVAALLVNSDKEGTEKEKEVEENSDMAVYFNEKGVLAREITLAAGDMLKIQ 120					
Qy	65	---FTYSLLKDLIDLITSVGTETKLSFSANGNKVNITSPDKLNFKAETAGTNGDPTVHLN 120					
Db	121	NGTNFTYSLKKDLIDLITSVGTETKLSFSANGNKVNITSPDKLNFKAETAGTNGDPTVHLN 180					
Qy	121	GIGSTLND-----RAASYKDVLLNAGNINIKYK-----NDF 151					
Db	181	GIGSTLIDDTLLNTGATNTVTDNDVYTDDEKKRAASYKDVLLNAGNINIKYKPGTFTASDND 240					
Qy	152	VRTDYVTEFLSADRTTTTVNYESKONGKKTETKICAKTSYLKERKGLVYTGDKDENGSS 211					
Db	241	VRTDYVTEFLSADRTTTTVNYESKONGKKTETKICAKTSYLKERKGLVYTGDKDENGSS 300					
Qy	212	TDEGEGLVTAKEVIDAANKAGMRKMTTANGOTGOADFEETVSGTNVTFASGKGTATV 271					
Db	301	TDEGEGLVTAKEVIDAANKAGMRKMTTANGOTGOADFEETVSGTNVTFASGKGTATV 360					
Qy	272	SKDOGNTITVAADVAVGALAVNQLQNSGWNLDAAVAGSSSKVTSISGVNSPBGKMDREV 331					
Db	361	SKDOGNTITVAADVAVGALAVNQLQNSGWNLDAAVAGSSSKVTSISGVNSPBGKMDREV 420					
Qy	332	NINAGNNIEIIRNCKNIDIAISMTPQFSSVSLGAGADAPTLSVDDALANVSGKKNKPEVR 391					
Db	421	NINAGNNIEIIRNCKNIDIAISMTPQFSSVSLGAGADAPTLSVDDALANVSGKKNKPEVR 480					
Qy	392	ITNAAPGVKEGDVTVAQLKGAQVQNLNRRIDNVGDNARAGIAQAIATAGLVQAYLPGKSM 451					

Db 481 ITNAPGVKESDVTNVAQLKGVANLNNRIDNVDGNARAGIAQAIALATAGLVQAYLPGRSM 540
Qy 452 MAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 502
Db 541 MAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 591

RESULT 6
US-09-669-974-11
; Sequence 11, Application US/09669974
; Patent No. 6333173

GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-11

Query Match 96.2%; Score 2447.5; DB 4; Length 591;
Best Local Similarity 84.6%; Pred. No. 1.3e-186;
Matches 500; Conservative 1; Mismatches 1; Indels 89; Gaps 4;

Qy 1 MNKIYRIIWSNALNAVYVSELTRNHTKRASATYKAVLATLLFATVOASAN----- 52
Db 1 MNELIRIIMNSALNAVYVSELTRNHTKRASATYKAVLATLLFATVOASANNEQEBDL 60
Qy 53 -----TLKAGNLKIKQ 64
Db 61 YLDPLRTVAALVINSDEKTEKEKEVENSMDWAYFENEKGLTAREITLAKGDMLKIKQ 120
Qy 65 -----FTYSLKLDLTLVSYTEKLSFSANGKVKNTSPTKGLNFAKETAGTGTTHLN 120
Db 121 NGTNFTYSLKLDLTLVSYTEKLSFSANGKVKNTSPTKGLNFAKETAGTGTTHLN 180
Qy 121 GIGSLTD-----RAASYKDVNLNAGWNKIGVK-----NYDF 151
Db 181 GIGSLTDTLNTGATNTVNDNTYDDEKRAASVKDVLNAGWNKIGVKPGTTASDNDF 240
Qy 152 VRTDYVEFLSADTKTTTVNVEESKDNKKTEVKIGAKTSVIERKDGKLVTKGKENGSS 211
Db 241 VRTDYVEFLSADTKTTTVNVEESKDNKKTEVKIGAKTSVIERKDGKLVTKGKENGSS 300
Qy 212 TDEGGLTAKEDVDAVNAKGRMKTITANGOTGADFEVYTGSTNTFASGKGTATV 271
Db 301 TDEGGLTAKEDVDAVNAKGRMKTITANGOTGADFEVYTGSTNTFASGKGTATV 360
Qy 272 SKDDGNTTVADVAVGDLNVLNOLONGSNMILDSKAVVSGSKYISGVNVSFKGMDPTV 331
Db 361 SKDDGNTTVADVAVGDLNVLNOLONGSNMILDSKAVVSGSKYISGVNVSFKGMDPTV 420
Qy 332 NINAGNNIETIRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDGALNVGSKKDNKPEVR 391
Db 421 NINAGNNIETIRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDGALNVGSKKDNKPEVR 480
Qy 392 ITNAPGVKESDVTNVAQLKGVANLNNRIDNVDGNARAGIAQAIALATAGLVQAYLPGRSM 451
Db 481 ITNAPGVKESDVTNVAQLKGVANLNNRIDNVDGNARAGIAQAIALATAGLVQAYLPGRSM 540

Qy 452 MAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 502
Db 541 MAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 591

RESULT 7
US-09-377-155-15
; Sequence 15, Application US/09377155
; Patent No. 6197312

GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-15

Query Match 93.2%; Score 2371.5; DB 3; Length 599;
Best Local Similarity 81.6%; Pred. No. 1.5e-180;
Matches 489; Conservative 2; Mismatches 11; Indels 97; Gaps 5;

Qy 1 MNKIYRIIWSNALNAVYVSELTRNHTKRASATYKAVLATLLFATVOASAN----- 52
Db 1 MNKIYRIIWSNALNAVYVSELTRNHTKRASATYKAVLATLLFATVOANNTDEDEEBEL 60
Qy 53 -----TLKAGNLKIKQ 64
Db 61 EPVYASALVQPMIDKEGNGENESTGNIGWISYDNNHTLHGATVYTLKAGNLKIKQNTN 120
Qy 65 -----FTYSLKLDLTLVSYTEKLSFSANGKVKNTSPTKGLNFAKETAGTNG 113
Db 121 KTNENTNDSSFTYSLKLDLTLVSYTEKLSFGANGKVKNTSPTKGLNFAKETAGTNG 180
Qy 114 DTYVHLNGIGSLTD-----RAASYKDVNLNAGWNKIGVK----- 147
Db 181 DTYVHLNGIGSLTD-----RAASYKDVNLNAGWNKIGVK----- 240
Qy 148 --NDFVRYDYVEFLSADTKTTTVNVEESKDNKKTEVKIGAKTSVIERKDGKLVTKGD 204
Db 241 ASDNDFVRYDYVEFLSADTKTTTVNVEESKDNKKTEVKIGAKTSVIERKDGKLVTKGD 300
Qy 205 KGENSSYDEGGLTAKEDVDAVNAKGRMKTITANGOTGADFEVYTGSTNTFASG 264
Db 301 KGENSSYDEGGLTAKEDVDAVNAKGRMKTITANGOTGADFEVYTGSTNTFASG 360
Qy 265 KGTATVSKDDGNTTVADVAVGDLNVLNOLONGSNMILDSKAVVSGSKYISGVNVSFK 324
Db 361 KGTATVSKDDGNTTVADVAVGDLNVLNOLONGSNMILDSKAVVSGSKYISGVNVSFK 420
Qy 325 GKMDPTVINAGNNIETIRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDGALNVG 383
Db 421 GKMDPTVINAGNNIETIRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDGALNVG 480
Qy 384 KDNKPEVRITNAPGVKESDVTNVAQLKGVANLNNRIDNVDGNARAGIAQAIALATAGLVQ 443
Db 481 KDNKPEVRITNAPGVKESDVTNVAQLKGVANLNNRIDNVDGNARAGIAQAIALATAGLVQ 540
Qy 444 AYLPEKSMALIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 502
Db 541 AYLPEKSMALIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 599

RESULT 8
US-09-669-974-15
; Sequence 15, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-15

Query Match 93.28; Score 2371.5; DB 4; Length 599;
Best Local Similarity 81.68; Pred. No. 1.5e-180;
Matches 489; Conservative 2; Mismatches 11; Indels 97; Gaps 5;

QY 1 MNKIRIIMNSALNANWVSELTNRHTRKASATVATVLTLLFATVQASAN----- 52
DB 1 MNKIRIIMNSALNANWVSELTNRHTRKASATVATVLTLLFATVQASANDEDEEEL 60
QY 53 -----TLKAGDNLIKQ----- 64
DB 61 EPVRSALVLOFMIDKEGNGENESTGNIGSIYYDNHNTLHGATVTLKAGDNLIKQNTN 120
QY 65 -----FTYSLKKDLDLTLSVTEKLSFSANGKNVNTSDTKGLNFAKETAGTNG 113
DB 121 KNTNENTNDSFTYSLKKDLDLTLSVTEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180
QY 114 DTTVHLNGISLTLD-----RAASVKDVLNAGNNIKGVK----- 147
DB 181 DTTVHLNGISLTLDLTNTGATTNTVNDVNTDCKKRAASVKDVLNAGNNIKGVKGT 240
QY 148 ---NVDFVRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSVYIKKDKGLVTGKD 204
DB 241 ASDNVDFVRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSVYIKKDKGLVTGKG 300
QY 205 KGENGSSTDEGEGLVTAKEVIDAVNKAQGMKTTTANGOTGADKFEVTSNTVTFASG 264
DB 301 KGENGSSTDEGEGLVTAKEVIDAVNKAQGMKTTTANGOTGADKFEVTSNTVTFASG 360
QY 265 KGTATATSKDQGNITFYMYDVNVDALNVNOLONGSNLDSKAVAGSSGVISGNVPSK 324
DB 361 KGTATATSKDQGNITFYMYDVNVDALNVNOLONGSNLDSKAVAGSSGVISGNVPSK 420
QY 325 GKMDETVNIAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLISVDG--DALNVGS 383
DB 421 GKMDETVNIAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLISVDGKALNVGS 480
QY 384 KKNKPPRTTNVAPVKEGSDVTVNQAOLKGYAQNINNRIDVNDGNARAGIAQATAGLVQ 443
DB 481 KDNKPPRTTNVAPVKEGSDVTVNQAOLKGYAQNINNRIDVNDGNARAGIAQATAGLVQ 540
QY 444 AYLPGKSMALIGGTYRGEAGYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 502
DB 541 AYLPGKSMALIGGTYRGEAGYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 599

RESULT 9

US-09-377-155-9
; Sequence 9, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-9

Query Match 93.08; Score 2366; DB 3; Length 594;
Best Local Similarity 82.08; Pred. No. 4.1e-180;
Matches 487; Conservative 4; Mismatches 11; Indels 92; Gaps 5;

QY 1 MNKIRIIMNSALNANWVSELTNRHTRKASATVATVLTLLFATVQASAN----- 52
DB 1 MNKIRIIMNSALNANWVSELTNRHTRKASATVATVLTLLFATVQASANDEDDLYLE 60
QY 53 -----TLKAGNLKIKQ----- 64
DB 61 PVQRTAVVLSFRSDKEGTGEKTEVEDSNMGVYFDPKKCVLAGTITLLAAGDNLIKQVNE 120
QY 65 -----FTYSLKKDLDLTLSVTEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVH 118
DB 121 NTNASFTYSLSKKDLDLTLSVTEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVH 180
QY 119 LNGISLTLD-----RAASVKDVLNAGNNIKGVK-----NV 149
DB 181 LNGISLTLDLTNTGATTNTVNDVNTDCKKRAASVKDVLNAGNNIKGVKPGTTASDNV 240
QY 150 DVEVRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSVYIKKDKGLVTGDKGNG 209
DB 241 DVEVRTYDVEFLSADTKTTTVNVEESKDKGKTEVKIGAKTSVYIKKDKGLVTGDKGEND 300
QY 210 SSTDEGEGLVTAKEVIDAVNKAQGMKTTTANGOTGADKFEVTSNTVTFASGKGT 269
DB 301 SSTDEGEGLVTAKEVIDAVNKAQGMKTTTANGOTGADKFEVTSNTVTFASGKGT 360
QY 270 TVSKDQGNITVMDVNVGALNVNOLONGSNLDSKAVAGSSGVISGNVPSKGMDE 329
DB 361 TVSKDQGNITVMDVNVGALNVNOLONGSNLDSKAVAGSSGVISGNVPSKGMDE 420
QY 330 TVNINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLISVDG--ALNVSSKDNK 388
DB 421 TVNINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLISVDGKALNVSSKDNK 480
QY 389 PVRTTNVAPVKEGSDVTVNQAOLKGYAQNINNRIDVNDGNARAGIAQATAGLVQAVLP 448
DB 481 PVRTTNVAPVKEGSDVTVNQAOLKGYAQNINNRIDVNDGNARAGIAQATAGLVQAVLP 540
QY 449 KSMALIGGTYRGEAGYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 502
DB 541 KSMALIGGTYRGEAGYAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 594

RESULT 10
US-09-669-974-9
; Sequence 9, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm
 ; APPLICANT: JENNINGS, Michael Paul
 ; APPLICANT: MOXON, E. Richard
 ; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
 ; FILE REFERENCE: 065064/0128
 ; CURRENT APPLICATION NUMBER: US/09/669,974
 ; PRIORITY FILING DATE: 2000-09-26
 ; PRIOR APPLICATION NUMBER: US 09/377,155
 ; PRIOR FILING DATE: 1999-08-19
 ; PRIOR APPLICATION NUMBER: PCT/AU98/01031
 ; PRIOR FILING DATE: 1998-12-14
 ; PRIOR APPLICATION NUMBER: GB 9726398.2
 ; PRIOR FILING DATE: 1997-12-12
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 9
 ; LENGTH: 594
 ; TYPE: PRT
 ; ORGANISM: Neisseria meningitidis
 ; US-09-669-974-9

Query Match 93.0%; Score 2366; DB 4; Length 594;
 Best Local Similarity 82.0%; Pred. No. 4,1e-180;
 Matches 487; Conservative 4; Mismatches 11; Indels 92; Gaps 5;

QY 1 MNKIRIITNSALNMAVVSSELTNRNHTKRASATVATLTLFATVOASAN----- 52
 DB 1 MNKIRIITNSALNMAVVSSELTNRNHTKRASATVATLTLFATVOASATDDDDLYLE 60
 QY 53 -----TLKAGDNLIKIQ----- 64
 DB 61 PVQRTAVVLSFRSDEKGEKTEEDSMWVYFDEKRVLKAGATITLKAGDNLIKIQNTNE 120
 QY 65 -----FTYSLAKDLTDLTSVTEKLSFSAANGKNVITSDTKGLNFAKETAGTNGDTVH 118
 DB 121 NTNASSFTYSLAKDLTDLTSVTEKLSFSAANGKNVITSDTKGLNFAKETAGTNGDTVH 180
 QY 119 LINGISSTLTLD-----RAASVADVNLNAGNINIGVK-----NV 149
 DB 181 LINGISSTLTDLTLNLTGATTNTNDVNTDEKKRAASVADVNLNAGNINIGVKPGTTASDV 240
 QY 150 DEVRTYDVEFLSADTKTTTVNVEESKDKGKTEVRIKAGTSYIKERDKLVTGKDKENG 209
 DB 241 DEVRTYDVEFLSADTKTTTVNVEESKDKGKTEVRIKAGTSYIKERDKLVTGKDKENG 300
 QY 210 SSTDEGELVTAKEVIDAVNKAAGRMKTTTANGOTGOADKFEFTVSGTNVTFASGKGT 269
 DB 301 SSTDEGELVTAKEVIDAVNKAAGRMKTTTANGOTGOADKFEFTVSGTNVTFASGKGT 360
 QY 270 TVSKDQDGNITVYVNVNVDALNVNQLONGNLDLSKAVAGSSGKVIISGNVSPSKGKDE 329
 DB 361 TVSKDQDGNITVYVNVNVDALNVNQLONGNLDLSKAVAGSSGKVIISGNVSPSKGKDE 420
 QY 330 TVNINAGNNIETTRNGKNIDITATSMTPQSSVSLGAGADAPTLVSDGD-ALNVGSKDNK 388
 DB 421 TVNINAGNNIETTRNGKNIDITATSMTPQSSVSLGAGADAPTLVSDGDALNVGSKDNK 480
 QY 389 PVRTINVAAPVKEGQVTVNAOLKGYAONLNNRIDVNDGNARAGIAQIATATAGLVAYLP 448
 DB 481 PVRTINVAAPVKEGQVTVNAOLKGYAONLNNRIDVNDGNARAGIAQIATATAGLVAYLP 540
 QY 449 KSMAIIGGTYRGEAGYALIGYSSISDGNMIITKGTASNSRCHFGASASVGYOW 502
 DB 541 KSMAIIGGTYRGEAGYALIGYSSISDGNMIITKGTASNSRCHFGASASVGYOW 594

RESULT 11
 US-09-377-155-7
 ; Sequence 7, Application US/09377155
 ; Patent No. 6197312
 ; GENERAL INFORMATION:
 ; APPLICANT: PEAK, Ian Richard Anselm
 ; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard
 ; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
 ; FILE REFERENCE: 065064/0128
 ; CURRENT APPLICATION NUMBER: US/09/377,155
 ; PRIORITY FILING DATE: 1999-08-19
 ; PRIOR APPLICATION NUMBER: PCT/AU98/01031
 ; PRIOR FILING DATE: 1998-12-14
 ; PRIOR APPLICATION NUMBER: GB 9726398.2
 ; PRIOR FILING DATE: 1997-12-12
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 594
 ; TYPE: PRT
 ; ORGANISM: Neisseria meningitidis
 ; US-09-377-155-7

Query Match 92.7%; Score 2359; DB 3; Length 594;
 Best Local Similarity 82.0%; Pred. No. 1,5e-179;
 Matches 487; Conservative 2; Mismatches 13; Indels 92; Gaps 5;

QY 1 MNKIRIITNSALNMAVVSSELTNRNHTKRASATVATLTLFATVOASAN----- 52
 DB 1 MNKIRIITNSALNMAVVSSELTNRNHTKRASATVATLTLFATVOANATDDDDLYLE 60
 QY 53 -----TLKAGDNLIKIQ----- 64
 DB 61 PVQRTAVVLSFRSDEKGEKTEEDSMWVYFDEKRVLKAGATITLKAGDNLIKIQNTNE 120
 QY 65 -----FTYSLAKDLTDLTSVTEKLSFSAANGKNVITSDTKGLNFAKETAGTNGDTVH 118
 DB 121 NTNASSFTYSLAKDLTDLTSVTEKLSFSAANGKNVITSDTKGLNFAKETAGTNGDTVH 180
 QY 119 LINGISSTLTLD-----RAASVADVNLNAGNINIGVK-----NV 149
 DB 181 LINGISSTLTDLTLNLTGATTNTNDVNTDEKKRAASVADVNLNAGNINIGVKPGTTASDV 240
 QY 150 DEVRTYDVEFLSADTKTTTVNVEESKDKGKTEVRIKAGTSYIKERDKLVTGKDKENG 209
 DB 241 DEVRTYDVEFLSADTKTTTVNVEESKDKGKTEVRIKAGTSYIKERDKLVTGKDKENG 300
 QY 210 SSTDEGELVTAKEVIDAVNKAAGRMKTTTANGOTGOADKFEFTVSGTNVTFASGKGT 269
 DB 301 SSTDEGELVTAKEVIDAVNKAAGRMKTTTANGOTGOADKFEFTVSGTNVTFASGKGT 360
 QY 270 TVSKDQDGNITVYVNVNVDALNVNQLONGNLDLSKAVAGSSGKVIISGNVSPSKGKDE 329
 DB 361 TVSKDQDGNITVYVNVNVDALNVNQLONGNLDLSKAVAGSSGKVIISGNVSPSKGKDE 420
 QY 330 TVNINAGNNIETTRNGKNIDITATSMTPQSSVSLGAGADAPTLVSDGD-ALNVGSKDNK 388
 DB 421 TVNINAGNNIETTRNGKNIDITATSMTPQSSVSLGAGADAPTLVSDGDALNVGSKDNK 480
 QY 389 PVRTINVAAPVKEGQVTVNAOLKGYAONLNNRIDVNDGNARAGIAQIATATAGLVAYLP 448
 DB 481 PVRTINVAAPVKEGQVTVNAOLKGYAONLNNRIDVNDGNARAGIAQIATATAGLVAYLP 540
 QY 449 KSMAIIGGTYRGEAGYALIGYSSISDGNMIITKGTASNSRCHFGASASVGYOW 502
 DB 541 KSMAIIGGTYRGEAGYALIGYSSISDGNMIITKGTASNSRCHFGASASVGYOW 594

RESULT 12
 US-09-669-974-7
 ; Sequence 7, Application US/09669974
 ; Patent No. 6333173
 ; GENERAL INFORMATION:
 ; APPLICANT: PEAK, Ian Richard Anselm
 ; APPLICANT: JENNINGS, Michael Paul
 ; APPLICANT: MOXON, E. Richard
 ; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
 ; FILE REFERENCE: 065064/0128
 ; CURRENT APPLICATION NUMBER: US/09/669,974

PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PRF
; ORGANISM: Neisseria meningitidis
US-09-669-974-13

Query Match 92.1%; Score 2344; DB 4; Length 598;
Best Local Similarity 80.9%; Pred. No. 2.3e-178;
Matches 484; Conservative 3; Mismatches 15; Indels 96; Gaps 5;

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QY 1 MNKIRIIMNSALNMAVYSELTRNHTKRASATVATLTLFATVOASAN----- 52
DB 1 MNKIRIIMNSALNMAVYSELTRNHTKRASATVATLTLFATVOANATDDDDLYLE 60
QY 53 -----TLKAGDNLIKIQ----- 64
DB 61 PVQRTAVVLSFRSDEKGEKTEGSDSNMAYVFDEKRVLKAGATILKAGDNLIKIQNTNE 120
QY 65 -----FTYSLKKDLTDLTSVTEKLSFSGANGKNVITSDTKGLNFAKETAGTNGD 114
DB 121 NTNENTNDSFTYSLKKDLTDLTSVTEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
QY 115 TTVHLNGIGSTLTD-----RAASVKDVLNAGNNIGVK----- 147
DB 181 PTVHLNGIGSTLTDLTLNTGATTNTNDVTDDEKRAASVADVNLNAGNNIGVKPGTTA 240
QY 148 --NVDVFRTYDVEFLSADTKTTVNVESKDKNGKTEVKIGAKTSVIREKDKLVTGKDK 205
DB 241 SDNVDFRTYDVEFLSADTKTTVNVESKDKNGKTEVKIGAKTSVIREKDKLVTGKDK 300
QY 206 GENGSSTDEBGLVTAKEVIDAVNKAQWPKTTTANGOTGQADKEFTYSGTNTVPASGK 265
DB 301 DENGSTDEBGLVTAKEVIDAVNKAQWPKTTTANGOTGQADKEFTYSGTNTVPASGN 360
QY 266 GTTATVSKDDQGNITVMTDVNVGDLNVLNQLNSGMNIDSKAVAGSSGKVISGNVSPSG 325
DB 361 GTTATVSKDDQGNITVMTDVNVGDLNVLNQLNSGMNIDSKAVAGSSGKVISGNVSPSG 420
QY 326 KMDETVNIAGNNIEITRNGKNIDTATSMTPQFSSVSGAGADAPTLVSDDGALNVGSK 384
DB 421 KMDETVNIAGNNIEITRNGKNIDTATSMTPQFSSVSGAGADAPTLVSDDGALNVGSK 480
QY 385 KDNKVRITTNVAPGVEGDTVNAOLKGYAQNLRNIDVNDGNARAGIAQATATAGLYOA 444
DB 481 DANKVRITTNVAPGVEGDTVNAOLKGYAQNLRNIDVNDGNARAGIAQATATAGLYOA 540
QY 445 YLPGRSMAAIGGGTYRGEAGVTAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 502
DB 541 YLPGRSMAAIGGGTYRGEAGVTAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 598
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RESULT 15
US-09-377-155-5
; Sequence 5, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377.155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5

LENGTH: 598
; TYPE: PRF
; ORGANISM: Neisseria meningitidis
US-09-377-155-5

Query Match 91.8%; Score 2335; DB 3; Length 598;
Best Local Similarity 80.6%; Pred. No. 1.2e-177;
Matches 482; Conservative 4; Mismatches 16; Indels 96; Gaps 5;

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QY 1 MNKIRIIMNSALNMAVYSELTRNHTKRASATVATLTLFATVOASAN----- 52
DB 1 MNKIRIIMNSALNMAVYSELTRNHTKRASATVATLTLFATVOANATDDDDLYLE 60
QY 53 -----TLKAGDNLIKIQ----- 64
DB 61 PVQRTAVVLSFRSDEKGEKTEGSDSNMAYVFDEKRVLKAGATILKAGDNLIKIQNTNE 120
QY 65 -----FTYSLKKDLTDLTSVTEKLSFSGANGKNVITSDTKGLNFAKETAGTNGD 114
DB 121 NTNENTNDSFTYSLKKDLTDLTSVTEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
QY 115 TTVHLNGIGSTLTD-----RAASVKDVLNAGNNIGVK----- 147
DB 181 PTVHLNGIGSTLTDLTLNTGATTNTNDVTDDEKRAASVADVNLNAGNNIGVKPGTTA 240
QY 148 --NVDVFRTYDVEFLSADTKTTVNVESKDKNGKTEVKIGAKTSVIREKDKLVTGKDK 205
DB 241 SDNVDFRTYDVEFLSADTKTTVNVESKDKNGKTEVKIGAKTSVIREKDKLVTGKDK 300
QY 206 GENGSSTDEBGLVTAKEVIDAVNKAQWPKTTTANGOTGQADKEFTYSGTNTVPASGK 265
DB 301 DENGSTDEBGLVTAKEVIDAVNKAQWPKTTTANGOTGQADKEFTYSGTNTVPASGN 360
QY 266 GTTATVSKDDQGNITVMTDVNVGDLNVLNQLNSGMNIDSKAVAGSSGKVISGNVSPSG 325
DB 361 GTTATVSKDDQGNITVMTDVNVGDLNVLNQLNSGMNIDSKAVAGSSGKVISGNVSPSG 420
QY 326 KMDETVNIAGNNIEITRNGKNIDTATSMTPQFSSVSGAGADAPTLVSDDGALNVGSK 384
DB 421 KMDETVNIAGNNIEITRNGKNIDTATSMTPQFSSVSGAGADAPTLVSDDGALNVGSK 480
QY 385 KDNKVRITTNVAPGVEGDTVNAOLKGYAQNLRNIDVNDGNARAGIAQATATAGLYOA 444
DB 481 DANKVRITTNVAPGVEGDTVNAOLKGYAQNLRNIDVNDGNARAGIAQATATAGLYOA 540
QY 445 YLPGRSMAAIGGGTYRGEAGVTAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 502
DB 541 YLPGRSMAAIGGGTYRGEAGVTAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 598
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Search completed: October 6, 2003, 09:35:51
JOB time : 15.4245 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:35 ; Search time 14.3699 Seconds
(without alignments)
3359.577 Million cell updates/sec

Title: US-09-771-382-27
Perfect score: 2544
Sequence: 1 MNKIYRIIWNLSALNAMYVVS.....TASGNSRGHFASASVGYQW 502

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2459.5	96.7	591	2 G81133	adhesin NMB0992 [i
2	2351	92.4	592	2 A81888	adhesin surface f
3	523.5	20.6	298	2 I64138	adhesin homolog HI
4	380.5	15.0	1190	2 A82615	surface protein XF
5	360.5	14.2	1588	2 A86036	probable adhesin z
6	350.5	14.2	1588	2 H91188	probable adhesin E
7	358.5	14.1	2059	2 D82671	surface protein XF
8	351.5	13.8	1107	2 AC0976	probable autotrans
9	346.5	13.6	658	2 AH0110	probable surface p
10	226.5	8.9	1325	2 A64905	yadek protein - Esc
11	224.5	8.8	1004	2 C82672	surface-exposed h
12	210.5	8.3	1910	2 AF0394	probable adhesin h
13	210	8.3	1286	2 S28634	adhesin ALDA-I pre
14	208.5	8.2	1343	2 E90893	hypothetical prote
15	208	8.2	1091	2 G64964	hypothetical prote
16	203.5	8.0	1343	2 D85724	hypothetical prote
17	197	7.7	1018	2 H83135	probable adhesin p
18	194	7.6	936	2 I40711	sapB protein - Cam
19	192	7.5	1417	2 A83080	hypothetical prote
20	192	7.5	3705	2 AD0123	probable autotrans
21	192	7.5	4919	2 T31105	hypothetical prote
22	191	7.5	1536	2 A43855	high-molecular-we
23	190	7.5	949	2 D90803	ALDA-I adhesin-lik
24	188.5	7.4	1005	2 H85611	probable adhesin z
25	188.5	7.4	365	2 AB3486	cell surface prote
26	188.5	7.4	1477	2 AB3486	high-molecular-we
27	185.5	7.3	585	2 P90961	flagellin [Importe
28	185.5	7.3	585	2 F85809	hypothetical prote
29	185.5	7.3	5291	2 F90696	hypothetical prote

30	183.5	7.2	1335	2 T17508	glycoprotein Vp260
31	182.5	7.2	920	2 I40614	surface array prot
32	181	7.1	584	2 C48658	flagellin - Escher
33	181	7.1	3029	2 S76109	hypothetical prote
34	180.5	7.1	5188	2 B85347	probable RTX fam11
35	180	7.1	1109	2 A56143	surface-array prot
36	180	7.1	3013	2 AB0480	adhesin/invasin y
37	178.5	7.0	364	2 A81019	probable adhesin z
38	176.5	6.9	1341	2 H98323	hypothetical prote
39	176	6.9	1275	2 T33369	hypothetical prote
40	175.5	6.9	2020	2 C48399	ABC-type transport
41	174	6.8	1487	2 A62560	hypothetical prote
42	173	6.8	1608	2 A28182	hemolysin A - Serr
43	173	6.8	2249	2 A41477	190K surface antiq
44	172.5	6.8	1366	2 S57664	IGA-specific metal
45	172	6.8	1369	2 T17504	hypothetical prote

ALIGNMENTS

RESULT 1					
G81133					
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)					
C:Species: Neisseria meningitidis					
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001					
C:Accession: G81133					
R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qiu, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masiugnani, V.; Pizze, M. Science 287, 1809-1815, 2000					
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappapoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: A81000; MUID:20175755; PMID:10710307					
A:Accession: G81133					
A:Status: preliminary					
A:Molecule type: DNA					
A:Residues: 1-591 <TEF>					
A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAI41395.1; PID:g722					
A:Experimental source: serogroup B, strain MC58					
C:Genetics: A:Gene: NMB0992					
Query Match	96.7%	Score 2459.5	DB 2	Length 591	
Best Local Similarity	84.9%	Pred. No. 5.8e-124			
Matches 502	Conservative 0	Mismatches 0	Indels 89	Gaps 4	
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DB	1	MNKIYRIIWNLSALNAMYVVS	ELTRNHTRKASATVKTAVLATLFPATVOASAN	NEGEEDL	60
QY	53	-----	-----	TLACGNLAKIKQ	64
DB	61	YLDEPQRTVAVLIVNSDEKTEGTEKKEEENSDMAVYENKGVLTAREITLAKGDNLEKIKQ			120
QY	65	-----FTYSLKKDLFDLISVGTSEKLSFSANGKRVNITSPTGKLNPAKETAAGNGDTYHLN			120
DB	121	NGTFTYSLKKDLFDLISVGTSEKLSFSANGKRVNITSPTGKLNPAKETAAGNGDTYHLN			180
QY	121	GIGSTLND	-----FAASVKDVLNAGNIIKGVK	-----NVDF	151
DB	181	GIGSTLNDTLTNGGATTTNVTNDVTTDDEKKRAASVQDVLNAGNIIKGVKPTTASDNVDF			240
QY	152	VRTDYVEFLSADTKTTTVNYESKDNKGKTYKIGAKTSVYKEKDGKLYTKDKGENGSS			211
DB	241	VRTDYVEFLSADTKTTTVNYESKDNKGKTYKIGAKTSVYKEKDGKLYTKDKGENGSS			300
QY	212	TDEEGVLTAKEVVIDAVNKKAGRMKTTTANGCQADFEFTVSGTNTVTFASGKTATV			271
DB	301	TDEEGVLTAKEVVIDAVNKKAGRMKTTTANGCQADFEFTVSGTNTVTFASGKTATV			360
QY	272	SKDDGNTVYVDVNGDALNVNOLNSGWNLDKRAVAGSSGKVIISGNVSPSKGMDET			331

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QY 332 NINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDGALNVGSKKDKPVR 391

Db 421 NINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDGALNVGSKKDKPVR 480

QY 392 ITNVAGVKEGDTYNTAOLKGAQONLNKRDINDVGNARAGIAQALITAGLVQAYLPKGS 451

Db 481 ITNVAGVKEGDTYNTAOLKGAQONLNKRDINDVGNARAGIAQALITAGLVQAYLPKGS 540

QY 452 MAIGGTYRGEAGYATIGYSSISDGNMIIKGTASGSRGHPGASASVGYOM 502

Db 541 MAIGGTYRGEAGYATIGYSSISDGNMIIKGTASGSRGHPGASASVGYOM 591

RESULT 2

A81888

probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain Z249)

C:Species: Neisseria meningitidis

C:date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001

C:Accession: A81888

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000

A:title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A:Reference number: A81775; M01D:2022356; PMID:10761919

A:Accession: A81888

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-592 <PAR>

A:Cross-references: GB:A162755; GB:A157959; NID:g7379742; PIDN:CAM84461.1; PID:g737989

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: NMA1200

Query Match 92.4%; Score 2351; DB 2; Length 592;

Best Local Similarity 81.6%; Pred. No. 3.6e-118;

Matches 463; Conservative 6; Mismatches 13; Indels 90; Gaps 5;

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Db 1 MNKRIIINNSALNMAVYSELTRNHTKRASATVKTAVATLTLFATVQANATDEDEEEL 60

QY 53 -----TLKAGNLIKQ----- 64

Db 61 ESVORSVGSIOASMEGSELETTISLMTNDSKEFVDPYIVYTLKAGDNLIKQINNT 120

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Db 121 MASSFTYSLKDDLTGLINETKLSFGANGKRVNIISDPKGLNFAKETAGTNGDTTVHLN 180

QY 121 GIGSTLTD-----RAASVQDVLNAGMNIKGVK-----NVDF 151

Db 181 GIGSTLTDLGLASSASHVDAGNOSTHYTRAASIKVDLNMGMNKGKTSSTTGQSNVDF 240

QY 152 VRTYDVEFLSADFTKTYNVNDSKNGKTEVKGAKTSVIREKDGKLVTKDGKGENSS 211

Db 241 VRTYDVEFLSADFTKTYNVNDSKNGKTEVKGAKTSVIREKDGKLVTKDGKGENSS 300

QY 212 TPEGSELTAKEVYAVNKGARMKTTTANGOTGQDKREYVTSCTNNMFTASGKTATV 271

Db 301 TPEGSELTAKEVYAVNKGARMKTTTANGOTGQDKREYVTSCTNNMFTASGKTATV 360

QY 272 SKDDGNTIVMTDVNVDALNNVQLONSGMNLDKRAVASSCKGVISGNVSPSKGKDEIV 331

Db 361 SKDDGNTIVMTDVNVDALNNVQLONSGMNLDKRAVASSCKGVISGNVSPSKGKDEIV 420

QY 332 NINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDGALNVGSKKDKPVR 390

Db 421 NINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDGALNVGSKKDKPVR 480

QY 391 RTTNVAPGVKEGDTYNTAOLKGAQONLNKRDINDVGNARAGIAQALITAGLVQAYLPKGS 450

Db 481 RTTNVAPGVKEGDTYNTAOLKGAQONLNKRDINDVGNARAGIAQALITAGLVQAYLPKGS 540

QY 451 MAIGGTYRGEAGYATIGYSSISDGNMIIKGTASGSRGHPGASASVGYOM 502

Db 541 MAIGGTYRGEAGYATIGYSSISDGNMIIKGTASGSRGHPGASASVGYOM 592

RESULT 3

I64138

adhesin homolog H11732 - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C:date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997

C:Accession: I64138

R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; M01D:95350630; PMID:7542800

A:Accession: I64138

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-298 <TIGR>

A:Cross-references: GB:U32846; GB:I42023; NID:g1574586; PID:g1574589; TIGR:H11732

Query Match 20.6%; Score 523.5; DB 2; Length 298;

Best Local Similarity 43.5%; Pred. No. 4.2e-21;

Matches 128; Conservative 25; Mismatches 60; Indels 81; Gaps 7;

QY 1 MNKRIIINNSALNMAVYSELTRNHTKRASATVKTAVATLTLFATVQ----- 49

Db 1 MNKRIIINNSALNMAVYSELTRNHTKRASATVKTAVATLTLFATVQ----- 49

QY 50 -----SANTLKAGDNKTI-----KQFTYSLKDDLTDLISV 79

Db 61 STEDDIEDSAATKRDKNKALAGDTLTAKAGNKLAKIDGCKSVTFPLAADLVQYAK 120

QY 80 GTEKLSFSAN-----GNKVNITSDTKGLNFAKETAGTNGDTTVHLNIGSTLTD--- 128

Db 121 VSDTLTIGGNTPAAGATPKVTSITSPADGLKLAK---GNGDPVHLNGLASTLDTVTN 177

QY 129 -----RAASVQDVLNAGMNIKGVK-----NVDFVRTYDVEFLSAD 164

Db 178 TGASTVTFPSDIDETRAATITKDVLMAGMNIKGVAGAGNTENVDLVAGYNVETIGD 237

QY 165 TKTTVTVNVSCKNGKTEVKGAKTSVIREKDGKLVTKDGK-----KGENGSTDEGE 216

Db 238 KNTLDVLTAKENGKTEVKGAKTSVIREKDGKLVTKDGK-----KGENGSTDEGE 291

RESULT 4

A82615

surface protein XPI981 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: A82615

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Nature 406, 151-157, 2000

A:title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; M01D:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: A82615

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1190 <SIM>

A:Cross-references: GB:AE004017; GB:AE003849; NID:g9107083; PIDN:AAF84783.1; GSPDB:GN

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Artuda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Britson, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier as-Neto, E.; Docena, C.; El-Deiry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmiter, D.A.
Rodrigues, V.; Rosa, A.J.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savaia
A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva
M.; Tshakro, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
C:Contents: annotation
C:Genetics:
A:Gene: xrl981

Query Match 15.0%; Score 380.5; DB 2; Length 1190;
Best Local Similarity 26.2%; Pred. No. 9.9e-13;
Matches 148; Conservative 72; Mismatches 211; Indels 133; Gaps 22;

QY 17 VVSELRNHTKASATKTAVALTLTLPATVQASANTLAKAGNLKIKOFTYS--LKKDLT 74
DB 682 VTSGISAGNOKITTNAAAGTADDAVAFSOLAQVSSASTASKGMILLASGANSWVAPCESV 741
QY 75 DLTSV--GTEKLSFSAANGKV--NITSPTKGLNFAKETAG-----TNGDPT---VHLNGIG 123
DB 742 DLKNTGDNIVISSESGNDVLFNLSS--SLKLDKLTGDTMTTNGVTVSGVTLGSGW 798
QY 124 STLDRASVQVLYNLNG--WNI-----KGVKNVDEVRVDTV 158
DB 799 LVITDPSVTSVSSGINAGSOKITTNVAGTADDAVNLSQLNTAMAGSAAKVVHYSTYD-- 856
QY 159 EFLSADTKITTVVESKDNCKTEVKIGAKTSVIREKDKLVTKGKGENG--SSTDEGEG 217
DB 857 ---GGTGGNNGDGDATGTRSLAVGVGLTASA---EGATAVGSGMAAGKSGSTAIGRN 908
QY 218 LVTAKETIDAVNKAGMKTATTANGOTGADKFEVTSNTNPFASGKGTATVSKDDOG 277
DB 909 AVASAGSVALGD--GAKDGARCAESTTGKISGLNNNTVGVSGDASKGETRTVS----- 962
QY 278 NITVMTDVNVDALNNQI---QNSGMNLSKRAVAGSSGKVISGNVSPSKGMDTVNI 333
DB 963 NVADAKEAT--DAVNLRQDLDRVAQDANRYVDNKIESLSEGTQF-----YKV 1006
QY 334 NAGNNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSTV-----DGLALNYSK--- 384
DB 1007 NSLNN-----SATP-----IAAGVDATAIGVATASGADSIAMGNKASAS 1046
QY 385 KDKKPV-----RITTVAPGVKEGDVNNVQALGVAAQNLNRID 422
DB 1047 ADNAVAALGNHNVADRANTVSVSGASGEROYTNVAGTADDAVNVSLNOGLITTAKOYTD 1106
QY 423 NVDGNMR---AGIAQAIATAGLVQAVYLPGRKSMALIGGTYRGEAGYAIGYSSISDGMV 478
DB 1107 GVGVSRLRBDTGDGVAAAIATANLPQAVIPGRGNTSVGSYSYROSATAVGVSSVSEGRW 1166
QY 479 IITGTASGNSRGHFGASASVGYOW 502
DB 1167 VFKFSGSANTRSGVIGAGVGYOW 1190

RESULT 5

A86036
probable adhesin Z5029 [imported] - Escherichia coli (strain 0157:H7, substrain EDL933)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_rev1510 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: A86036
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoultis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A86036
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1588 <STO>
A:Cross-references: GB:AE005174; NID:G13518349; PIDN:AA658749.1; GSPDB:GN00145; UWGP:Z50

A:Experimental source: strain 0157:H7, substrain EDL933
C:Genetics:
A:Gene: Z5029

Query Match 14.2%; Score 360.5; DB 2; Length 1588;
Best Local Similarity 28.3%; Pred. No. 1.7e-11;
Matches 141; Conservative 55; Mismatches 181; Indels 121; Gaps 21;

QY 46 TVQASANTLAKAGNLKIKOFTYSLKDLDTLTSVGEKLSFSA-----NGKK-----VNIT 96
DB 1171 TVRQLOALGAIVATTPPKYFHFANSTEE--DSLAVGTDLSLAMGAKTYVNGKIGIGYGAY 1228
QY 97 SDPTKGLNFAKETAGTNGDPTVHLNGI-----GSTLTDRASVQVLYN--AGMNTKSG---VK 147
DB 1229 VDNALNLNGI--ALGSNAG--VIHNSIALIGNSSTTRKACQNTYATNMDAQNVSGERSVG 1285
QY 148 NVDVFTVTVVEFLSADTKITTVVESKDNCKTEVKIGAKTSVIREKDKLVTKGDKG- 206
DB 1286 SADGQROITVVAAGSADTDVAVNG-----OLKVTDAQVSONTQISITNLDNR-VTNLDSRV 1339
QY 207 ---ENG-----SSTDEGGLVTAKEVIDAVNKKAGRMKTATTANGOTGADKFEVTSNTN 259
DB 1340 TNIENGIGDITVGTSTKTYFTNTDGVDA--SAGKDSVAIGSISIAAD--NSVALGTG- 1394
QY 260 TPAAGKGTATVSKDDGNT--VMYDVNVDALNNQI---GNNLSKRAVAGSSGKV 315
DB 1395 SVATFEENTISVGSSTNRRTTNVAGKNATDAVNAOLKSEAGVRYDTKA----- 1446
QY 316 ISGNVSPSKGMDTVNINAGNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSTV 375
DB 1447 -----DGSID-----YSNITLGGNGGT----- 1465
QY 376 GDALNYSKDKNKPRTTNVAPGVKEGDVNNVQALGVAAQ-----NINNRIDNV 424
DB 1466 -----RISNVAGVNNNDVNVVQALQSVQETQOYTDQREVDNKLST 1510
QY 425 DGNARAGIAQAIATAGLVQAVYLPGRKSMALIGGTYRGEAGYAIGYSSISDGMNIIKTA 484
DB 1511 ESKLSGSIASAMMTGLPQAVIPGRGNTSVGSYSYROSATAVGVSSVSEGRW 1570
QY 485 SGNSRGHFGASASVGYOW 502
DB 1571 STNSGGRYSALAGAGIOW 1588

RESULT 6

H91188
probable adhesin ECs4480 [similarity] - Escherichia coli (strain 0157:H7, substrain R
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_rev1510 18-Jul-2001 #text_change 02-Nov-2001
C:Accession: H91188
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinaigawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and 9
A:Reference number: A9629; MUID:21156231; PMID:11258796
A:Accession: H91188
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1588 <HAV>
A:Cross-references: GB:BA000007; PIDN:BA837903.1; PID:G13363955; GSPDB:GN00154
A:Experimental source: strain 0157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECs4480

Query Match 14.2%; Score 360.5; DB 2; Length 1588;
Best Local Similarity 28.3%; Pred. No. 1.7e-11;
Matches 141; Conservative 55; Mismatches 181; Indels 121; Gaps 21;

QY 46 TVQASANTLAKAGNLKIKOFTYSLKDLDTLTSVGEKLSFSA-----NGKK-----VNIT 96
DB 1171 TVRQLOALGAIVATTPPKYFHFANSTEE--DSLAVGTDLSLAMGAKTYVNGKIGIGYGAY 1228

Qy 126 LTRDAASVDVLAGMNIKGVK-----NVDFRYTDFEFLSADTKTTTVN-----VE 173
 Db 530 STDA-----INSQLEYETMMLISQYNESSISQLAGDISEYITFENGTVKIR 576
 Qy 174 SKDNGKTEYKIGAKTSVIEKDGKLVYTKDK-----GENGSSTDEG----- 215
 Db 577 TNDNGLEGO-----DAYATNGATVAGYDAVASGAGCIALGONSSSSIEGSLALSGS 629
 Qy 216 -----EGLY-----TAKEVIDAVNKA-----GWRMTTTTANGOTGO--- 246
 Db 630 TSNRAITTTGIRETSATSDGVYIGYNTDRELGLSLGCTDGESTRQITTNVADSEADAV 689
 Qy 247 -----ADKFEYVTSGTNTVTFASGKGTAA-----TVSKDDOG-----NITVM 282
 Db 690 TVRQLONAIGAVTTPTKRYHANSTEDSLAVGTDSLAMGAKTIVNADAGIGLINTLNV 749
 Qy 283 YDVAVGALNVN-----OLNSGNWLSK-----AVAGSSGK 314
 Db 750 ADAINGIAIGSNABANHANSIAMGNSQTRGACQTDYATVNMPTPONSVEGEFVSBDGQ 809
 Qy 315 VISGNVSPSKGMDJETVNING-----NNIETTRGKN----- 348
 Db 810 RQITNVNAGSADTDA---VNVGLKVTDAQVSRNTOSTITLNTQVSNLDTVTNIENGIG 866
 Qy 349 DIATSMTPOF-----SSVSLGAGADAP-----TLSDVGDALNVGS 383
 Db 867 DIVTGTSTKRYKFTDGDANAGADSVAIQSSISIAAENSVALGTSVADENATVVSQS 926
 Qy 384 KDKKPVRTNVAPGVKEGDTNVYAOLK----- 411
 Db 927 STQOR--RITNVAGVNNVTDAVNVYAOLKSEAGSVREYNADGSVNVSVLMIGDGSQGT 984
 Qy 412 -----GVAO-----NUNNRIDVNDVAGNAGIAQATATA 439
 Db 985 RIGVNSAANDTDAVNVYAOLKRSVEANTTYTDQKMEKNSKIKGIEKMSGCIASAMMA 1044
 Qy 440 GLVQAYLPKSKMAIGGTYRGEAGYAGYSSISDGNMIIKGTASGNSRHFEGASASVG 499
 Db 1045 GLPQAVAPGANMTSIAGTGFGEASAVAIQVMSVSESGWYKLGCTSNSSQDYSALGAG 1104
 Qy 500 YQW 502
 Db 1105 FQW 1107

Qy 68 SLKRDLDLTVSGTEKLSFSGANKNVNTSDTKLNFPAKETAGTNGD---TVHLNGIG 123
 Db 261 -----TALGNRKITGVAG-----SASSADVANNQGLTA---VGQVQONTANTISLG 304
 Qy 124 STLDRAASVYKDVINAGNINIKGVNVDFTYDVEFLSADTKTTTVNVEKDKKT-- 181
 Db 305 GRVTTIEGSMASIANGC---GVKY---FHANSTQPDVASGTNSVAIGPASTLASGNALA 358
 Qy 182 -----EVKIGAKTSVIEKEDGKLVYTKDKGENGSSTDEEGLVTKKEVIDAVNKAQWAKT 237
 Db 359 SGAGAVAIIG--DGAASADSGVAIQSGSGDGKREVENTIG-----KYS 399
 Qy 238 TTANGOTGOADKFEYVTSGTNTVTFASGKGTATVFSKDDQGNITVMYDVNVDALNVQLO 297
 Db 400 NASNTSSG-----TVSGNAT-----GERTYNSVADG-----LQATDANVLQOLD 441
 Qy 298 NSGNWLSKAVAGSSGKVIQSGVSPSKGMDJETVNINGNNI--BITRGNKIDI--ATSM 354
 Db 442 G-----IAASIVVENNVSGLQNGTGMFQVNNSSGLAKRPSATGANSATGAGSV 491
 Qy 355 TPQFSSVSLGAGADAP-----TLSDVGDALNVGSKKDKNPVRTNVAPGVKEGDV 404
 Db 492 ASGNNSVTFPGSGARATPANSALCANSVADRPANSVSGVGNER--DITNVAPATQGTDA 549
 Qy 405 TNVQOLKGVACN-----LNMRIDVNDGNAR-----AGIAQIATAGIYQAYLPKSKMA 453
 Db 550 VNFQOLKISQNTAAYTNQKRSKELKODLRKQNSVLSAGIASAMASISLTQYTGSSSMTT 609
 Qy 454 IGGTYRGEAGYAGYSSISDGNMIIKGTASGNSRHFEGASASVQW 502
 Db 610 IGAASVYQGSALSLGVSSISDSGRWVSKLOASSMTQGFQIGVGVQW 658

RESULT 9
 AH0110
 Probable surface protein (partial) YP00902 [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
 C:Accession: AH0110
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tiltball, R.W.; Holden, M.T.G.; Prentice, M.B.
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.;
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,
 Nature 413, 523-527, 2001.
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AH0110
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-658 <KUR>
 A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:915978974; GSPDB:GN00175
 C:Genetics:
 A:Gene: YP00902

Query Match 13.6%; Score 346.5; DB 2; Length 658;
 Best Local Similarity 25.3%; Pred. No. 3,1e-11;
 Matches 134; Conservative 76; Mismatches 198; Indels 121; Gaps 21;

Qy 12 ALNMMVVSSELTNRHTRKASATVKT-----AVLATLPLFATVQASANTLKAGCNLKIKQPTTY 67
 Db 213 ALGAGAVTSQ--ANSIALGAASINTVGAQSSYSAYALTAPASVGEIGIG----- 260

RESULT 10
 A64905
 ydek protein - Escherichia coli (strain K-12)
 N:Alternate names: protein T
 C:Species: Escherichia coli
 C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
 C:Accession: A64905; I52440; S34315
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: A64905
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1325 <BLAT>
 A:Cross-references: GB:AE000248; GB:U00096; NID:91787783; PIDN:ANC74583.1; PID:917877
 A:Experimental source: strain K-12, substrain MG1655
 R:Cartwright, P.; Tims, M.; Litigow, T.; Hoj, P.; Hoogenraad, N.
 Biochim. Biophys. Acta 1153, 345-347, 1993
 A:Title: An Escherichia coli gene showing a potential ancestral relationship to the g
 A:Reference number: I52440; MUID:94100243; PMID:8274505
 A:Accession: I52440
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 689-883, 'K', 885-1316, 'S', 1318-1325 <RES>
 A:Cross-references: EMBL:X73295; NID:9312392; PIDN:CA651730.1; PID:9312393
 A>Note: the difference in length is due to a frameshift error at pos 653
 C:Genetics:
 A:Gene: ydek
 C:Function:
 A:Description: probably involved in protein translocation apparatus
 C:Keywords: nucleotide binding; P-loop
 F:712-719/Region: nucleotide-binding motif A (P-loop)

Query Match 8.9%; Score 226.5; DB 2; Length 1325;
 Best Local Similarity 24.8%; Pred. No. 0.00018;
 Matches 146; Conservative 67; Mismatches 241; Indels 135; Gaps 27;

Qy 1 MNKIYRIIMNSALNMMVVSSELTNR-----NHTKRASATVKT--VLATLPLFATVQAS 50

```

Db      1 MRRITRVWNCITLQVFOACSELTFRAGKTSVTNLRKSSLTFRKSLTGLVLLALSGSAS 60
OY      51 AMTLKAGNDLAKIKOFTYSLKKDLTDLTSVTEKLSFSAANGKNVNIISDPTKGNFAKETAG 110
Db      61 GASLVEY-DMDQITNIDTVAAYDAYLVGWGTGVLNLAAGN-ASLTFTTTSV-----IG 112
OY      111 TNGDPTTHLNGIGST--LTDRASVYKVDLNA-----WNIKVKNVD--FWRPTDVEF 160
Db      113 AAEDESGTAVNNVLGGTWRLTDSGNMNAAP-LNVGSGTGTILNIKOKGHVDGGLR----- 164
OY      161 LSADT-KTTTAVVESKDNCKTEV-----KIGAKTS 190
Db      165 LGSSTGGVGTAVNEGDSVLTTELEIGSYGTGSLNITDKGYVTSSIVAILIGYOAGSNGQ 224
OY      191 VIKERDKG-LVYKGDG-----ENGSTDEGELVTAKEVIDAVNKAQRMKTTTAN 241
Db      225 VVVEKGEMLINKNDSISIEFOIGNOGTGEATIREGLVTAEMTIIIGNMTG-----IGTLN 280
OY      242 GGTGQADKFEYTSSTNTTTPASGKGTATVSKDDGNTVTWVDVNGDALN-VNOLONS 299
Db      281 VO--DODSVITVRRLYNGYFGNG--TVNISNNGLINNKESLVGVODSHGVVNTDKG 335
OY      300 GNNL-----DSKAVAGSSGKYISGNVSPSKGMDT-----V 331
Db      336 HNNFLCTGEAFRYIYIGADGDELNVSSSEKVDSGITITG--MKETGTGNTVYKDKNSV 392
OY      332 NINAGNNIEITRNGKNIDTATSMTPQFSVSLGADAPTLTVDGDALVWGSKKD-NKPV 390
Db      393 ITNLGTLNGIDGHEKNISNOGLVYVNSGGSLGYG---ETGVGNVSIITGGMWEVKNKV 448
OY      391 RTTNVAPYKEDGYTNVAOLKGYAQNLRINVDGNARAGIAQAIATVGLQVATLP-G 448
Db      449 YTTIGVAGYGNLNISSDG--KEVSQNIITPLGDKASIGITLNLMDATSSSDPTFGVINGNG 506
OY      449 KSMMAIGGTYRGEAGYAT-----GYSSISDGSNMWIKGTASGNSR 489
Db      507 SCIVVNSCATLNTSTGYRIGGNASGKGLVNISTDLSMNLK-TSSTNAQ 554

RESULT 11
C82672
surface-exposed outer membrane protein XF1516 [imported] - xylella fastidiosa (strain 9e
C:Species: xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: C82672
R:anonymous, The xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: C82672
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1004 <SIM>
A:Cross-references: GB:AE003981; GB:AE003849; NID:g9106543; PIDN:AAF84325.1; GSPDB:GN001
A:Experimental source: strain 9a3c
R:Simpton, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Bilones, M.R.S.; Bueno, M.R.P.; Camargo, H.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir, H
as-Neto, E.; Docena, C.; El-Poriry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kltajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, H
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miranca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
C:Genetics: annotation
A:Gene: XF1516

```

```

Query Match      8.8%; Score 224.5; DB 2; Length 1004;
Best Local Similarity 23.2%; Pred. No. 0.00017;
Matches 132; Conservative 74; Mismatches 207; Indels 157; Gaps 23;

OY      2 NKIYRIWNSALNANVYVSELT-----RNHT-----K 28
Db      4 NOIYRFFNLISGWSVASHMTNDGGSDVYLRHSGVRRRSVLVLAIGLALTSVTHAOSVK 63
OY      29 RASATVTKAVLTLLFAFVOASANTLKAQDNLIKOFYTSCLKDLTDLTSVTEKLSFSA 88
Db      64 SPAMTASGVMAAHVDSQVNRTRADRIPIGDSGL-----MTHMALDKKFPF 110
OY      89 NGKNVNTSDTKGLNFAKETAGTNGDTTVHLN--GISSTLTDRASVYKVDVLAQMNKIG 145
Db      111 GNNISLIGYFSKAFAPNALALGYNSSVTQSANNGVALGSNST-----VSG 155
OY      146 VKNVDFVRYDVEFLSLADTKTTVNVESKDKCKTEYKIGAKTSVIKEKOKLYTGDK 205
Db      156 VNSV-----ALGASMASSELNVISVGSG--DGYTGPRVRRIVNVGD5--IGNND 200
OY      206 GENGSTDEGELVTAKEVIDAVNKAQRMKTTTANQGTQADKFEYTSSTNTVTFASGK 265
Db      201 ANKSGQLDS--VTA-----SYNDVAASVKTIALTNQ-----VTSSVASASGK 241
OY      266 GTTATVS-KDDGNTVTWVDVNGDALNVNOLONGMNLDSKAVAGSSGKYISGNVSPSK 324
Db      242 ESTALISGAQVADNTVAF--CGRAIANAAGASALGDFSHAKINSTVYGTQGSVLQ 297
OY      325 GKMDFTVNNAG-----NNIEITRNG--KNIDTATSMTPQFSVSLGADAPTLTAV-- 374
Db      298 GGVSLIGYFVEGSEFNGALGSLNVLQGDV-----SVALLSGSMASEPNVVS 347
OY      375 --DGDALNWSKKDNKPVRITVAPYKEDGYTNVAOLKGYAQNLRINVDN----- 424
Db      348 VESGGLRQPAVR-----RIVAVGDCIGNNDAVNKNSQOLDGYTASVNDVYASVKNLGAALQ 402
OY      425 -DGNARAGIAQAIATAGLVQAVLPKKSMAIG-----GTYGCEAGYATGYSISDG 475
Db      403 ITGSGVAVSYSGDSTFAGASAOAGDSSIALGARSANNAIGSSALGVGDHAGANSTALG 462
OY      476 GNMIIKGT-----SGNSRGH--FGASASVG 499
Db      463 G-----QSTAIRSEGTSLGINSFVGOSATNG 488

RESULT 12
AF0394
probable adhesin hmwA [imported] - Yersinia pestis (strain C092)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AF0394
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlball, R.W.; Holden, M.T.G.; Prentice, M
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AF0394
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1910 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC92482.1; PID:g15981183; GSPDB:GN00175
A:Genetics: hmwA

Query Match      8.3%; Score 210.5; DB 2; Length 1910;
Best Local Similarity 22.6%; Pred. No. 0.0021;
Matches 133; Conservative 80; Mismatches 196; Indels 179; Gaps 26;

OY      1 MNKIYRIIWSALNANVYVSE--LTRNHTKASATVTAVALT-----LLFATVQSA 51
Db      734 LSKSGRLVFD--INGNIYVKNYGLRVNNSQLSADKVFAYVAVTGYDGLLRDSHVYATRS 791

```


A:Gene: ECS2117

Query Match 8.2%; Score 208.5; DB 2; Length 1343;
Best Local Similarity 23.6%; Pred. No. 0.0017;
Matches 140; Conservative 72; Mismatches 239; Indels 141; Gaps 27;

QY 1 MKIRIITNSALNMAVYSELTR-----NHTRKASATVKA--VLAATLLPFAVQS 50
DB 1 MKIRIITNSALNMAVYSELTR-----NHTRKASATVKA--VLAATLLPFAVQS 60
QY 51 ANTLKAGDNLKIKQFYSLSKDLTDLTYSCTEKLSPSANGKNVNTSDTKGLNFAKETAG 110
DB 61 GASLEV-DNGQITNIDTDAVAYDAIYVGMVGTGLNLAAGN-ASLFTITTSV-----IG 112
QY 111 TNGDPTVHLNGIGST--LTDRAASVADVLNAGMNIKGVNVDFTVTEELFADPKTT 168
DB 113 GNEDEGTVNVLGTFMRLYDSCNNARP-LNVGSGTGTLINIKOKHVDG-GYLRIGCTQA 170
QY 169 ---TVNVEKDKGKTEV-KIG-----AKTSVKEKD 196
DB 171 GVGTAVNEDESVLTLELFEISYGTSLNITDKGVTSIVALLGYQANSNGKVVVEKG 230
QY 197 GK-LVTGKDKG-----ENGSTDEGEGLYTAKEVIDAVNKAQRMKTTANGOTGA 247
DB 231 GEMLIKNDSSIEFOIGNOGTGEBATIREGLITAEHTIIGNATG-----VGLNVO--DQ 284
QY 248 DKEFTVTSCTNVTFAAG-----KGTATVSKDDOGNITVWYDVN 286
DB 285 DSVITVRLYNGYFGGAVNISNGLINNKKEYSLGVGDGSHGVAVVTDKGMNLF--G 341
QY 287 VDDALNVNOLNSGMNLDKAAVAGSSGKYISGNVSPSKMDETVINANGN-----NIE 340
DB 342 TEAFARYIYIGDAG--DDELNVSRGKVDSGIITAG--MKET--GTGNLTVKDKNSV 392
QY 341 ITRNGKNIDIASMTPOFSSVSLGAGADAPTLSDVDALNVGSK-----KDN 387
DB 393 ITNLGNLGYDHGEMINISNEGL-----VYNSGSSIGYETGVGKYSITTGGEWPN 445
QY 388 KPVRTITNAPGVKESDVTNVAOLKGYAQNLRNIDNVGNARAGIAQAIATAGLVQAYLP 447
DB 446 KNYTTIGVAGVGNINISDGC--KFVSQNTIFLGKASGICITLNLMDATSSPDVGINVG 503
QY 448 ---GKSMMAIGGTYRGEAGYAI-----GYSSISDGGNWIIGKASGNSR 489
DB 504 NFGSLIVNNGATLNTSTGYFTIGNAGSKGIVNISTDSLWMLK--TSSSTNAQ 554

RESULT 15

G64964
Hypothetical protein b2000 - Escherichia coli (strain K-12)

C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: G64964

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC
A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: G64964

A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-1091 <BLAT>
A:Cross-references: GB:AE000291; GB:U00096; NID:g1788298; PIDN:MAC75061.1; PID:g1788309;

A:Experimental source: strain K-12, substrain MG1655
C:Keywords: nucleotide binding; P-loop
F:683-690/Region: nucleotide-binding motif A (P-loop)

Query Match 8.2%; Score 208; DB 2; Length 1091;
Best Local Similarity 23.2%; Pred. No. 0.0014;
Matches 130; Conservative 65; Mismatches 197; Indels 168; Gaps 32;
QY 1 MKIRIITNSALNMAVYSELTRNHTRKASATVTAVALATLLPFAVQA-----S 50
DB 1 MKIRIITNSALNMAVYSELTRNHTRKASATVTAVALATLLPFAVQA-----S 50

DB 57 LNTCYRLVWNHMTGAFVVAASELARRARCKGVAVALSLAATVSLFVLAADIVYHGETVN 116
QY 51 ANTLKAGDNLKIKQFYSLSKDLTDLT-----SVTEKLSFSANGKNVNTSDTK 100
DB 117 GGTLANHND---QIVFGTNGMTISTGLEYPDNEAMTGGWQDGGTANKTIVTSG-- 170
QY 101 GINPAKETAGTGDPTVHLNGIGSTLTLDRAASVADVLN-----GM 141
DB 171 GIQ-RVNPBGSVSDPVISAGG--GOSILOGRA--VNTTLNGGEQOMHEGAIAATGTVINDGM 226
QY 142 NI-----KGVKNVDFRTPDVEFLSADTKTTTVNVEKDKGKTEVKIG-A 187
DB 227 QYVKGCTVATDVTNVTGABGCPDAENGDTGQVRBDATRTIN-----KNGRIYAAEGTA 282
QY 188 KTSVKEKDKGLVTKDKGNGSSSTDE---GEGLY---TAKEVIDAVNKAQWMA--- 235
DB 283 NTVV-----YAGDDQTVHGHALDPTLNGSYQYVHNGGTFASDPTV--VNSDGMQIVKNG 333
QY 236 ---KTTTANGOTGQADKEFTVTSCTNVTFAAG-----KGTATVSKDDOG-NITVWYDVN 287
DB 334 GVAGNTTVN-OKGRL-QVDAGGTATNVTLKOGALVTSAAVTV-----GINRLGAFSVYE 387
QY 288 GDALNVNOLNSGMNLDKAAVAGSSGKYISGNVSPSKMDETVINANGNIEIRNGKN 347
DB 388 GKADNV-VLENGG-RLD-----VLTGHTATN-----TVYDGGTLDV-RNG-- 425
QY 348 IDIATSMTPPOFSSVSLGAGADAPTLSDVDALNVGSKDKMDKPVRTITNAPGVKESDVTNV 407
DB 426 ---GTAAT-----VSMGNG--VLLADSGAAVSGTRSDGK-----AFSIGGOADAL 467
QY 408 AOLKGYAQNLRNIDNVGNARAGIAQAIATAGLVQAYLPKGSMAIGGTYRGEAGYAI 467
DB 468 MLEKSSFTLN-----AGDTARDTT-----VNGGLETFARGTGLA 501
QY 468 GYSSISDGGNWIIGKATASGN 487
DB 502 GTTILNNGAIIFLSGKTYVN 521

Search completed: October 6, 2003, 09:33:25
Job time : 17.369 secs

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:06:20 ; Search time 7.75217 Seconds
(without alignments)
3045.266 Million cell updates/sec

Title: US-09-771-382-27
Perfect score: 2544
Sequence: 1 MNKIRIIMNSALNANVVS.....TASGSRGHGASASVGYQM 502

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	226.5	8.9	1325	YDEK_ECOLI	P32051 escherichia
2	210	8.3	1286	AIDA_ECOLI	Q03155 escherichia
3	208	8.2	1039	AG43_ECOLI	P39180 escherichia
4	175.5	6.9	2003	YDBA_ECOLI	P33666 escherichia
5	173	6.8	1608	HLVA_SERMA	P15320 serratia ma
6	173	6.8	2249	OMPA_RICRI	P15921 rickettsia
7	172	6.8	1567	ICEN_XANCT	P18177 xanthomonas
8	169.5	6.7	1577	HLVA_PROMT	P16466 proteus mir
9	169	6.6	1655	OMPB_RICCN	Q9Kk43 r outer mem
10	168.5	6.6	1654	OMPB_RICRI	Q53047 r outer mem
11	165	6.5	1645	OMPB_RICRY	P96989 r outer mem
12	165	6.5	1025	MAPA_BACSU	Q07883 bacillus su
13	164.5	6.5	1234	MAPA_CAOCR	P35828 caulobacter
14	164.5	6.5	1861	APU_THETU	P38536 t amylopull
15	164	6.4	1933	BIGA_SALTY	P25927 salmonella
16	163.5	6.4	933	SLAP_CAMEF	P35827 campylobact
17	161.5	6.3	1148	ICERK_PSEBSX	Q30611 pseudomonas
18	161.5	6.3	2021	OMPA_RICCN	Q52657 rickettsia
19	160.5	6.3	1300	120K_RICRI	P14914 rickettsia
20	160.5	6.3	1643	OMPB_RICPR	Q53020 r outer mem
21	158.5	6.2	507	FLIC_SALON	Q06974 salmonella
22	158	6.2	1153	YPJA_ECOLI	P52143 escherichia
23	157	6.2	1569	PVDB_PLAKN	P50493 plasmodium
24	156.5	6.2	507	FLIC_SALBE	Q06968 salmonella
25	156.5	6.2	928	PM10_CHIRN	Q06965 chlamydia p
26	156.5	6.2	1656	OMPB_RICUA	Q06653 r outer mem
27	155.5	6.1	350	FLIC_SALFL	Q08860 shigella fl
28	155.5	6.1	2358	YEEL_ECOLI	P76347 escherichia
29	154	6.0	497	FLIC_SALRO	Q06982 salmonella
30	153.5	6.0	497	ICEN_PSEBSY	P04949 escherichia
31	153	6.0	1200	ICEN_PSEBSY	P06620 pseudomonas
32	152	6.0	504	FLIC_SALBU	Q06969 salmonella
33	152	6.0	504	FLIC_SALBU	Q06971 salmonella

34	151	5.9	1196	ICEN_PSEBSX	Q33479 pseudomonas
35	151	5.9	1848	CBPA_CLOCL	P38058 clostridium
36	150.5	5.9	880	LYTD_BACSU	P39848 bacillus su
37	150.5	5.9	918	YMB_CAEEL	P34487 caenorhabdi
38	150	5.9	504	FLIC_SALMC	Q06981 salmonella
39	150	5.9	504	FLIC_SALSE	Q06983 salmonella
40	150	5.9	917	HXA3_HAEIN	P45355 haemophilus
41	149.5	5.9	1288	VACA_HELPTJ	Q92Kw5 helicobacte
42	149	5.9	504	FLIC_SALNA	O52959 salmonella
43	148.5	5.8	2660	YEEL_ECO57	O8x8v7 escherichia
44	148	5.8	948	HPTI_DEIRA	P56867 deinococcus
45	147.5	5.8	1167	CAGA_HELPJ	Q921c1 helicobacte

ALIGNMENTS

RESULT 1
YDEK_ECOLI STANDARD: PRT; 1325 AA.
AC P32051: P76140; P77168:
DF 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical lipoprotein ydek precursor (ORF1).
GN YDEK OR ORF1 OR B1510.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC SRRAIN-K12; MGI655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC SRRAIN-K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Nakano K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Sempel G., Seki Y., Sivasubramanian S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 595-1325 FROM N.A.
RX MEDLINE=94100243; PubMed=8274505;
RA Cartwright P.J., James M.W., Lithgow T., Hoef P.B., Hoogenraad N.J.;
RT "An Escherichia coli gene showing a potential ancestral relationship
to the genes for the mitochondrial import site proteins ISP42 and
KOW38.";
RL Biochim. Biophys. Acta 1153:345-347(1993).
CC - SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
(potential).
CC - SIMILARITY: TO E. COLI YFAL.
CC - SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
ISP42 AND KOW38.
CC - CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT IN POSITION 653.
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CC -----
CC EMBL; AE000248; AAC74583.1; -
DR EMBL; D90793; BAA15190.1; ALT_INT.
DR EMBL; D90794; BAA15197.1; ALT_INT.
DR EMBL; X73295; CAA51730.1; ALT_FRAME.
DR PIR; A64905; A64905.
DR Ecogene; EG11780; ydek.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN. 1.
KW Hypothetical protein; Membrane; Lipoprotein; Signal;
KW Complete proteome.
KW SIGNAL 1 18
FT CHAIN 19 1325 POTENTIAL.
FT LIPID 19 1325 HYPOTHETICAL LIPOPROTEIN YDEK.
FT CONFLICT 884 884 N -> K (IN REF. 3).
FT CONFLICT 1317 1317 M -> S (IN REF. 3).
SO SEQUENCE 1325 AA; 136514 MW; 26A2AD06EFA19AD7D CRC64;

Query Match	8.9%;	Score 226.5;	DB 1;	Length 1325;
Best Local Similarity	24.8%;	Pred. NO. 0.00018;		
Matches 146;	Conservative 67;	Mismatches 241;	Indels 135;	Gaps 27;

```

OY      1 MNKYYRIITMNSALNAAVYVSSLETR-----NHTKRASATVTKA--VLATLLEFATQAS 50
Db      1 MNRYYRIYRNTCTLOVFOACSELTFRAGKTSTVYNLRKSSGLTTKTSRLTLGVLLAISGSAS 60
OY      51 ANTLKAGDNLEKIOFTYSLKDKDLTDLSVTEKLSFSANGKRVNITSDTKLNFKEATGAG 110
Db      61 GASLEW-DNDDITNIDTDVAAYDALVGVYGVYGLVNLIAAGN-ASLTITTTTSV-----IG 112
OY      111 TNGDTFYHLNGIGST--LTDRASVYKDYLANG-----WNTRKYKND--FVRTYDVEF 160
Db      113 ANESSEGVNVLGGTWMRLYDSGNMARP-LVNGSGGTGLTNIKQGHVDGYLR-----164
OY      161 LSADP-KTTYVNVESKDMGKTEV-----RIGAKTS 190
Db      165 LGSSTGVGVTVNVGSEDSVLTTELFELIGSYGTSINTDKGYVYTSIVAILGYQAGSNGQ 224
OY      191 VIKERDKG-LVTGKDKG-----ENGSTDEGEGLTAYAKEVIDAIVAKRAGRMKTTAN 241
Db      225 VVVEKGGEWMLKNNDSSTLEFQIGNQGTGEALITREGGLVTAENTIIIGNATG---IGTLN 280
OY      242 GQTQOADKEFTVTSGTNTVTFASGKGTATATVSKDDOGNITVWYDVNVGDALN--VNOLONS 299
Db      281 VQ--DODSVIYRRLYNGYFENG---TYNINNNGLINKEXSLVGOVDSHGAVVATDKG 335
OY      300 GWNL-----DSKAVAGSSGCVIGSVNSPSKGMDET-----Y 331
Db      336 HWNLTGTEGEAFRYIYIGDAGGELNVSSSEGVDSGLITAG--KKEGTGNTIYKDKNSV 392
OY      332 NINAGNNIETIRNCKNIDDIATSMTPPESSVSLAGADAPTLSDVDGALNVSSKRD-NKPV 390
Db      393 ITNLTGNLTGYCHHEMINSNGGLVYVNSGSSSLG---ELGVGVNVSTITGGMNEVKNV 448
OY      391 RITVAPGVKEGDVTNVAQLKGAQNLNRIIDVNGNARAGIAQAIATAGLVQAYLP--G 448
Db      449 YTTIGVAGVGNLNTISDGG--KFVSQNTITFLDKKASIGICTLMLMATSFDVIGLVNGEG 506
OY      449 KSMALIGGGYRGEGAGYAI-----GYSSISDGGNMTIIGTASGNSR 489
Db      507 SGIVNVSNGATLNSTGYEFIGGNASGKGIYVNSTDSIMNLK-TSTSTNAQ 554

RESULT 2
AIDA_ECOLI
ID      AIDA_ECOLI      STANDARD;      PRT; 1286 AA.
AC      Q03155;
DT      01-JUN-1994 (Rel. 29, Created)
DT      01-JUN-1994 (Rel. 29, Last sequence update)
DT      26-FEB-2003 (Rel. 41, Last annotation update)
DE      Adhesin aidA-I precursor.

```

```

GN      AIDA-1.
OS      Escherichia coli.
OC      plasmid p186.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Escherichia.
OX      NCBI_TaxID=562;
RN      [1]
RP      SEQUENCE FROM N.A., AND SEQUENCE OF 50-56.
RC      STRAIN=O126:H27 / 2787;
RX      MEDLINE=9232638; PubMed=1625582;
RA      Benz I., Schmidt M.A.;
RT      "AIDA-1, the adhesin involved in diffuse adherence of the
RT      diarrhoeagenic Escherichia coli strain 2787 (O126:H27), is
RT      synthesized via a precursor molecule.";
RL      Mol. Microbiol. 6:1539-1546(1992).
CC      -1. FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE
CC      ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI
CC      TO EPITHELIAL CELLS.
CC      -1 SUBCELLULAR LOCATION: Outer membrane.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      or send an email to license@isb-sib.ch).

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CC	EMBL; X65022; CAA46156.1; -. PIR; S28634; S28634. InterPro: IPR006315; Autotransport. InterPro: IPR005546; Autotransporter. InterPro: IPR004899; Pertactin. PIfam; PF03797; Autotransporter; 1. PIfam; PF03212; Pertactin; 1. TIGFAMS; TIGR01414; autotrans_bar1; 2. Cell adhesion; Signal; Outer membrane; Plasmid. SIGNAL 1 49 CHAIN 50 ? PROPEP ? 1286 SEQUENCE 1286 AA; 132271 MW; B2A00E72AC05FB34 CRC64;
ADHESIN AIDA-I.	

Query Match	8.3%	Score 210	DB 1	Length 1286
Best Local Similarity	21.1%	Pred. No. 0.0012		
Matches 139	Conservative 83	Mismatches 226	Indels 210	Gaps 31
QY	1	MNKIRIIRIINSAALAAWVYSELTRNNH-----IKRASATYKTA-VLATILFETVQAASA	51	
Db	1	MNKAVSIITWSSROAMIVAYASELARGHGVLAKNLTLLVLAAYSTIGMAFAVNISCTV-SSG	59	
QY	52	NTLACGDNLKKKQFTYSLSK-KDLIDLTSVGTETKLSFSAKGNKVNITSDPKQLNFAKETAG	110	
Db	60	GTVSSGET-----QIVYSGRGNSNATVNSGCTQIYVN---NGCKTATATVNS--GSONVG	109	
QY	111	TNG---DTYVHLNIGSTLIDTRAAVNDVYLAAGNINIGYKRVKVDVRRYDTEFLSDPK-	166	
Db	110	TSGATISTIVYNSGGIQRVSSGCVASATNLLSGGAONIYNLGNAS-----NTVIFSGNQTTI	164	
QY	167	-----TTTVVNESKDNGKTEVKGACTV-----IKEHDGLVYTKDGEN-?-?-G	209	
Db	165	FSGGITDSTNISGGQQRVSSGGVAVASNTTINSGAONILSEGAISTHIISSGNGQIYASG	224	
QY	210	SSTDEGEGLYAKEYIDAVYKAGKRMKT-----TTANGT-----GQADKREYIYSG	256	
Db	225	ANATE-----TIYNSGGQFORVNSGAVATGTVLISGCTQNVSSGGSIASTISVYNSG	273	
QY	257	TNTVFASGKGTATATVSKD-----DQGNITVAYDVNV-----GDLANVN-----OLQN	298	
Db	274	VQYFACAGATYDITVNSGGNGNISGGIVSEFTYIVNVSCTQNIYSGSALSANINIGSQIYV	333	
QY	299	S-GMNLDSKAVAG-----SSGKVI--SGVNSPSKGMDETIVINAGNIEITRNG	345	
Db	334	SEGAINITLVSDGGYOHIRNGIANGIASGITVNSGAVINISGGYASSTIINSGGTLRYVLSDG	393	

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OY 346 -----KNID----- -TATSTPPESSSLGAGD 36
Db 394 YARGITLLNSNGEENVSNGCVSTNMAINTGNOYIISDGEATAIYVTSQFORIN--SGGT 451
OY 369 AP-----TLS-----VDGDALNVGSK-----DNKPRVITVAPGVKEGDVT 405
Db 452 APVONSVVYTRVTSAAKPFDAEYVSGKQFYVLMRGIVSYNPLTAVMSMFPETASGANV 511
OY 406 NVA-QLKGVAAQNLNKRIDNVGN----- -ARAGI 432
Db 512 NLSGRLNFAAGVAVGTITLNOEGRQYVYSGATATSTVGNNGREYVYSGITDGTVLNSG 571
OY 433 AQAITAGLVAQYVL--PCKSMATIG-----GGTYRGAGYAIGYSSIPDGN 477
Db 572 LQAVSSGKASATVINEGGAQFYVDDGQVYTGINKRGITTRDSCASALNTIALSSGN 629

RESULT 3
AG43_ECOLI
ID AG43_ECOLI STANDARD: PRT: 1039 AA.
AC P39180: P75614: P76360: P97241: Q46771:
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 43 precursor (AG43) (Fluifing protein).
GN FLU OR B2000.
OC Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655:
RX MEDLINE-97426617; PubMed-9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Berna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12:
RX MEDLINE-97251358; PubMed-9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasei H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Masubuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,
RA Siyansundaram S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horiiuchi T.;
RA "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-ML 308-225;
RA Henderson I.R., Owen P.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PRELIMINARY SEQUENCE OF 53-78.
RC STRAIN-ML 308-225;
RX MEDLINE-89291704; PubMed-2661530;
RA Caffrey P., Owen P.;
RT "Purification and N-terminal sequence of the alpha subunit of antigen
RT 43, a unique protein complex associated with the outer membrane of
RT Escherichia coli.";
RL J. Bacteriol. 171:3634-3640(1989).
RN [5]
RP SEQUENCE OF 53-63.
RC STRAIN-K12 / EMG2;
RX MEDLINE-97443975; PubMed-9298666;
RA Link A.-J., Rodison K., Church G.M.;

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Query Match	Best Local Similarity	Score 208	DB 1	Length 1039
Matches 130;	Conservative	65;	Mismatches 197;	Indels 168; Gaps 32;


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OY 1 MAKIIRITWNSALNMYVVSSELTNRNHTRASATVTAVALTLFFATVQA-----S 50
DB 5 LNTICRLVNMHTGFAFYFARARGRGVAVALSLPVLADIYVHGERTV 64
OY 51 ANTLKAGDNLIKQOTYSILKNDLPDLT-----SVGTCKLSFSAANGKVNITSDPK 100
DB 65 GGTLLNHNH-----QIVFGTTNGMTISTGLETPDNEANTGGVODGGTANKTIVTSG-- 118
OY 101 GINFAKETAGTNGDTVHLNGISGTLTDRASVKKDLNA-----GM 141
DB 119 GLQ-RVNPBGVSVDIVISAGG-QGSLQGRA--VNTTLNGEQGMHEGAIATGTVINDKGM 174
OY 142 NI-----KQYKANDFVRTYVEFLSADTKTTTVNVESSKNGKTEYKIG-A 187
DB 175 QYVKKPGVATVDIVNTVGAEGGPDANGDTCFVRDPAVKTITN-----KNGROIYRAEGTA 230
OY 188 KTSVKEKDKGLVTKDKGNGSSTDE-----GEGLV-----TAKEYIDANVKAQWBM----- 235
DB 231 NTTVV-----YAGDDQVYGHADDTLTLNGSYQYVHNGGTRASDVI--VNSGMOIVKNG 281
OY 236 ---KTTTANGQTGAQDFEYVTSNTVTFASG---KGTATVSKDDOG-NITVMYDVNV 287
DB 282 GYAGNTTVV-OKGRL-QVDAGGTATNTLKQGGALVTSTAATVT---GINELGAFSYVE 335
OY 288 GDLVNVNLONGNMLDSKAVAGSSGKYISGNVSPSKGMDTVNIMNNGNIEITRNKGN 347
DB 336 GQADV-VLENGG-RLD-----VLTGHTATN-----TRVDGGTLDV-RNG-- 373
OY 348 IDIATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKDKNRPVRLTNVAPGVEGDVTVV 407
DB 374 ---GTATTT-----VSMGNGC---VLLADSGAAVSGTRSGK-----AFSIGGGQADAL 415
OY 408 AOLKVAONLNRIIDVNGDNARAGIAQAIATAGLVQAVLPGKSMAGGGTTRGEGAVAI 467
DB 416 MLEKSSSEFLN-----AGDTATDTT-----VNGELTFARGGTFLA 449
OY 468 GYSSISDGNMIIKGTASGN 487
DB 450 GTTTLNNGAILTLTSGKTVNN 469

RESULT 4
YDBA_ECOLI
ID YDBA_ECOLI STANDARD: PRT: 2003 AA.
AC P3366; P76087; P76088; P76856; P76857; P76859;
DC 01-FEB-1994 (Rel. 28, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ydba.
GN YDBA OR B1401/B1405.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=9742617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12.
RX MEDLINE=9725157; PubMed=9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishino Y., Oshima T., Saio N.,
RA Sampei G., Seki Y., Sivasubram S., Tagami H., Takeda J.,

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RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 464-2003 FROM N.A.
RC STRAIN-K12;
RX MEDLINE=92190338; PubMed=1665988;
RA Moszer I., Glasner P., Danchin A.;
RT "Multiple IS insertion sequences near the replication terminus in
RT Escherichia coli K-12.";
RL Biochimie 73:1361-1374(1991).
CC -I- SIMILARITY: TO S.TYPHIMORIUM ORF NEAR CYSG (AC P25928).
CC -I- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR
CC THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT
CC BETWEEN AMINO ACIDS 839 AND 840.
CC -----
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CC -----
DR EMBL: AE000237; AAC74483.1; ALT_SEQ.
DR EMBL: AE000237; AAC74487.1; ALT_SEQ.
DR EMBL: D90778; BAA15009.1; ALT_SEQ.
DR EMBL: D90778; BAA18880.1; ALT_SEQ.
DR EMBL: D90779; BAA18881.1; ALT_SEQ.
DR EMBL: X62680; -, NOT_ANNOTATED_CDS.
DR Ecogene: EG11307; ydba.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 489 I -> V (IN REF. 2).
FT CONFLICT 495 I -> V (IN REF. 2).
SQ SEQUENCE 2003 AA; 205949 MW; B83A12C8B5220BE CRC64;

Query Match 6.9%; Score 175.5; DB 1; Length 2003;
Best Local Similarity 22.8%; Pred. No. 0.12;
Matches 119; Conservative 69; Mismatches 184; Indels 151; Gaps 27;

OY 33 TYKTAVLATLLEFATYQASANTLKADNLKIQFYSLKK-----DLTDLTSVGTCKL 84
DB 151 TEKTLTIDSVFTYENADGTTISLDS-NGRATATLMOIDEANTVALLEGVSAGATRW 209
OY 85 SESANGKNVNTISDTKGIN-----FAKETAGT-----NGDTVHLNGISGTL 126
DB 210 QYNHNGELY-ITGDNAIYNNNNKTYVDKDSGTETINNNKGVIODGLDVSGGHGIDI 268
OY 127 TDRAA-----SVKDVLMGWNITKGVKANDVFRTYVEFLSADTKTTTVNVESSKNG 178
DB 269 TGD SATVDNKGITMTYTDDESMGQIDGDKAIYNNGEESTITNGGTGTQINGDDATAANNNG 328
OY 179 KTEVKIKAKTSV---IKEKDGKLYTKDKGNG-----SSTDEGGLVTAKE-- 223
DB 329 KTT---VQKDSGTETIENGNNKGVIODGLDVSGGHGIDITGDSATVDNKGITMTYDPE 385
OY 224 ---VID-----AVNRAGMRKTTTANGQTGAQDFEYVTSNTVTFASGKGTATVASKDD 275
DB 386 SIGIYDDQDAVYVNEG---ESALINGGT-----TQINGDDAT-ANNNGKTTVDKDS 435
OY 276 QGNITVMTDVNVGDLANVNLONGNMLDSKAVAGSSGKYI-SGNVSPSKGMDTVNIN 334
DB 436 TGT-----EIAGNNGKVIODGDLVSG----- 458
OY 335 AGNNIEITRNKGNIDIAATSMT---PQFSSVSLGAGADAPTLSDGDALNVGSKDKNRPVR 391
DB 459 -GHGIDITGDSATVYVNGKGTMTYDPE---SIG-----TQIDSDQAVNNEGS---T 503
OY 392 ITNVAPGVKEGDVTVVLAOLKVAONLNRI-IDVNGDNARAGIAQAIATAGLVQAVLPGKS 450
DB 504 ITNGGTG-----TQINGNDATANNKSKTTVYDCKRSTG-TKTAGNIGIYV--LDG-S 550

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OY 451 MMAIGGTYRGEAGYAIYSSISDGNWIKTASGNSRCHFG 493
Db 551 LFTVGG-----AHGVENIGDNGTVNNKGDIVYSDGSIG 584

RESULT 5
HLA_SERMA
ID HLA_SERMA STANDARD: PRT: 1608 AA.
AC P15320;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN SHLA.
OS Serratia marcescens.
OC Bacteria: Proteobacteria: Gammaproteobacteria: Enterobacteriales:
OC Enterobacteriaceae: Serratia.
OX NCBI_Taxid=615;
RN [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
RC STRAIN-SNB;
RX MEDLINE=88257037; PubMed=3290200;
RA Poole K., Schiebel E., Braun V.,
RT "Molecular characterization of the hemolysin determinant of Serratia
RT marcescens."
RL J. Bacteriol. 170:3177-3188(1988).
CC -1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
CC DEFINED.
CC -1- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM
CC ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA
CC REQUIRES SHLB FUNCTION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -1- SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M22618; AAA50323.1; -
DR PIR: A26182; A26182.
KM Hemolysis; Toxin; Outer membrane; Signal.
FT SIGNAL
FT CHAIN
FT SQUENCE 1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;

Query Match 6.84; Score 173; DB 1; Length 1608;
Best Local Similarity 21.54; Pred. No. 0.12; Indels 232; Gaps 30;
Matches 141; Conservative 71; Mismatches 213;

OY 24 RNHTKR-----ASATVKTAVLATLFAVQASANTLAKADNLKIKQFTYSJKDL 73
Db 460 RNTTSSLRTGRMSNDESESLKASELRS-----EGELTKKGRNVTGCAVHQRDL 512
OY 74 T-----DLTSVTEKLSFSANG--NKVNITSPTKLNFAKEKTAGTNGDT 115
Db 513 TIDADNOIOYOVOKTANAKAVRDKTSMWIGIGGDKNN--SNRREISHASEL--TSGC- 567
OY 116 TVHLNG-IGSTLDRASVADVLANAGNINIGVKNVDFVRV-----DVEPELSAD 164
Db 568 TILNKGOGVTIT-----GSKARGQKGEGTATHGRLIDNALSTVDKIDAR 615
OY 165 TKTT---TVNVESEKDNKK---TEVKGAKTSVIREKDEKLV-----TG 202
Db 616 TGTAFNITSSSHKADNSYSSSTASBELKSDTNLTVSHKADVDIGSQVASGGLSVESKIG 675
OY 203 K---DKGENGSSSTDEGEGLVT---AKEVIDAVNKAQWRM-----KTT----- 238
Db 676 NINVKAEROONIDEOKTALTIVNGYAKADKQYRAGLRIRHTRDSEKTRTENSASLS 735

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OY 239 -----TANGOTGADKFEETVSTGNTVFAHGKOTTA----- 269
Db 736 GGSVKLKAEDVTFSSGSLVADKGDASVSQAKSFLLAADKTASNTBQRIIGGCFYTTGG 795
OY 270 -----TVSKDQGNITVMDVNVGDLANVNOQNSGMNLD 304
Db 796 IDKLGSGVEAGYENNNKTOAQSSKAITSGSDVKGNLT-----INARDKLTQOGAGHSVGAV 851
OY 305 SKVAGSSGKIVISGNVSPSKGMDERYINAGNIEITRNGKNDIATSMTPPPSSVSLG 364
Db 852 QENAGVDHLAADTASTTTTKTDVGNV-----GANVDYSAVTRPVERAAGKA 900
OY 365 A-----GADAPTSLVDGDLNMGSK--DNKPVRITNVAPGV---KEGPV-- 404
Db 901 AKLDATGVINDIGGICGAPNVGLDIGAGGSSSEKSSSSQAVSSVQAQSIDINAKGEYRD 960
OY 405 -TNVAQLKGVQNLN-----NRIDNVGNMRAGITQAIAVAGLVQAVLPKSKMM 452
Db 961 QGTQYQASKG-AVNLTADSHRSEPAANRDEQSRDTR-----GSAG-VRYVTTTGSGL 1011
OY 453 AIG-----GGTYREAGYAIYSSISDGNW-----IKGTASGNSRCHGASA 496
Db 1012 TVDAKGEGETQRNSNSASQAVTGSIDAANGINNVKKAIDYQGTALNGRGTAYNA 1068

RESULT 6
OMPA_RICRI
ID OMPA_RICRI STANDARD: PRT: 2249 AA.
AC P15921;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface
DE antigen) (rOmpA) (rOmp A).
GN OMPA.
OS Rickettsia rickettsii.
OC Bacteria: Proteobacteria: Alphaproteobacteria: Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_Taxid=783;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-R;
RX MEDLINE=90354033; PubMed=2117568;
RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;
RT "A protective protein antigen of Rickettsia rickettsii has tandemly
RT repeated, near-identical sequences."
RL Infect. Immun. 58:2760-2769(1990).
CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -1- PTM: GLYCOSYLATED (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
CC -----
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CC -----
DR EMBL: M31227; AAA26380.1; -
DR PIR: A41477; A41477.
DR InterPro: IPR006315; Autotransport.
DR InterPro: IPR005546; Autotransporter.
DR Pfam: PF03797; Autotransporter; 1.
DR TIGRFAMs: TIGR01414; autotransp_bar1; 3.
KM Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.
FT SIGNAL
FT CHAIN
FT DOMAIN 29 2249
FT REPEAT 212 1180
FT 212 286
FT A (TYPE 1).

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FT REPEAT 287 358 B (TYPE II).
FT REPEAT 359 430 C (TYPE II).
FT REPEAT 431 505 D (TYPE I).
FT REPEAT 506 577 E (TYPE II).
FT REPEAT 578 652 F (TYPE II).
FT REPEAT 653 724 G (TYPE II).
FT REPEAT 725 799 H (TYPE I).
FT REPEAT 800 874 I (TYPE I).
FT REPEAT 875 949 J (TYPE I).
FT REPEAT 950 1021 K (TYPE II).
FT REPEAT 1022 1093 L (TYPE II).
FT REPEAT 1094 1165 M (TYPE II).
FT REPEAT 1166 1180 TYPE I (INCOMPLETE).
SQ SEQUENCE 2249 AA; 224333 MW; A9D6646C089DF087 CRC64;

```

Query Match 6.8%; Score 173; DB 1; Length 2249;

Best Local Similarity 24.8%; Pred. No. 0.18; Mismatches 225; Indels 168; Gaps 31;

```

Matches 148; Conservative 56; Mismatches 225; Indels 168; Gaps 31;

QY 27 TKRASATVKTAVIATLLFATVQASANTLKAGDNLIKQFTYSLKK---DLTDLTSVGT 81
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 714 TFGTGNSTVTGIDIGNTNALTAVNAGATATGAGV-IKATFTKLTNASVLTLTNANAVLT 772
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 82 EKLSFSANGKRVNTSDTKGNFA-KETAGTNGPT-----TVHLNG--IGSTLT 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 773 GADINTTGGDNVGLN---LNGALSOYTGIDIGNTSLATISVGAGTATGGAIVIKATTT 828
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 128 --DRAASVDKLVNAGNMIKGVKNDPFRITYDVEFLSADTKTTVYNESKDKGKTEYKI 185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 829 KLTNAAVSLTLTNANAVLTGA--VDNNTGGDNVGLNGLALSOYTGIDIGNTSLATISV 886
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 186 GAKT---SVYKEDKGL-----V 200
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 887 GAGTATGGAIVIKATTTKLTNASVLTLTNANAVLTGADNTTGGDNVGLNGLALSOV 946
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 201 TGNKKGNGSST-DEGEIVT---AKEVIDANNAKGMKRTTANGQNGQADKEFYVT 254
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 947 TGDIGNTNLSLATISVGATATGGAIVIKATTTKLTDASAVKFTNPVYVGTADINTGNAN 1006
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 255 SGTNVTFASGKGTATVASKDOGNITVYDVNVDALNVQLONSGMNLDKAVAGSSGK 314
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1007 NGI-VTFGTNGSTVGNV-----GNTNALTAVNAGV--LQVQGVKANTINLTNDSA 1058
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 315 VTSNVSPEKSKMDEYVNIANG-----NIEITRNKNIDIAITSMTPQFSSVSLGAGADA 369
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1059 VTFNPNVYVGTADINTGNANNGIVTFGTNGSTVGNVGN-----TNALATVNVGAG-- 1108
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 370 PTLSDVDGAL--NVGSKKDN-KPVRTINVAPGVKEGDTTNAQLKGVANQNNRINDVDG 426
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1109 -LLQVQGVKANTINLTNDSAVTFN--PVVVTGALIDNTG-----NANNGIVTFGTG 1158
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 427 NARA-----GLAQAIAT-----AGL-VQAVLPGKSMMA-----IGGTYRG 461
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1159 NSYTGIDIGNTNALTAVNAGVIGTLQA---GGSILANNIDFGASTLEFNPDLGG----- 1211
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 462 EAGTAIGT---SSISDGNWIIK-----GTASGNSRGH---FGASASVG 499
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1212 --GRAIIFYEKGALANGNNAILNVNFKLLTFASHLITIGVAEINIGAGNLFTIDASVG 1266
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 7

```

ID ICEN_XANCT STANDARD; PRG; 1567 AA.
AC P18127;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ice nucleation protein.
GN INAX.
OS Xanthomonas campestris (pv. translucens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=343;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=X56S;
RX MEDLINE=91080859; PubMed=2259339;
RA Zhao J., Orser C.S.;
RT "Conserved repetition in the ice nucleation gene inax from
   Xanthomonas campestris pv. translucens.";
RL Mol. Gen. Genet. 223:163-166(1990).
CC -I- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
   CRYSTALLIZATION IN SUPERCOOLED WATER.
CC -I- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
   OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
   REGIONAL 48-RESIDUE PERIODICITY IS SUGGESTED IN WHICH THE ICE
   NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
CC -I- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
   FAMILY.
CC -----
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CC -----
DR EMBL; X52970; CAA37140.1; -.
DR HSSP; P06620; 11NA.
DR InterPro; IPR000258; Ice_nucleatn.
DR Pfam; PF00818; Ice_nucleation; 81.
DR PRINTS; PR00327; ICENUCLEATN.
DR PROSITE; PS00314; ICE_NUCLEATION; 57.
DR K W Ice nucleation; Repeat; Outer membrane.
SQ SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;

```

Query Match 6.8%; Score 172; DB 1; Length 1567;

Best Local Similarity 20.9%; Pred. No. 0.13; Mismatches 237; Indels 94; Gaps 21;

```

Matches 107; Conservative 74; Mismatches 237; Indels 94; Gaps 21;

QY 20 SELFRNHTKRASATVKTAVIATLLFATVQASANTLKAGDNLIKQFTYSLKDLTDLT-- 77
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 808 SDITAGYGTGTAAADSTLIAGYGTQTSQSDSLTLAGY-----STQARRESDYTAG 861
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 78 -----SVTEKLSFANGKNVNTSDTKGNLFAKETAGTNGDTTVHLNGIGSTLTLDRAAS 132
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 862 YGSGTGAADSTLISGV-----STQFAGSDSLTA---GYGSGTARKGS 904
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 133 VKDVLNAGNMIKGVKND--FRTIYDVEFLSADTKTTVYNESKDKGKTEYIKAKTS 190
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 905 --DV-TAGYGTGTAGADSTLIAGYGTQTSQSDSLTLAGYGTQFARKGSDMTAGYGST 961
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 191 VIREKDKLVYKRGKNGSGSTDEGEIVYAKEVIDAVNNAKGMKRTTANGQNGQADKEF 250
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 962 GTAGADSTLIAG-----YGTQTSQS-----DSSLTLAGYGTQFARBSVYTAGY 1007
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 251 ETVTSGTNVTFASGKGTATVASKDOGNITVYDVNVDALNVQLONSGMNLDKAVAG 310
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1008 STGTAGADSTLIAGYGTQFAGSD--SSLTLAGY-----GSTQFARBSVYTAGY 1061
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 311 SSGKVISGNSVPSKGMDEYVNIANGNIEITRNKNIDIAITSMTPQFSSVSLGAGADAP 370
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1062 ADSTLIAGYGTQFARBSVSLTLAGYGT--QFARBSGSD-----TAGYGTGT--AGADSS 1113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 371 TLSVDGALNVGSKDKMKPVRTINVAGV-----KEGDTTNAQLKGVANQNNRINDN 423
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1114 LIAGYGTQFAGYD-----SMTAGYGTQFARBSVSLTLAGYGTSTAGHSSSLIAG 1165
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 424 VDGNNARAGIAQAIATA-GLVQAVLPGKSMMAIGGTYRGAGY---AIGYSSISDGC-- 476
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1166 YGSGTQFAGYNSILTLTGYSGTQFAGESSLTLAGYGST--STAGYDSTLIAGYGTQFAGYK 1223
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 477 NWIIKGTASGNSRGH-----FGASASVGTQ 501

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Db      92 LLNTANNLAVTSEDTTLTGTINNVNNAHSFNTLNAGKTLTTTQ-----GVTN 142
QY      49 ASANTLKAGDNLIKQFTYSLKKDLTDLTSV-----TEKL-----84
Db      143 AQAAPAKNAQNV-VQVFNNGCAIDNNDLKGRIIDEGAPASTVLENLAPTTQAPLILG 201
QY      85 -SEFANG--NKVNT-----SDTKGLNFAKETAGTN-----GDT 115
Db      202 DNVIANGVNGTLNVTGFIQVSNKSFATYKAINIAGOGGIIFFITDANNNTLNLOAGT 261
QY      116 TVHLNGIGST-----LTDRAASYKVDL--NAGNINIKVKNVD-----VRYDVEFLSAD 164
Db      262 TINFETGDTGTRLVLLSKHAATAATNFNTGSLGRLKGV--IEFTVAVDQITFANAGAN 319
QY      165 TKTTTVV-----VESKNGKRTV--KIGAKTSYIKERDGLVYTK-----KGE 207
Db      320 AVIGTNGAGRAAGFVVSVDNGKVATIDGOVYAKDAVIOASAN--ATGOVNFRIHVDVA 376
QY      208 NGS-----STDEGEGLVTAKEVIDAV-----NKAGMR 234
Db      377 DGTAFKTAASKVTTIGDSNFGNMDFG-NLAQIKVPMNATITGNTFGDASNPENTAG-- 433
QY      235 MKTTTANG--QTGOADKFEVTSCTNVTASGKT-----TATVSKDDGNTTMYDV 285
Db      434 VITFDANGTLESASADANVAVTNNITAIASGAGVVOIGSTHAELRLGNAGSIFKLAD- 492
QY      286 NVDGALN--VNOJONGSMNLSKAVAGSSKVISGKSPSKGM-----327
Db      493 -GTIVNGKVNQALVGALAACTITLDGSAATTITDIGNMGAAALORTILANDAKTLT 550
QY      328 -----DEVNINA--GNNEITPENGKNI-----DIATSMPEQFSVSLGAGADAPT 372
Db      551 LGGANITGAGGGTIDLGANGTITKLTSTONNIIVVDPLALIA-TDQTEVNVASSLTNNQ 609
QY      373 SVDS-----DALVGSK--DNKEPRTVNAAGVKEGV-----TNVA 408
Db      610 TINKKIGTIGANNKTLIGOFNIGSSKTVLSNGNVAINELVIG-NDGAVQFAHDTYLITRT 668
QY      409 QLKGAONLNRIIDNVGNARAGIAQAIATAGLQAVLTPK-----SMMAIGGTYRGEA 463
Db      669 MAAGGKIIFNPVYNNCTTTLAAGTINLGSATNPILAETINFGSKGVAVDTLVNGBSVL- 725
QY      464 GYA-----IGYSISDGGNMWIIKGTASGNSRGHGASA 496
Db      726 -YATNTTTDANVGSFVFNAGGTIVSGTVGGGQGNKFNHYA 766

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RESULT 11
OMP_RICITY STANDARD; PRT; 1645 AA.
ID OMPB_RICITY STANDARD; PRT; 1645 AA.
AC P96989;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scat) (rOMP)
DE (Comp B) [Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
CN OMPB OR SLP.
OS Rickettsia typhi.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_Taxid=785;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Williamston;
RX MEDLINE=94040787; PubMed=8224886;
RA Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;
RT Cloning and sequence analysis of the gene encoding the crystalline
RT surface layer protein of Rickettsia typhi.";
RL Gene 133:129-133(1993).
RN [2]

```

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RP PARTIAL SEQUENCE.
RC STRAIN=Williamston;
RX MEDLINE=92114896; PubMed=1370573;
RA Ching W.M., Carl M., Dasch G.A.;
RT Mapping of monoclonal antibody binding sites on CNR fragments of
RT the S-layer protein antigens of Rickettsia typhi and Rickettsia
RT prowazekii.";
RL Mol. Immunol. 29:95-105(1992).
RN [3]
RP IDENTIFICATION OF CLEAVAGE SITE.
RX MEDLINE=92104668; PubMed=1729180;
RA Hackstadt T., Messer R., Cieplak W., Peacock M.G.;
RT Evidence for proteolytic cleavage of the 120-kilodalton outer
RT membrane protein of rickettsiae: identification of an avirulent
RT mutant deficient in processing.";
RL Infect. Immun. 60:159-165(1992).
CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
CC -----
CC THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION
CC BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION -
CC THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS
CC USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY
CC MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL
CC ENTITIES REQUIRES A LICENSE AGREEMENT (SEE HTTP://WWW.ISB-SIB.CH/ANNOUNCE/
CC OR SEND AN EMAIL TO LICENSE@ISB-SIB.CH).
CC -----
DR EMBL: L04661; JAB4987.1; -.
DR PIR: JN0896; JN0896.
DR InterPro: IPR006315; Autotransport.
DR InterPro: IPR005546; Autotransporter.
DR Pfam: PF03797; Autotransporter; 1.
DR TIGRFAMs: TIGR01414; autotransp_bar1; 1.
KW Antigen; S-layer; Transmembrane; Cell wall.
FT CHAIN 1 1353 120 KDA SURFACE-EXPOSED PROTEIN.
FT TRANSMEM 1415 1645 32 KDA BETA PEPTIDE.
FT CONFLICT 657 657 MEMBRANE ANCHOR (POTENTIAL).
FT CONFLICT 842 842 H -> N (IN REF. 2).
FT CONFLICT 1071 1071 V -> I (IN REF. 2).
FT CONFLICT 1306 1306 G -> A (IN REF. 2).
FT CONFLICT 1306 1306 G -> S (IN REF. 2).
SQ SEQUENCE 1645 AA; 169698 MW; 0CB5641C7EB185EE CRC64;

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Query Match 6.5%; Score 165; DB 1; Length 1645;
Best local similarity 21.6%; Pred. No. 0.32;
Matches 117; Conservative 77; Mismatches 210; Indels 138; Gaps 25;

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QY 46 TVQASANTLKAAGNLKIKQFTYSLKKDLTDLTSVTEKLSFSANGKNVNTSDPKGLNFA 105
Db 141 TQAQAAAT-ksaQNVVSKVNGAIAIND-NLDSGSGIDFPAAPVLEFENLNP-----T 193
QY 106 KETAGTNGDPTVHLNGIGSTL--TDRASASYKVDVLAAG--WNIGKVKNVDVFRYDVEFL 160
Db 194 QEAPLTIGDNNAKIYNGANGILINTNGFVYKSDKFAKIKTINIGDNGLGFNPTPDANA 253
QY 161 LSAIDTKTTTVNVESKD-----NGKRTVKI--GAKTSYIKERD-----GKL- 199
Db 254 LNLGGGNTITNFNGRDGTGLVLSKNGNATFENVGSLGNLKGIVLEFDTAAAGKILIA 313
QY 200 -----VTGKDKGENS-----STDG-----EGVTAKEVIDAVKAKGRMKTTPANG 242
Db 314 NGGAANAIVGTDNAGRAAGFIYVDNGNNAATISGVYADIV-----IQSANAGG 364
QY 243 QT-----GGADFEFVTSCTNVTASGKKTITVSDOGNTTMYDVN-----286
Db 365 QVTFEHLVDVGLGKTKFKAADSIVITTEANSEST-----DEGNLAVQIVPNKMLIT 418
QY 287 ---VGDALNVNQLONGSMNLSKAVAGSSKVISGKSPS-----KGKDETVNI----- 333

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Db 419 GNFIDA-----KNG--NTAGVTFNANGTLVSGTDPNIVTNIKIEVEGAGIYOLS 471
Oy 334 -----NAGNNEITRNCKNIDIAITSMTPOSSVSLGADAPLTVSDGL---N 380
Db 472 GHHGAEHLGNAGSIFKLA-DGVINGPVNONPLVNNALAG-----STLDGSAITIGD 526
Oy 361 VGSKDKNPVRITTVNAPGVKEGDTVTVNAQLKGVAONLNNRIDVDGNARAGIAQAIATAG 440
Db 527 ICGAVNALADIDITLA-----NDASKILTLSCA-----NIGANAGAGIHFQANCG 572
Oy 441 LVQALPRKSMALIGCGTTRGAGATGSSISDGNMIKT-----ASGSRHFGAS 495
Db 573 TQLTSTGNLILVDFDLDTDTQTSVAVSSLTNNQTLTNGSIGTIGANTKTILGRFNVG 632
Oy 496 AS 497
Db 633 SS 634

RESULT 12
WAPA_BACSU
ID WAPA_BACSU STANDARD: PR1: 2334 AA.
AC 007833:
DF 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Wall-associated protein precursor.
GN WAPA OR N17G.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168:
RX MEDLINE=93302506; PubMed=8316082;
RA Foster S.D.;
RT "Molecular analysis of three major wall-associated proteins of
RT Bacillus subtilis 168: evidence for processing of the product of a
RT gene encoding a 258 kDa precursor two-domain ligand-binding
RT protein."
RL Mol. Microbiol. 8:299-310(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / BGSC1A1;
RX MEDLINE=95219088; PubMed=7704263;
RA Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;
RT "Cloning and sequencing of a 29 kb region of the Bacillus subtilis
RT genome containing the hut and wapa loci."
RL Microbiology 141:337-343(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / BGSC1A1;
RX MEDLINE=97124196; PubMed=8969509;
RA Yoshida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai N.,
RA Miwa Y., Fujita Y.;
RT "Sequencing of a 65 kb region of the Bacillus subtilis genome
RT containing the ltc and cel loci, and creation of a 177 kb contig
RT covering the gut-sacxy region."
RL Microbiology 142:3113-3123(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerthon I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Erlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,

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RA Guisepi G., Guy B.J., Haga K., Hitech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Kjaer-Blanchard M., Klein C.,
RA Kobayashi Y., Koester P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogilawa A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Preece E., Puig P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha F., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serro P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassaretto A.,
RA Viari A., Wambuit R., Wedler E., Wedler H., Weitzneger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
CC -I- FUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM,
CC MOTILITY, SECRETION OR DIFFERENTIATION. MAY BE RELEASED
CC -I- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
CC INFO THE MEDIUM.
CC -I- DOMAIN: HAS TWO LIGAND-BINDING DOMAINS; THE N-TERMINUS, HAS THREE
CC 101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE
CC C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED
CC MOTIF REPEATED 31 TIMES.
CC -I- SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME
CC SIMILARITY TO THE REPEAT IN E.COLI RBS GROUP OF PROTEINS (RHSA-D).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL: L05634; AAA22883.1; -
DR EMBL: D31856; BAA06656.1; -
DR EMBL: D29985; BAA06260.1; -
DR EMBL: D83026; BAA11683.1; -
DR EMBL: Z99124; CAB15959.1; -
DR PIR: S32920; S32920.
DR Subtilist; BG10797; wapa.
DR InterPro: IPR003305; CBM_Cenc.
DR InterPro: IPR006530; YD.
DR Pfam: PF02018; CBM_4_9; 1.
DR TIGRFAMS: TIGR01643; YD_repeat_2x; 17.
KW Cell wall; Repeat; Signal; Complete proteome.
FT SIGNAL 1 28 OR 32 (POTENTIAL).
FT CHAIN 29 2334 WALL-ASSOCIATED PROTEIN.
FT DOMAIN 504 869 3 X 101 AA APPROXIMATE TANDEM REPEATS.
FT REPEAT 504 605 1-1.
FT REPEAT 606 736 1-2.
FT REPEAT 737 869 1-3.
FT DOMAIN 1021 2139 31 X 21 AA APPROXIMATE TANDEM REPEATS OF
FT REPEAT 1021 1040 X(4)-G-X(4)-[YF]-X-D-X(2)-G-X(4).
FT REPEAT 1041 1061 2-1.
FT REPEAT 1062 1082 2-2.
FT REPEAT 1083 1102 2-3.
FT REPEAT 1103 1128 2-4.
FT REPEAT 1129 1148 2-5.
FT REPEAT 1149 1169 2-6.
FT REPEAT 1170 1193 2-7.
FT REPEAT 1194 1218 2-8.
FT REPEAT 1219 1238 2-9.
FT REPEAT 1239 1265 2-10.
FT REPEAT 1266 1286 2-11.
FT REPEAT 1287 1307 2-12.

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FT REPEAT 1690 1709 2-13.
FT REPEAT 1711 1730 2-14.
FT REPEAT 1732 1751 2-15.
FT REPEAT 1753 1772 2-16.
FT REPEAT 1795 1814 2-17.
FT REPEAT 1820 1839 2-18.
FT REPEAT 1840 1859 2-19.
FT REPEAT 1861 1880 2-20.
FT REPEAT 1887 1906 2-21.
FT REPEAT 1908 1927 2-22.
FT REPEAT 1929 1948 2-23.
FT REPEAT 1969 1982 2-24. (APPROXIMATE).
FT REPEAT 1983 2002 2-25.
FT REPEAT 2008 2027 2-26.
FT REPEAT 2028 2047 2-27.
FT REPEAT 2051 2070 2-28.
FT REPEAT 2071 2090 2-29.
FT REPEAT 2093 2112 2-30.
FT REPEAT 2120 2139 2-31.
SQ SEQUENCE 2334 AA; 258329 MW; B75138CD278BAA3 CRC64;

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Query Match 6.58; Score 165; DB 1; Length 2334;
Best Local Similarity 22.58; Pred. No. 0.49;
Matches 106; Conservative 64; Mismatches 181; Indels 120; Gaps 22;

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QY 23 TRNHTKRSATVK--TAVLATL-----LFATVQASANTLAKGDLK-----IKQ 64
DB 970 THRTTKRADGTGPTGVLELEFETADQFLKTKEDQNAFENKKGKGLQVNDGHNAATV 1029
QY 65 FTVSLKADLTDLFSVTEKLSFS--ANGKNVNTS--DTKGLNFA-----KETAGTNGDT 115
DB 1030 YTVYNDKQQLATIDTASGRKLTFTYDENGHTSITGPKNKVTVSYENDLLKVTDTGTV 1089
QY 116 TVH-----LNGISLTLDRAASVADVNLAGNIN---GVKNVDVPRYDIYEFISAD 164
DB 1090 TSYDYDESEGLVQVYANSSTEARFVTEYQYSGHLEKAINAKKETVYSID-----AD 1143
QY 165 TKTTTVAVESKDNKKTVEV--KIGAKTSVKEKDGKLV-----GKDKGENGSTDEG 215
DB 1144 KKTILM---TQPNKRKQVQYVNEGNPIQYIDAEGLKITTNKYEENNVVEDDPDVG 1200
QY 216 EGLVTAKEVIDAVNKAQRMKTTTANGQGOADKFETVS-----GTVTFASGKGTAT 270
DB 1201 TGRAT-----ESYQYDKQGNVTSVKDAYGTE--TYEYKKNNDVT 1237
QY 271 VSKRDQGNIT--VMYDVAVGDLANNOJLNSGNMNDLSKAVAGSSGKTVSGNVSPEKG--KMD 328
DB 1238 KMKDTGNAVTDIAD-----GLDAVSETDQSGKSSSAAYDKYGNQIQ 1280
QY 329 ETVVINGNNIETIRNCKNIDIASMTPOFSSVSLGAGADAPTLVGDALNVSCKDKN 388
DB 1281 SSKRLSASTN--ILKDG-----SFEAKSGMWLTKSKDRKRTSVIADSGVLSGSKAL 1331
QY 389 PVRTTNVAPGVKEG--DVTNVAQLKGVAQNLNINRDNVDGNARAGIAQATA 437
DB 1332 EVLSQTSAGTDHGYSSATQTELE-----PNTTYLTSKIKTKDLAKSRA 1376

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RESULT 13
SLAP_CAUCR STANDARD; PRT; 1025 AA.
AC P35828; Q46015; Q9RF12;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE S-layer protein (Paracrystalline surface layer protein).
GN RSPA OR CC1007.
OS Caulobacter crescentus.
OC Bacteria: Proteobacteria: Alphaproteobacteria: Caulobacteriales:
CC Caulobacteraceae; Caulobacter.
CX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21; 646-660 AND 1021-1025.

```

```

RC STRAIN-ATCC 19089 / CB15;
RX MEDLINE=93007489; PubMed=1393820;
RA "Glichrist A., Fisher J.A., Smit J.K.;
RT "Nucleotide sequence analysis of the gene encoding the Caulobacter
RL crescentus paracrystalline surface layer protein.";
RN Can. J. Microbiol. 38:193-202(1992).
RP REVISIONS TO 376; 636 AND 842-843.
RA Awram P.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-JS3001;
RA Bingle W.H., Awram P.A., Nomellini J.F., Smit J.K.;
RT "The secretion signal of C. crescentus S-layer protein is located in
RL the C-terminal 82 amino acids of the molecule.";
RN Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RP [4]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Niernan W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Onta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA Deboy R.T., Dodson R.J., Durkin A.S., Gwin M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Unterhark T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RL "Complete genome sequence of Caulobacter crescentus.";
RC Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
RN [5]
RP SEQUENCE OF 1-313 FROM N.A., AND SEQUENCE OF 1-20.
RC STRAIN-ATCC 19089 / CB15;
RX MEDLINE=8908089; PubMed=3049545;
RA Fisher J.A., Smit J.K., Agabian N.;
RT "Transcriptional analysis of the major surface array gene of
RL Caulobacter crescentus.";
RN J. Bacteriol. 170:4706-4713(1988).
RP [6]
RP CHARACTERIZATION.
RC STRAIN-ATCC 19089 / CB15;
RX MEDLINE=98292737; PubMed=9620954;
RA Awram P., Smit J.K.;
RT "The Caulobacter crescentus paracrystalline S-layer protein is
RL secreted by an ABC transporter (type I) secretion apparatus.";
RN J. Bacteriol. 180:3062-3069(1998).
RP [7]
RP FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. PROBABLY ACTS AS A
PHYSICAL BARRIER TO PARASITES AND LYTIC ENZYMES.
-1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
LAYER WITH HEXAGONAL SYMMETRY. SECRETED BY AN ABC TRANSPORTER
(TYPE I) SECRETION APPARATUS.
-1- MISCELLANEOUS: THE CALCIUM BINDING OF THIS PROTEIN MAY MEDIATE
SURFACE ATTACHMENT BY IONIC BRIDGING BETWEEN THE S-LAYER AND A
SPECIFIC MEMBRANE-ASSOCIATED OLIGOSACCHARIDE.
-----
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EMBL; AF062345; AAC38665.2; -
EMBL; AF193063; AAF19365.1; -
EMBL; AE005779; AAK22991.1; ALT_INIT.
PIR; A48995; A48995.
HSSP; P22629; 1SMC.
TIGR; CC1007; -
InterPro; IPR001343; Hemlysn_Ca_bind.
Pfam; PF00353; hemolysincabind; 3.
PRINTS; PR00313; CAMDNGRPT.

```


KW Cell wall; S-layer; Calcium-binding; Complete proteome.
 FT INIT_MET 0
 SQ SEQUENCE 1025 AA; 98001 MW; AD7A326E1363D8AC CRC64;
 Query Match 6.5%; Score 164.5; DB 1; Length 1025;
 Best Local Similarity 22.9%; Pred. No. 0.2; Mismatches 220; Indels 165; Gaps 28;
 Matches 135; Conservative 66; Mismatches 220; Indels 165; Gaps 28;
 34 VRTAVLATL-----FATVQAS-AMTLKAG---DNLK-IKOFYSLHKDLTDLT 77
 191 VKAALIGTILNATVSGIGVATATAAMINDSLDNLSDNAGVNLFTAYSSGVSGST 250
 78 ---SVTEKLSFSAN-----GKNVNTSDTKGLNFAKETAGTNGDTT 117
 251 ISLTGTDTLTGTAGNDTFVAGEVAGAAATLVGDTLSGAGAGDVINWVOAAVTAALPGV 310
 118 HNGTIGSTLTDRASVSKVDLNGMNIKGVK--NVPEFVRTYDV-----EELSADRTTV 170
 311 TISGLEIMNVISGAI--TLNTSSGVTLTALNTISGAQVTVAGAGONLTATTAAQAA 368
 171 NVESKDNCKTEVKIGAKTSVIERKDKLVTKDKENG-----SSTDEGEGLVTA 221
 369 NNVAVDGGAIVTV--ASTGV---TSGTTVGANSAAGTGSVSVAANSSTTTTGAIAVYG 422
 222 KEVIDAVNKAGRKAKTT-----TANG-----OTGQADKEEYVTSCTN--VTF-- 261
 423 GTAVTVAOTAGNAVNTTLTADVTVGNSSTTAVTGTAAATAGATVAGRVAGVATTTD 482
 262 ---ASGKGTATVSKDQGNITV---MYDVNVGD-----AL 291
 483 SAAASATTAGKATVATLTSFGAATIDSSALITVNLISGIGTSIGIRGALTANPTANTLT 542
 292 NVNOLNSGWNLSKAVAGS-----SGKVISGNVSPSKMKDETVINAGNIEITEN 344
 543 NVNGLTTGATIDSEAADDEFTTINAGSTASSTIASLVAAADATLNTISGARVTTISH 602
 345 -----GKNI--DIATSMTPQFSSVSGAGADAPTLVSDDALNVGSKKDK 388
 603 TAAALTGTITVNSVATLGAELATGLV--FTG--GAGADSLTIGATTKAIYMGAGDDTV 657
 389 PVRTNNVAPG--VKEGDTVNVAKLGVAONLNRRIDNV-----GNARAG--- 431
 658 TVSSATLGAAGSVNGDGDIV-----LVANVGSSFSADPRAGGETTLRVAGAAAGSHN 712
 432 ----IAQAIATAGLVQ---AYLPKSKMAIGGTYRGEAGYAIGYSSI 472
 713 ANGFTALQIGATAGATFTTNVAVNVGLFVLAFTGTTVTLTANAGTSDV 762
 RESULT 14
 APU_THERU STANDARD; PRT; 1861 AA.
 ID APU_THERU
 AC P38536;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Amylopullulanase precursor (Alpha-amylase/pullulanase) (Pullulanase type II) [Includes: Alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase); Pullulanase (EC 3.2.1.41) (1,4-alpha-D-glucan glucanohydrolase) (Alpha-dextrin endo-1,6-alpha-glucosidase)].
 GN AMVB.
 OS Thermoaerobacter thermosulfurogenes (Clostridium
 OS Thermosulfurogenes).
 OC Bacteria; Firmicutes; Clostridia; Thermoaerobacteriales;
 OC Thermoaerobacteriaceae; Thermoaerobacterium.
 OX NCBI_TaxID=33950;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 3896 / EML;
 RX MEDLINE=9425298; PubMed=8195085;
 RA Matuschek M., Burchardt G., Sahm K., Bahl H.;
 RT "Pullulanase of Thermoaerobacterium thermosulfurogenes EML
 RT (Clostridium thermosulfurogenes): molecular analysis of the gene,

RT composite structure of the enzyme, and a common model for its
 attachment to the cell surface.";
 RL J. Bacteriol. 176:3295-3302(1994).
 CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 linkages in oligosaccharides and polysaccharides.
 CC -I- CATALYTIC ACTIVITY: Hydrolysis of (1->6)-alpha-D-glucosidic
 linkages in pullulan and in amylopectin and glycogen, and the
 alpha- and beta-limit dextrans of amylopectin and glycogen.
 CC -I- SUBCELLULAR LOCATION: CELL-BOUND. IF C-TERMINUS MAY SERVE AS AN
 S-LAYER ANCHOR.
 CC -I- PTM: GLYCOSYLATED.
 CC -I- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC -I- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -I- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 or send an email to license@isb.ch).
 CC
 DR EMBL: M57692; AAB00841.1; .
 DR HSPD: Q08751; IBV2.
 DR InterPro: IPR006589; ALP_amy1_cat-sub.
 DR InterPro: IPR006048; Alpha_amy1_C.
 DR InterPro: IPR006047; Alpha_amy1_cat.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR004185; Glyco_hydro_131g.
 DR InterPro: IPR004193; Glyco_hydro_13N.
 DR InterPro: IPR001119; SLH.
 DR Pfam: PF00128; alpha-amylase; 1.
 DR Pfam: PF02806; alpha-amylase; 1.
 DR Pfam: PF02903; alpha-amylase; 1.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF02922; Isoamylase; 1.
 DR Pfam: PF02935; SLH; 3.
 DR SMART: SM00642; Aamy; 1.
 DR SMART: SM00632; Aamy_C; 1.
 DR SMART: SM00060; FN3; 2.
 DR PROSITE: PS01072; SLH_DOMAIN; 3.
 DR PROSITE: PS01072; SLH_DOMAIN; 3.
 KW Hydrolyase; glycosidase; Carbohydrate metabolism; Signal; Repeat;
 DR Multi-functional enzyme; Glycoprotein.
 FT SIGNAL 1 35
 FT CHAIN 36 1861
 FT DOMAIN 928 1018
 FT DOMAIN 1157 1248
 FT ACT_SITE 628 628
 FT ACT_SITE 657 657
 FT ACT_SITE 734 734
 FT DOMAIN 1681 1739
 FT DOMAIN 1740 1803
 FT DOMAIN 1804 1861
 FT CONFLICT 1734 1734
 SQ SEQUENCE 1861 AA; 206104 MW; 06C23070E453B574 CRC64;
 Query Match 6.5%; Score 164.5; DB 1; Length 1861;
 Best Local Similarity 20.8%; Pred. No. 0.4; Mismatches 229; Indels 155; Gaps 26;
 Matches 122; Conservative 81; Mismatches 229; Indels 155; Gaps 26;
 2 NKIYRIWNSALNA-----WVVSSELTFRNHRKASATVKTAVL----- 39
 1208 NEVNYIDTVSYANGTVYKVAVDLSENRRESNVVTKIPVIVFTVDPYDTPDA 1267
 40 ----ATLFAIVQASANTLKAGDNLIKQFIYSLKDLTDSVTEKLSASGNKNKVI 95
 1268 VNLAGTFPNAWDPQAQOM-----TKIDNNYTSITLTDE---GTQLEYRYARCSMDKV 1318
 96 TSDTGLNFA---KTAGTNGDTVHLNGI-----GSTLT-DRASVSKDV 137
 1319 EKDEYGNFASNRKVTIYNGNENKTIINDIYRMRDIFIFLYSPSSNMFTVDSNISTMEV- 1377

Db 808 VNNGSLIIGDDSVVDVNVSYIPTGYTYNALLMADGEGSTIENKGDITSHGVSVIRAD 867
Oy 468 GYSISIDGGMWIKGTASGNSRGHFGASAVG 499
Db 868 NGSEVNSGDIIVYATSSNSSEDRAAIRASG 899

Search completed: October 6, 2003, 09:24:06
Job time : 10,7522 secs

.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:10 : Search time 36.8701 Seconds
(without alignments)
3513.485 Million cell updates/sec

Title: US-09-771-382-27
Perfect score: 2544
Sequence: 1 MKKIRIINSLNMAWVVS.....TASGNSRGHFGASASGYQW 502

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2459.5	96.7	591	09JPR18	09JPR18 neisseria m
2	2455.5	96.5	591	09JPS7	09JPS7 neisseria m
3	2455	96.5	592	09AOF0	09AOF0 neisseria m
4	2447.5	96.2	591	09JPS3	09JPS3 neisseria m
5	2400	94.3	600	09JPS6	09JPS6 neisseria m
6	2388	93.9	590	09JPS3	09JPS3 neisseria m
7	2375.5	93.4	595	09JPH0	09JPH0 neisseria m
8	2371.5	93.2	599	09JPR8	09JPR8 neisseria m
9	2369	93.1	598	09JPR7	09JPR7 neisseria m
10	2367.5	93.1	599	09JPS2	09JPS2 neisseria m
11	2367	93.0	594	09JPS8	09JPS8 neisseria m
12	2365	92.9	594	09JRY4	09JRY4 neisseria m
13	2363	92.8	594	09JPR3	09JPR3 neisseria m
14	2361	92.7	592	09JPS9	09JPS9 neisseria m
15	2359	92.7	594	09JPH7	09JPH7 neisseria m
16	2357	92.6	598	09JPR9	09JPR9 neisseria m

17	2351	92.4	592	16	09JQW4	09JQW4 neisseria m
18	2344	92.1	598	2	09JPS0	09JPS0 neisseria m
19	2344	92.1	598	2	09JPR0	09JPR0 neisseria m
20	2335	91.8	598	2	09JQY5	09JQY5 neisseria m
21	2329.5	91.6	589	2	09JPR10	09JPR10 neisseria m
22	2327	91.5	592	2	09JQY2	09JQY2 neisseria m
23	2317.5	91.1	589	2	09JQY1	09JQY1 neisseria m
24	2317	91.1	600	2	09JPS5	09JPS5 neisseria m
25	2207.5	86.8	526	2	09JPS4	09JPS4 neisseria m
26	2205.5	86.7	530	2	09JPS1	09JPS1 neisseria m
27	1009.5	39.7	2353	2	P71401	P71401 haemophilus
28	974	38.3	1098	2	Q48152	Q48152 haemophilus
29	970	38.1	1096	2	Q8GM79	Q8GM79 haemophilus
30	901	35.4	1210	2	Q8GM74	Q8GM74 haemophilus
31	893	35.1	1210	2	Q8GM75	Q8GM75 haemophilus
32	888	33.7	1204	2	Q8GM76	Q8GM76 haemophilus
33	678	26.7	1004	2	Q8GM77	Q8GM77 haemophilus
34	663	26.1	1002	2	Q8GM78	Q8GM78 haemophilus
35	426.5	16.8	1299	16	Q9F3X6	Q9F3X6 pasteurella
36	380.5	15.0	1190	16	Q9PC04	Q9PC04 xylella fas
37	372.5	14.6	2314	2	Q8KQW8	Q8KQW8 moraxella c
38	370.5	14.6	1964	2	Q8KQW9	Q8KQW9 moraxella c
39	360.5	14.2	1588	16	Q8XDG4	Q8XDG4 escherichia
40	358.5	14.1	2059	16	Q9PD50	Q9PD50 xylella fas
41	352.5	13.9	1461	16	Q8ZL64	Q8ZL64 salmonella
42	351.5	13.8	1107	16	Q9FZD8	Q9FZD8 salmonella
43	351	13.8	1778	16	Q8FCB2	Q8FCB2 escherichia
44	346.5	13.6	641	16	Q8CKM1	Q8CKM1 yersinia pe
45	346.5	13.6	658	16	Q8ZHU0	Q8ZHU0 yersinia pe

ALIGNMENTS

RESULT 1
ID 09JPR18 PRELIMINARY; PRT: 591 AA.
AC 09JPR18;
DT 01-OCT-2000 (TREMURel. 15, Created)
DT 01-OCT-2000 (TREMURel. 15, Last sequence update)
DE 01-OCT-2002 (TREMURel. 22, Last annotation update)
DE Outer membrane protein GNA992 (Adhesin) (Mha outer membrane protein).
GN GNA992 OR NM00992 OR NMHA.
OS Neisseria meningitidis, and
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487, 491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B, BZ169, BZ83, and HA4/76;
RX MEDLINE=20175756; Pubmed=10710308;
RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartoloni E., Cepechi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Brooker M., Hurd E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappelli R.;
RT Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.*;
RL Science 287:1816-1820(2000).
[2]
RA SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; Pubmed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., Deboy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Ciftone H., Clark E.B., Cotton M.D., Uitterback T.R., Khouri H., Qin H., Vamathevan J.,

RA Gill J., Scariato V., Masignani V., Pizza M., Grandi G., Sun L.,
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
 RT "Complete genome sequence of *Neisseria meningitidis* serogroup B strain
 RT MC58.";
 RL Science 287:1809-1815 (2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=*N.meningitidis*; STRAIN=PMC21;
 RA Peak I.R., Strikhantha Y., Dieckelman M., Moxon R., Jennings M.P.;
 RT "Identification and characterization of a gene encoding a novel outer
 RT membrane protein of *Neisseria meningitidis*.";
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBD databases.
 DR EMBL: AF226375; AAF42524.1; -
 DR EMBL: AE002450; AAF41395.1; -
 DR EMBL: AF226367; AAF42516.1; -
 DR EMBL: AF226370; AAF42519.1; -
 DR EMBL: AF226374; AAF42523.1; -
 DR EMBL: AF157611; AAK68872.1; -
 DR TIGR: NMB0992; -
 DR InterPro: IPR005594; Yada.
 DR Pfam: PF03895; Yada; 1.
 KW Complete proteome.
 SQ SEQUENCE 591 AA; 62112 MW; 7C22F3CAE7F73BC6 CRC64;

Query Match 96.7%; Score 2459.5; DB 16; Length 591;
 Best Local Similarity 84.9%; Pred. No. 2.6e-100;
 Matches 502; Conservative 0; Mismatches 0; Indels 89; Gaps 4;

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OY 1 MNKIRIITNSALNMAVYSELTRNHTKRASATVTAVALTLFATVOASAN----- 52
DB 1 MNKIRIITNSALNMAVYSELTRNHTKRASATVTAVALTLFATVOASANNEQEDL 60
OY 53 -----TLKAGDLKIKQ 64
DB 61 YLDPVQRTVAVLIVNSDEKGEKEKEVEENSDMAVYFNEKGVLTAREITLKKAGDLKIKQ 120
OY 65 -----FTYSLKKDLTLTSVGTSEKLSFSAANGKVNITSDPTKGLNFAKETAGTNGDTTVALN 120
DB 121 NGTNTFTYSLKKDLTLTSVGTSEKLSFSAANGKVNITSDPTKGLNFAKETAGTNGDTTVALN 180
OY 121 GIGSTLTLD-----RAASVKDVLNAGMNIKGVK-----NYDF 151
DB 181 GIGSTLTLDLNTGATNTVNDVTDDKKRAASVKDVLNAGMNIKGVKPGTTASDNDF 240
OY 152 VRTYDVEFLSADRTTTVNVEKDKNGKTEVYKIGAKTSVIREKDGKLVTKGDKGENSS 211
DB 241 VRTYDVEFLSADRTTTVNVEKDKNGKTEVYKIGAKTSVIREKDGKLVTKGDKGENSS 300
OY 212 TDEGGGLVTAKEVIDAVNKAAGWRMKTTPANGOTGADKFEYVTSNTVTFASGKGTATV 271
DB 301 TDEGGGLVTAKEVIDAVNKAAGWRMKTTPANGOTGADKFEYVTSNTVTFASGKGTATV 360
OY 272 SKDDGNTITVMDVAVGDLANVNOLONSGMNDSKAVALSSGKVSIGNVSPSKGMDETV 331
DB 361 SKDDGNTITVMDVAVGDLANVNOLONSGMNDSKAVALSSGKVSIGNVSPSKGMDETV 420
OY 332 NINAGNNIETFRNGKNIDIASMTPOFSSVSLGACADAPTLISVDDALNVGSKKNKPYR 391
DB 421 NINAGNNIETFRNGKNIDIASMTPOFSSVSLGACADAPTLISVDDALNVGSKKNKPYR 480
OY 392 ITNVAPEGVGVTVVAOLKGYAQNUNNRIDVNDGNARAGTAAQATATAGLVQAYLPBGS 451
DB 481 ITNVAPEGVGVTVVAOLKGYAQNUNNRIDVNDGNARAGTAAQATATAGLVQAYLPBGS 540
OY 452 MAIGGGTYRGEAGYALIGYSSISDGGNWIITKGTASNSRGHFGASASVGYOW 502
DB 541 MAIGGGTYRGEAGYALIGYSSISDGGNWIITKGTASNSRGHFGASASVGYOW 591

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RESULT 2
 ID 09JPS7
 AC 09JPS7;
 PRELIMINARY; PRT: 591 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Outer membrane protein GNA992.
 GN GNA992.
 OS *Neisseria meningitidis*.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 RX NCBI_TaxID=487;
 RP SEQUENCE FROM N.A.
 RC STRAIN=B2147;
 RX MEDLINE=20175756; PubMed=10710308;
 RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
 RA Ratti G., Santini L., Savino S., Scarselli M., Storti E., Zuo P.,
 RA Brooker M., Hundi E., Knapp B., Blair E., Mason T., Tettelin H.,
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
 RA Moxon E.R., Grandi G., Rappuoli R.;
 RT "Identification of Vaccine Candidates Against serogroup B
 RT Meningococcus by Whole-Genome Sequencing.";
 RL Science 287:1816-1820 (2000).
 DR EMBL: AF226366; AAF42515.1; -
 DR InterPro: IPR005594; Yada.
 DR Pfam: PF03895; Yada; 1.
 SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;

Query Match 96.5%; Score 2455.5; DB 2; Length 591;
 Best Local Similarity 84.8%; Pred. No. 3.9e-100;
 Matches 501; Conservative 1; Mismatches 0; Indels 89; Gaps 4;

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OY 1 MNKIRIITNSALNMAVYSELTRNHTKRASATVTAVALTLFATVOASAN----- 52
DB 1 MNKIRIITNSALNMAVYSELTRNHTKRASATVTAVALTLFATVOASANNEQEDL 60
OY 53 -----TLKAGDLKIKQ 64
DB 61 YLDPVQRTVAVLIVNSDEKGEKEKEVEENSDMAVYFNEKGVLTAREITLKKAGDLKIKQ 120
OY 65 -----FTYSLKKDLTLTSVGTSEKLSFSAANGKVNITSDPTKGLNFAKETAGTNGDTTVALN 120
DB 121 NGTNTFTYSLKKDLTLTSVGTSEKLSFSAANGKVNITSDPTKGLNFAKETAGTNGDTTVALN 180
OY 121 GIGSTLTLD-----RAASVKDVLNAGMNIKGVK-----NYDF 151
DB 181 GIGSTLTLDLNTGATNTVNDVTDDKKRAASVKDVLNAGMNIKGVKPGTTASDNDF 240
OY 152 VRTYDVEFLSADRTTTVNVEKDKNGKTEVYKIGAKTSVIREKDGKLVTKGDKGENSS 211
DB 241 VRTYDVEFLSADRTTTVNVEKDKNGKTEVYKIGAKTSVIREKDGKLVTKGDKGENSS 300
OY 212 TDEGGGLVTAKEVIDAVNKAAGWRMKTTPANGOTGADKFEYVTSNTVTFASGKGTATV 271
DB 301 TDEGGGLVTAKEVIDAVNKAAGWRMKTTPANGOTGADKFEYVTSNTVTFASGKGTATV 360
OY 272 SKDDGNTITVMDVAVGDLANVNOLONSGMNDSKAVALSSGKVSIGNVSPSKGMDETV 331
DB 361 SKDDGNTITVMDVAVGDLANVNOLONSGMNDSKAVALSSGKVSIGNVSPSKGMDETV 420
OY 332 NINAGNNIETFRNGKNIDIASMTPOFSSVSLGACADAPTLISVDDALNVGSKKNKPYR 391
DB 421 NINAGNNIETFRNGKNIDIASMTPOFSSVSLGACADAPTLISVDDALNVGSKKNKPYR 480
OY 392 ITNVAPEGVGVTVVAOLKGYAQNUNNRIDVNDGNARAGTAAQATATAGLVQAYLPBGS 451
DB 481 ITNVAPEGVGVTVVAOLKGYAQNUNNRIDVNDGNARAGTAAQATATAGLVQAYLPBGS 540
OY 452 MAIGGGTYRGEAGYALIGYSSISDGGNWIITKGTASNSRGHFGASASVGYOW 502
DB 541 MAIGGGTYRGEAGYALIGYSSISDGGNWIITKGTASNSRGHFGASASVGYOW 591

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RESULT 3
Q9AOF0 PRELIMINARY; PRT; 592 AA.
AC Q9AOF0:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Outer membrane protein.
GN NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC SRAIN-MC58;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon E.R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF125375; AAK09243.1;
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada.
DR PIR; P03895; Yada.
SQ SEQUENCE 592 AA; 62290 MW; 168966A97381EFC5 CRC64;

Query Match 96.5%; Score 2455; DB 2; Length 592;
Best Local Similarity 84.6%; Pred. No. 4; Ie-100;
Matches 501; Conservative 0; Mismatches 1; Indels 90; Gaps 4;

QY 1 MNKTYRIIWSALNAMYVSELTRNHRKASATYKTAVALTLFATVQASAN----- 52
DB 1 MNKTYRIIWSALNAMYVSELTRNHRKASATYKTAVALTLFATVQASANRPKKD 60
QY 53 -----TLKAGDNLIK 63
DB 61 YLPDVLRTAVAVLIYNSDKEGTGEKEVEENSDMAVYFNEKGYLTAREITLKAGDNLIK 120
QY 64 Q-----FTYSLKKDLTDLTSVTEKLSFSANGKNVITSDTKGLNFAKETAGTGTIVHL 119
DB 121 QNGNFYYSLSKDLTDLTSVTEKLSFSANGKNVITSDTKGLNFAKETAGTGTIVHL 180
QY 120 NGIGSTLTD-----RAASVKVLANAGNKGK-----NVD 150
DB 181 NGIGSTLTDLTLNLTGATTNTNDVTDDEKKRAASVKVLANAGNKGKPGTTASDNDV 240
QY 151 FVRYDYVEFLSADTKTTTVNVEKNGKTEVKGATSVYKEKDGKLVYTKDGKNGSS 210
DB 241 FVRYDYVEFLSADTKTTTVNVEKNGKTEVKGATSVYKEKDGKLVYTKDGKNGSS 300
QY 211 STDEGGLVTAKEVIDAVNKAQWRRKTTTANGQTQADKFEVYSGTNVTFASGKTAT 270
DB 301 STDEGGLVTAKEVIDAVNKAQWRRKTTTANGQTQADKFEVYSGTNVTFASGKTAT 360
QY 271 VSKDQGNITVAVDVGALNVNQLNSGWNLDKAVAGSSGKVISGNSPSKGMDET 330
DB 361 VSKDQGNITVAVDVGALNVNQLNSGWNLDKAVAGSSGKVISGNSPSKGMDET 420
QY 331 VNINAGNNIEITRNKKNIDIAATSMTPQSSVSLGAGADAPTLISVDGALNVGSKDKMPV 390
DB 421 VNINAGNNIEITRNKKNIDIAATSMTPQSSVSLGAGADAPTLISVDGALNVGSKDKMPV 480
QY 391 RITNAPGVKEGADVTVNAQLKGVANLNRRIDNVGNARAGIAQAIAITAGLVQAYLPGKS 450
DB 481 RITNAPGVKEGADVTVNAQLKGVANLNRRIDNVGNARAGIAQAIAITAGLVQAYLPGKS 540
QY 451 MAIGGTYRGEGAGYAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYOW 502
DB 541 MAIGGTYRGEGAGYAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYOW 592

RESULT 4
Q930Y3 PRELIMINARY; PRT; 591 AA.
ID Q930Y3
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AC Q930Y3;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE NHA outer membrane protein.
GN NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC SRAIN-EG329;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157606; AAK68867.1;
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada.
DR PIR; P03895; Yada.
SQ SEQUENCE 591 AA; 62048 MW; CODC600798859C65 CRC64;

Query Match 96.2%; Score 2447.5; DB 2; Length 591;
Best Local Similarity 84.6%; Pred. No. 8; Ie-100;
Matches 500; Conservative 1; Mismatches 1; Indels 89; Gaps 4;

QY 1 MNKTYRIIWSALNAMYVSELTRNHRKASATYKTAVALTLFATVQASAN----- 52
DB 1 MNKTYRIIWSALNAMYVSELTRNHRKASATYKTAVALTLFATVQASANNEQEDL 60
QY 53 -----TLKAGDNLIK 64
DB 61 YLPDVLRTAVAVLIYNSDKEGTGEKEVEENSDMAVYFNEKGYLTAREITLKAGDNLIK 120
QY 65 -----FTYSLKKDLTDLTSVTEKLSFSANGKNVITSDTKGLNFAKETAGTGTIVHL 120
DB 121 NGTFYYSLSKDLTDLTSVTEKLSFSANGKNVITSDTKGLNFAKETAGTGTIVHL 180
QY 121 GIGSTLTD-----RAASVKVLANAGNKGK-----NVD 151
DB 181 GIGSTLTDLTLNLTGATTNTNDVTDDEKKRAASVKVLANAGNKGKPGTTASDNDV 240
QY 152 VRYDYVEFLSADTKTTTVNVEKNGKTEVKGATSVYKEKDGKLVYTKDGKNGSS 211
DB 241 VRYDYVEFLSADTKTTTVNVEKNGKTEVKGATSVYKEKDGKLVYTKDGKNGSS 300
QY 212 TDEGGLVTAKEVIDAVNKAQWRRKTTTANGQTQADKFEVYSGTNVTFASGKTAT 271
DB 301 TDEGGLVTAKEVIDAVNKAQWRRKTTTANGQTQADKFEVYSGTNVTFASGKTAT 360
QY 272 SKDQGNITVAVDVGALNVNQLNSGWNLDKAVAGSSGKVISGNSPSKGMDET 331
DB 361 SKDQGNITVAVDVGALNVNQLNSGWNLDKAVAGSSGKVISGNSPSKGMDET 420
QY 332 NINAGNNIEITRNKKNIDIAATSMTPQSSVSLGAGADAPTLISVDGALNVGSKDKMPV 391
DB 421 NINAGNNIEITRNKKNIDIAATSMTPQSSVSLGAGADAPTLISVDGALNVGSKDKMPV 480
QY 392 ITNAPGVKEGADVTVNAQLKGVANLNRRIDNVGNARAGIAQAIAITAGLVQAYLPGKS 451
DB 481 ITNAPGVKEGADVTVNAQLKGVANLNRRIDNVGNARAGIAQAIAITAGLVQAYLPGKS 540
QY 452 MAIGGTYRGEGAGYAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYOW 502
DB 541 MAIGGTYRGEGAGYAIGYSSISDGNMIITKGTASGNSRGHFGASASVGYOW 591

RESULT 5
Q9JPS6 PRELIMINARY; PRT; 600 AA.
ID Q9JPS6
AC Q9JPS6;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
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DT 01-OCT-2002 (TREMblrel. 22, last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
NCBI_TaxId=487;
OX NCBI_TaxId=487;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=E26;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Barolini E., Capocchi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappelli R.;
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226371; AAF42520.1; -
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0596CD1 CRC64;

Query Match 94.3%; Score 2400; DB 2; Length 600;
Best Local Similarity 82.0%; Pred. No. 1.1e-97;
Matches 492; Conservative 3; Mismatches 7; Indels 98; Gaps 4;

QY 1 MKKIRITNSALNMAVYSELTRNHTKRASATVKTAVATLLFATVOASAN----- 52
DB 1 MKKIRITNSALNMAVYSELTRNHTKRASATVKTAVATLLFATVOASADN 60
QY 53 -----TLKAGDNLK 61
DB 61 EEEETLEPVVTRAPVLSFSAEDTGEKEVTEMTWGIFFDKNGYIKACTITLKAGDNLK 120
QY 62 IKQ-----FTYSLKKDLTDLTSVTEKLSFSANGKNVITSDTKGLNFAKETAGT 111
DB 121 IKQNTDENTNASSFTYSLKKELDTLSVTEKLSFGANGKNVITSDTKGLNFAKETAGT 180
QY 112 NGDTTVHLNGISLTLD-----RAASVDVYLNAGNNIGVK-- 147
DB 181 NGDTTVHLNGISLTLDLTNLGATNTNDVTDDEKRAASVDVYLNAGNNIGVKPG 240
QY 148 -----NVDFVRYTVEEFLSADTKTTTVNVEESKDNCKTEVKIGAKTSYIKERDGLVYG 202
DB 241 TTASNDVDFVRYTVEEFLSADTKTTTVNVEESKDNCKTEVKIGAKTSYIKERDGLVYG 300
QY 203 KDKGENGSSTDEGEGLVTAKEVIDAVNKAQWBRKTTTANGQTGAQDKETVSGTNVFA 262
DB 301 KDKGENGSSTDEGEGLVTAKEVIDAVNKAQWBRKTTTANGQTGAQDKETVSGTNVFA 360
QY 263 SKGKTAAVSKDDQNTIVMVDVNGDALNVQNLQNSGNLDSKAVAGSSGCVISGNVSP 322
DB 361 SKGKTAAVSKDDQNTIVMVDVNGDALNVQNLQNSGNLDSKAVAGSSGCVISGNVSP 420
QY 323 SKGKDETVNINAGNNIETTRNGKNIDIASMTPOFSSVSLGAGADAPLTVSDGALANG 382
DB 421 SKGKDETVNINAGNNIETTRNGKNIDIASMTPOFSSVSLGAGADAPLTVSDGALANG 480
QY 383 SKDKNPKVRIITNVAPVEGDTNVAOLKGVQNLNRIIDNVGNARAGIAQAIATAGLV 442
DB 481 SKDKNPKVRIITNVAPVEGDTNVAOLKGVQNLNRIIDNVGNARAGIAQAIATAGLV 540
QY 443 QAYLPGKSMMAIGGTYGEGAGYAGYSISDGGNWIITKGTASGNSRGHFGASASVGYOW 502
DB 541 QAYLPGKSMMAIGGTYGEGAGYAGYSISDGGNWIITKGTASGNSRGHFGASASVGYOW 600

ID Q9JPS3 PRELIMINARY; PRT; 590 AA.
AC Q9JPS3;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
DT 01-OCT-2002 (TREMblrel. 22, last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
NCBI_TaxId=487;
OX NCBI_TaxId=487;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=NGE28;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Barolini E., Capocchi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappelli R.;
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226378; AAF42527.1; -
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 93.9%; Score 2388; DB 2; Length 590;
Best Local Similarity 83.2%; Pred. No. 3.5e-97;
Matches 491; Conservative 3; Mismatches 8; Indels 88; Gaps 5;

QY 1 MKKIRITNSALNMAVYSELTRNHTKRASATVKTAVATLLFATVOASAN----- 52
DB 1 MKKIRITNSALNMAVYSELTRNHTKRASATVKTAVATLLFATVOANATDEDEEDL 60
QY 53 -----TLKAGDNLKIKQ-- 64
DB 61 DPVQRTAVLIYNSDKEGTGEKEVEBNSDMAVYFNEKGVLTAGTTTLKAGDNLKIKQNG 120
QY 65 ---FTYSLKKDLTDLTSVTEKLSFSANGKNVITSDTKGLNFAKETAGTNGTVHLNGI 122
DB 121 TNYFTYSLKKDLTDLTSVTEKLSFSANGKNVITSDTKGLNFAKETAGTNGTVHLNGI 180
QY 123 GSTLTD-----RAASVKVYLNAGNNIGVK-----NVDFVR 153
DB 181 GSTLTDLTNLGATNTNDVTDDEKRAASVKVYLNAGNNIGVKFGCTTASDNVDYR 240
QY 154 TYDVEEFLSADTKTTTVNVEESKDNCKTEVKIGAKTSYIKERDGLVYKDKGENGSSTD 213
DB 241 TYDVEEFLSADTKTTTVNVEESKDNCKTEVKIGAKTSYIKERDGLVYKDKGENGSSTD 300
QY 214 EEEGLVTAKEVIDAVNKAQWBRKTTTANGQTGAQDKETVSGTNVFA 273
DB 301 EEEGLVTAKEVIDAVNKAQWBRKTTTANGQTGAQDKETVSGTNVFA 360
QY 274 DDQGNITVYVNVGDALNVQNLQNSGNLDSKAVAGSSGKYSISGNVSPSKMDETVNI 333
DB 361 DDQGNITVYVNVGDALNVQNLQNSGNLDSKAVAGSSGKYSISGNVSPSKMDETVNI 420
QY 334 NAGNNIETTRNGKNIDIASMTPOFSSVSLGAGADAPLTVSDG--ALNVGSKDKNPKVRI 392
DB 421 NAGNNIETTRNGKNIDIASMTPOFSSVSLGAGADAPLTVSDGALANGSKDKNPKVRI 480
QY 421 TNVAPVEGDTNVAOLKGVQNLNRIIDNVGNARAGIAQAIATAGLVQAYLPGKSM 452
DB 481 TNVAPVEGDTNVAOLKGVQNLNRIIDNVGNARAGIAQAIATAGLVQAYLPGKSM 540
QY 453 AIGGTYGEGAGYAGYSISDGGNWIITKGTASGNSRGHFGASASVGYOW 502
DB 541 AIGGTYGEGAGYAGYSISDGGNWIITKGTASGNSRGHFGASASVGYOW 590

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RESULT 7
ID Q9JPH0 PRELIMINARY; PRT: 595 AA.
AC Q9JPH0;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_Taxid=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=528, and 1000;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Moxon E.R., Grandi G., Saunders N.J., Granoff D.M., Venter C.,
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL: AF226360; AAF42509.1; -
DR EMBL: AF226356; AAF42505.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada. 1.
SQ SEQUENCE 595 AA; 62120 MM; 8212C96380142BFC CRC64;

Query Match 93.4%; Score 2375.5; DB 2; Length 595;
Best Local Similarity 81.6%; Pred. No. 1.2e-96;
Matches 487; Conservative 7; Mismatches 8; Indels 93; Gaps 5;

QY 1 MNKIRIIMNSALNANWVSELTRNHRKRSATYKAVLATLTFATYQASAN----- 52
DB 1 MNKIRIIMNSALNANWVSELTRNHRKRSATYKAVLATLTFATYQASATDEDEDEL 60
QY 53 -----TLKAGDNLKIKO--- 64
DB 61 EPPVRSALVLOPMIDKNGENESTGDIQSIYYDHNHTLHGATVTLKAGDNLKIKONTD 120
QY 65 -----FTYSLKKDLTDLTSVGTETKLSFSANGKNVITSDFKGLNFAKETAGTNGDTTV 117
DB 121 ENTNASFTYSLKKDLTDLTSVGTETKLSFGANGKNVITSDFKGLNFAKETAGTNGDTTV 180
QY 118 HLNGIGSTLTLD-----RAASYDVNLAAGNNIKGV-----N 148
DB 181 HLNGIGSTLTDLTLAGSSAHVDAGNOSTHYTRAASIKDVNLAAGNNIKGVGTGTTGSGEN 240
QY 149 VDEVRTDYVEFLSADTKTTTVNVEKDNCKKTEVKIGAKTSYIKKDGKLYTGKDGGEN 208
DB 241 VDEVRTDYVEFLSADTKTTTVNVEKDNCKKTEVKIGAKTSYIKKDGKLYTGKKGGEN 300
QY 209 GSSTDEGEGLVTAKEVIDAVNKAQWRRKTTTANGQTQADKFETVTSGTNVTFASGKGT 268
DB 301 GSSTDEGEGLVTAKEVIDAVNKAQWRRKTTTANGQTQADKFETVTSGTNVTFASGKGT 360
QY 269 ATYSKDDOGNTYMYDVNVDALNVNOLONGMNLDSKAVAGSSGKATSGNVSFSPSKMD 328
DB 361 ATYSKDDOGNTYMYDVNVDALNVNOLONGMNLDSKAVAGSSGKATSGNVSFSPSKMD 420
QY 329 ETVNINAGNNIETRNKNKNDIATSMTPQSSVSLGADAPTLVSVDG-ALNVGSKDN 387
DB 421 ETVNINAGNNIETRNKNKNDIATSMTPQSSVSLGADAPTLVSVDGALNVGSKDN 480
QY 388 KPVRTNVADGVKEGDTVNAQLKGAQNLRIDNVGNARAGIAQAIATAGLVQAYLP 447
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DB 481 KPVRTNVADGVKEGDTVNAQLKGAQNLRIDNVGNARAGIAQAIATAGLVQAYLP 540
QY 448 GKSMMAIGCGTYRGEAGYTAIGYSSISDGMNIIKGTASGNSRGHFASASGVQW 502
DB 541 GKSMMAIGCGTYRGEAGYTAIGYSSISDGMNIIKGTASGNSRGHFASASGVQW 595

RESULT 8
ID Q9JPR8 PRELIMINARY; PRT: 599 AA.
AC Q9JPR8;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992 (Nhha outer membrane protein).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_Taxid=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH38;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappunoli R.,
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL: AF226360; AAF42509.1; -
DR EMBL: AF226356; AAF42505.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada. 1.
SQ SEQUENCE 599 AA; 62844 MM; BBA16BBS3C1970C CRC64;

Query Match 93.2%; Score 2371.5; DB 2; Length 599;
Best Local Similarity 81.6%; Pred. No. 1.9e-96;
Matches 489; Conservative 2; Mismatches 11; Indels 97; Gaps 5;

QY 1 MNKIRIIMNSALNANWVSELTRNHRKRSATYKAVLATLTFATYQASAN----- 52
DB 1 MNKIRIIMNSALNANWVSELTRNHRKRSATYKAVLATLTFATYQASATDEDEDEL 60
QY 53 -----TLKAGDNLKIKO--- 64
DB 61 EPPVRSALVLOPMIDKNGENESTGDIQSIYYDHNHTLHGATVTLKAGDNLKIKONTN 120
QY 65 -----FTYSLKKDLTDLTSVGTETKLSFSANGKNVITSDFKGLNFAKETAGTNG 113
DB 121 KTNENTNDSSFYSLKKDLTDLTSVGTETKLSFGANGKNVITSDFKGLNFAKETAGTNG 180
QY 114 DTVVHLNGIGSTLTLD-----RAASYDVNLAAGNNIKGV----- 147
DB 181 DTVVHLNGIGSTLTDLTLLNAGTNTVNDVTDKRRKRSVYKDVNLAAGNNIKGVKGT 240
QY 148 ---NVDEVRTDYVEFLSADTKTTTVNVEKDNCKKTEVKIGAKTSYIKKDGKLYTGKD 204
DB 241 ASDNVDEVRTDYVEFLSADTKTTTVNVEKDNCKKTEVKIGAKTSYIKKDGKLYTGKG 300
QY 205 KGENGSSTDEGEGLVTAKEVIDAVNKAQWRRKTTTANGQTQADKFETVTSGTNVTFASG 264
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Db 301 KGENSSSTDEGEGLVTAKEVIDAVNKAQWRKTTTANGOTGADKEFEVVTSGTNTVFSAG 360
Qy 265 KGTATVSKDDGNTITVMDVNVGDALNVNOLONGSMWLDKAVAGSSGKVIISGNVSPSK 324
Db 361 KGTATVSKDDGNTITVMDVNVGDALNVNOLONGSMWLDKAVAGSSGKVIISGNVSPSK 420
Qy 325 GKMDVTVINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLISVDG-DALNVSK 383
Db 421 GKMDVTVINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLISVDGKDALNVSK 480
Qy 384 KDKNPEVRIITNVAPEGKEDVTNVAQLKGAQNLRNIDNVGNARAGIAQALATAGLVQ 443
Db 481 KDKNPEVRIITNVAPEGKEDVTNVAQLKGAQNLRNIDNVGNARAGIAQALATAGLVQ 540
Qy 444 AYLPGKSMAAIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHGASASVGYOW 502
Db 541 AYLPGKSMAAIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHGASASVGYOW 599

RESULT 9
Q9JPR7 PRELIMINARY; PRT; 598 AA.
ID Q9JPR7;
AC Q9JPR7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxId=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SM2107;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226385; AAF42534.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 598 AA; 62431 MW; 0881CC094F33B4D4 CRC64;

Query Match 93.1%; Score 2369; DB 2; Length 598;
Best Local Similarity 81.6%; Pred. No. 2.4e-96;
Matches 488; Conservative 2; Mismatches 12; Indels 96; Gaps 5;
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Db 241 SENVDPVRYDTVEFLSADTKTTTVNVESKDNKTEVAKISVIEKDGKLVTKGK 300
Qy 206 GENSSTDEGEGLVTAKEVIDAVNKAQWRKTTTANGOTGADKEFEVVTSGTNTVFSAGK 265
Db 301 KGENSSSTDEGEGLVTAKEVIDAVNKAQWRKTTTANGOTGADKEFEVVTSGTNTVFSAGK 360
Qy 266 GTTATVSKDDGNTITVMDVNVGDALNVNOLONGSMWLDKAVAGSSGKVIISGNVSPSK 325
Db 361 GTTATVSKDDGNTITVMDVNVGDALNVNOLONGSMWLDKAVAGSSGKVIISGNVSPSK 420
Qy 326 KMDVTVINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLISVDG-DALNVSK 384
Db 421 KMDVTVINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLISVDGKDALNVSK 480
Qy 385 KDKNPEVRIITNVAPEGKEDVTNVAQLKGAQNLRNIDNVGNARAGIAQALATAGLVQ 444
Db 481 KDKNPEVRIITNVAPEGKEDVTNVAQLKGAQNLRNIDNVGNARAGIAQALATAGLVQ 540
Qy 445 AYLPGKSMAAIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHGASASVGYOW 502
Db 541 AYLPGKSMAAIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHGASASVGYOW 599

RESULT 10
Q9JPS8 PRELIMINARY; PRT; 599 AA.
ID Q9JPS8;
AC Q9JPS8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxId=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A22;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226364; AAF42513.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 599 AA; 62693 MW; 46C2E974AF7F78E9 CRC64;

Query Match 93.1%; Score 2367.5; DB 2; Length 599;
Best Local Similarity 81.5%; Pred. No. 2.8e-96;
Matches 488; Conservative 3; Mismatches 11; Indels 97; Gaps 5;
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Db      181 DTTVHLNGIGSTLTDTLTLGSSASHVDAGNOSTHYTTRAAISIKDVLNAGMNIKGVKGTG 240
QY      148 ---NVDVFRTPDVEFLSADTKTTTIVNVESSKDNKGKTEVKIGAKTSVIREKDKLTGKD 204
Db      241 QSENVDFTYDTPVEFLSADTKTTTIVNVESSKDNKGKTEVKIGAKTSVIREKDKLTGKG 300
QY      205 KGENSSSTDEGEGLVTAKEVIDAVNKGMRMKTATTANGOTGADKFEFTVSGTNTVPASG 264
Db      301 KGENSSSTDEGEGLVTAKEVIDAVNKGMRMKTATTANGOTGADKFEFTVSGTNTVPASG 360
QY      265 KGTATVSKDDOGNTTVMYDVNVDALNNOLONGSMWLDKRAVAGSSGKVTISGNVSPSK 324
Db      361 KGTATVSKDDOGNTTVMYDVNVDALNNOLONGSMWLDKRAVAGSSGKVTISGNVSPSK 420
QY      325 GKMDEVNINAGNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSDVDG-DALNVSS 383
Db      421 GKMDEVNINAGNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSDVDG-DALNVSS 480
QY      384 KKDNRKVRITNVAPEGKEDVTNVAOLKGVANLNRIIDNVGNAFAGIAQAATAGLVQ 443
Db      481 KKDNRKVRITNVAPEGKEDVTNVAOLKGVANLNRIIDNVGNAFAGIAQAATAGLVQ 540
QY      444 AYLPGKSMATGGGTYRGEAGTAIGYSSISDGNMIIKGTASGNSRHFAGASVGYOW 502
Db      541 AYLPGKSMATGGGTYRGEAGTAIGYSSISDGNMIIKGTASGNSRHFAGASVGYOW 599

RESULT 11
Q9JPS2 PRELIMINARY; PRT; 594 AA.
ID 09JPS2 AC 09JPS2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE31;
RX MEDLINE=20175756; PubMed=10710308;
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Arico' B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Rattl G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tetteijn H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226379; AAF42528.1; -.
DR InterPro: IPR005594; Yada.
PFam: PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 93.0%; Score 2367; DB 2; Length 594;
Best Local Similarity 82.2%; Pred. No. 2.9e-96;
Matches 488; Conservative 1; Mismatches 13; Indels 92; Gaps 5;
QY 1 MNKIYIINMSALNANWVAVSELTRNHTKRASATVATLTLFATVQASAN----- 52
Db 1 MNKIYIINMSALNANWVAVSELTRNHTKRASATVATLTLFATVQASATDDDDLLYLE 60
QY 53 -----TLKAGDNLKIKO----- 64
Db 61 PVQRTAPVLSFHADSEGTGKEVTEDSNMGVYFDKKGVLTAGTITLKAGDNLKIKONTDE 120
QY 65 -----FTYSLKDLTDLTDSVGTGKLSFSANGKNKVNITSDTKLNAFAKTAGTNGDTYH 118

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Db      121 MNASSFTYSLKDLTDLTDSVTEKLSFGANGKRVNITSDTKLNAFAKTAGTNGDTYH 180
QY      119 LNCIGSTLTD-----RAASVKDVLNAGMNIKGVK-----NV 149
Db      181 LNCIGSTLTDLTNLCATTNVTNDVNTDDEKRAASVKDVLNAGMNIKGVKPEPTTASDNV 240
QY      150 DFRRTDTPVEFLSADTKTTTIVNVESSKDNKGKTEVKIGAKTSVIREKDKLTVGKDGENG 209
Db      241 DFRRTDTPVEFLSADTKTTTIVNVESSKDNKGKTEVKIGAKTSVIREKDKLTVGKDGENG 300
QY      210 SSTDEGEGLVTAKEVIDAVNKGMRMKTATTANGOTGADKFEFTVSGTNTVPASGCTTA 269
Db      301 SSTDEGEGLVTAKEVIDAVNKGMRMKTATTANGOTGADKFEFTVSGTNTVPASGCTTA 360
QY      270 TVSKDDOGNTTVMYDVNVDALNNOLONGSMWLDKRAVAGSSGKVTISGNVSPSKRMD 329
Db      361 TVSKDDOGNTTVMYDVNVDALNNOLONGSMWLDKRAVAGSSGKVTISGNVSPSKRMD 420
QY      330 TVNINAGNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKRDK 388
Db      421 TVNINAGNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKRDK 480
QY      389 PVRTNVAPEGKEDVTNVAOLKGVANLNRIIDNVGNAFAGIAQAATAGLVQAYLPG 448
Db      481 PVRTNVAPEGKEDVTNVAOLKGVANLNRIIDNVGNAFAGIAQAATAGLVQAYLPG 540
QY      449 KSMATGGGTYRGEAGTAIGYSSISDGNMIIKGTASGNSRHFAGASVGYOW 502
Db      541 KSMATGGGTYRGEAGTAIGYSSISDGNMIIKGTASGNSRHFAGASVGYOW 594

RESULT 12
Q93QY4 PRELIMINARY; PRT; 594 AA.
ID 093QY4 AC 093QY4;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Nha outer membrane protein.
GN NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E6327;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF157605; AAK68866.1; -.
DR InterPro: IPR005594; Yada.
PFam: PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62297 MW; 9DD448B04B3A8EA2 CRC64;

Query Match 93.0%; Score 2366; DB 2; Length 594;
Best Local Similarity 82.0%; Pred. No. 3.2e-96;
Matches 487; Conservative 4; Mismatches 11; Indels 92; Gaps 5;
QY 1 MNKIYIINMSALNANWVAVSELTRNHTKRASATVATLTLFATVQASAN----- 52
Db 1 MNKIYIINMSALNANWVAVSELTRNHTKRASATVATLTLFATVQASATDDDDLLYLE 60
QY 53 -----TLKAGDNLKIKO----- 64
Db 61 PVQRTAVVLSFRSDEGTGKEVTEDSNMGVYFDKKGVLTAGTITLKAGDNLKIKONTNE 120
QY 65 -----FTYSLKDLTDLTDSVGTGKLSFSANGKNKVNITSDTKLNAFAKTAGTNGDTYH 118
Db 121 NTAASSFTYSLKDLTDLTDSVGTGKLSFSANGKNKVNITSDTKLNAFAKTAGTNGDTYH 180
QY 119 LNCIGSTLTD-----RAASVKDVLNAGMNIKGVK-----NV 149

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181 LINGSTLTDTLLNTGATTNVTNDVTDDEKRRASVADVLMAGMNIKGKPGTTASDNV 240
Db
150 DFEVRYTDFEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVIEKDKGLVTGDKGNG 209
Oy
241 DFEVRYTDFEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVIEKDKGLVTGDKGNG 300
Db
210 SSTDEGGLVYAKEDVDAVNAKAGRMKTTTANGOTGADRFETVTSCTNTTFASGKTGA 269
Oy
301 SSTDKGGLVYAKEDVDAVNAKAGRMKTTTANGOTGADRFETVTSCTNTTFASGKTGA 360
Db
270 TVSKDDGNTTVMADVNGDALNVNOLNSGMNLDKRAVAGSSGKVTSGNVSPSKGKMD 329
Oy
361 TVSKDDGNTTVMADVNGDALNVNOLNSGMNLDKRAVAGSSGKVTSGNVSPSKGKMD 420
Db
330 TVNINAGNNEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKKDK 388
Oy
421 TVNINAGNNEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKDK 480
Db
389 PVRTTNVAPGVKEDVTVNAQLKGVAQNLNRIIDVNGNARAGIAQAIATAGLVQAVLP 448
Oy
481 PVRTTNVAPGVKEDVTVNAQLKGVAQNLNRIIDVNGNARAGIAQAIATAGLVQAVLP 540
Db
449 KSMVAIGGTYRGAGYAGTSSISDGMNIIKGTASGNSRHHGASASVGYOW 502
Oy
541 KSMVAIGGTYRGAGYAGTSSISDGMNIIKGTASGNSRHHGASASVGYOW 594
Db
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RESULT 13

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09JPI3 PRELIMINARY; PRT; 594 AA.
AC 09JPI3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
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RM [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88, and B232;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226376; AAF2525.1; -
DR EMBL: AF226369; AAF2518.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada. 1.
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B9D04B46 CRC64;
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Query Match 92.9%; Score 2363; DB 2; Length 594;
Best Local Similarity 82.0%; Pred. No. 4.4e-96;
Matches 487; Conservative 1; Mismatches 14; Indels 92; Gaps 5;

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Oy 1 MNKIYRIIWSALNAAVVSSELTRNHTRKASATYKTAVALTLATLFAVQASAN----- 52
Db 1 MNKIYRIIWSALNAAVVSSELTRNHTRKASATYKTAVALTLATLFAVQASATTTDDDLYLE 60
Oy 53 -----TLKGDMLKTKO----- 64
Db 61 PVQRTAPVLPFSLHADSEGTGEKEVTEBDSNWGVYFDKKGVLTAGTITTLAKAGNLIKONTDE 120
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Oy 65 -----FTYSLKDDLDLTSVTEKLSFSANGKNVNTSPTKGINFAKETAAGTNGDTTV 118
Db 121 NTNASSFTYSLKDDLDLTSVTEKLSFSANGKNVNTSPTKGINFAKETAAGTNGDTTV 180
Oy 119 LINGSTLTDT-----RAASVADVLMAGMNIKGKPGTTASDNV 149
Db 181 LINGSTLTDTLLNTGATTNVTNDVTDDEKRRASVADVLMAGMNIKGKPGTTASDNV 240
Oy 150 DFEVRYTDFEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVIEKDKGLVTGDKGNG 209
Db 241 DFEVRYTDFEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVIEKDKGLVTGDKGNG 300
Oy 210 SSTDEGGLVYAKEDVDAVNAKAGRMKTTTANGOTGADRFETVTSCTNTTFASGKTGA 269
Db 301 SSTDEGGLVYAKEDVDAVNAKAGRMKTTTANGOTGADRFETVTSCTNTTFASGKTGA 360
Oy 270 TVSKDDGNTTVMADVNGDALNVNOLNSGMNLDKRAVAGSSGKVTSGNVSPSKGKMD 329
Db 361 TVSKDDGNTTVMADVNGDALNVNOLNSGMNLDKRAVAGSSGKVTSGNVSPSKGKMD 420
Oy 330 TVNINAGNNEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKKDK 388
Db 421 TVNINAGNNEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKDK 480
Oy 389 PVRTTNVAPGVKEDVTVNAQLKGVAQNLNRIIDVNGNARAGIAQAIATAGLVQAVLP 448
Db 481 PVRTTNVAPGVKEDVTVNAQLKGVAQNLNRIIDVNGNARAGIAQAIATAGLVQAVLP 540
Oy 449 KSMVAIGGTYRGAGYAGTSSISDGMNIIKGTASGNSRHHGASASVGYOW 502
Db 541 KSMVAIGGTYRGAGYAGTSSISDGMNIIKGTASGNSRHHGASASVGYOW 594
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RESULT 14

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09JPS9 PRELIMINARY; PRT; 592 AA.
AC 09JPS9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
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RM [1]
RP SEQUENCE FROM N.A.
RC STRAIN=860800;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226361; AAF2510.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada. 1.
SQ SEQUENCE 592 AA; 61917 MW; 4A3471514FD3C879 CRC64;
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Query Match 92.8%; Score 2361; DB 2; Length 592;
Best Local Similarity 82.3%; Pred. No. 5.3e-96;
Matches 487; Conservative 2; Mismatches 13; Indels 90; Gaps 5;

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Oy 1 MNKIYRIIWSALNAAVVSSELTRNHTRKASATYKTAVALTLATLFAVQASAN----- 52
Db 1 MNKIYRIIWSALNAAVVSSELTRNHTRKASATYKTAVALTLATLFAVQANATDDEDEEL 60
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QY 53 -----TLKAGDNLIKIQ----- 64
 Db 61 ESQVRSVVSQASMEGSELETISLMTNDSKEFVDPYIVTLAKADNLIKQNTMENT 120
 QY 65 -----FTYSLKDKLDLTSVGTETKLSFSAANGKVNITSOTKLNPAKETAGTNGTTPVHLN 120
 Db 121 NASFTYSLKDKLDLTSVGTETKLSFSAANGKVNITSOTKLNPAKETAGTNGTTPVHLN 180
 QY 121 GIGSTLTD-----RAASVKDYLNAGNIRKGV-----NVDF 151
 Db 181 GIGSTLTDMLNTGATTNTNDVNTDDEKRRASVAVKDYLNAGNIRKGVKPGTTASDNVDF 240
 QY 152 VRTDYVEFLSADTKTTTVNVEKSKDKGKTEVIGAKTSVKEKDKGLVTKGDKGNGSS 211
 Db 241 VRTDYVEFLSADTKTTTVNVEKSKDKGKTEVIGAKTSVKEKDKGLVTKGDKGNGSS 300
 QY 212 TDBEGGLVTAKEVIDAVNKAAGMRKTTTANGOTGADKFEVTSVGTNTVFAAGKGTATV 271
 Db 301 TDBEGGLVTAKEVIDAVNKAAGMRKTTTANGOTGADKFEVTSVGTNTVFAAGKGTATV 360
 QY 272 SKDDGNTVAVDYNVGDALNVNOLNSGMNLDKRAVAGSSGKVIISGVNPSKGMDETV 331
 Db 361 SKDDGNTVAVDYNVGDALNVNOLNSGMNLDKRAVAGSSGKVIISGVNPSKGMDETV 420
 QY 332 NINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSDVG-DALNVGSKKDKPV 390
 Db 421 NINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSDVG-DALNVGSKKDKPV 480
 QY 391 RITNVAAGVKEGDTNVAQKGAQNLNRRIDNVGNARAGIAQAIATAGLVQAYLPDGS 450
 Db 481 RITNVAAGVKEGDTNVAQKGAQNLNRRIDNVGNARAGIAQAIATAGLVQAYLPDGS 540
 QY 451 MMAIGGTYRGEAGYAGISYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 502
 Db 541 MMAIGGTYRGEAGYAGISYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 592

RESULT 15

Q9JPH7 PRELIMINARY; PRT; 594 AA.
 AC Q9JPH7;
 DT 01-OCT-2000 (TREMBLERel. 15, Created)
 DT 01-OCT-2000 (TREMBLERel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMBLERel. 22, Last annotation update)
 DE Outer membrane protein GNA992 (Nha outer membrane protein).
 GN GNA992 OR NHA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_Taxid:487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-B2198; and 297-0;
 RC MEDLINE-20175756; PubMed-10710308;
 RA Piza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,
 RA Galeotti C.L., Iuzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
 RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H.,
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
 RA Moxon E.R., Grandi G., Rappuoli R.;
 RT "Identification of Vaccine Candidates Against Serogroup B
 RT Meningococcus by Whole-Genome Sequencing.";
 RL Science 287:1816-1820(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-B2198;
 RA Peak I.R., Srikanta Y., Dieckelman M., Moxon R., Jennings M.P.;
 RT "Identification and characterization of a gene encoding a novel outer
 RT membrane protein of Neisseria meningitidis.";
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF226358; AAF42517.1; -;
 DR EMBL; AF226358; AAF42507.1; -;

DR EMBL; AF157604; AAK6865.1; -;
 DR InterPro; IPR005594; Yada.
 DR Pfam; PF03895; Yada; 1.
 SO SEQUENCE 594 AA; 62361 MW; 436BDEDE68263C5C CRC64;
 Query Match 92.7%; Score 2359; DB 2; Length 594;
 Best Local Similarity 82.0%; Pred. No. 6,5e-96;
 Matches 487; Conservative 2; Mismatches 13; Indels 92; Gaps 5;

QY 1 MNKIRIINNALNAAVYSELTRNRHTRKASATYKTAVLATLLEPATYQASAN----- 52
 Db 1 MNKIRIINNALNAAVYSELTRNRHTRKASATYKTAVLATLLEPATYQANATDDDDLYLE 60
 QY 53 -----TLKAGDNLIKIQ----- 64
 Db 61 PVORTAVVLSFRSDEKTEGEGEDSWMNAVYFDEKRYLAKGATTLKAGDNLIKQNTNE 120
 QY 65 -----FTYSLKDKLDLTSVGTETKLSFSAANGKVNITSOTKLNPAKETAGTNGTTPVHLN 118
 Db 121 NTNDSFTYSLKDKLDLTSVGTETKLSFSAANGKVNITSOTKLNPAKETAGTNGTTPVHLN 180
 QY 119 LNGIGSTLTD-----RAASVKDYLNAGNIRKGV-----NV 149
 Db 181 LNGIGSTLTDLTLMTGATTNTNDVNTDDEKRRASVAVKDYLNAGNIRKGVKPGTTASDNV 240
 QY 150 DVFRTDYVEFLSADTKTTTVNVEKSKDKGKTEVIGAKTSVKEKDKGLVTKGDKGNG 209
 Db 241 DVFRTDYVEFLSADTKTTTVNVEKSKDKGKTEVIGAKTSVKEKDKGLVTKGDKGNG 300
 QY 210 SSTDGEGLVTAKEVIDAVNKAAGMRKTTTANGOTGADKFEVTSVGTNTVFAAGKGTATV 269
 Db 301 SSTDGEGLVTAKEVIDAVNKAAGMRKTTTANGOTGADKFEVTSVGTNTVFAAGKGTATV 360
 QY 270 TVSKDDGNTVAVDYNVGDALNVNOLNSGMNLDKRAVAGSSGKVIISGVNPSKGMDETV 329
 Db 361 TVSKDDGNTVAVDYNVGDALNVNOLNSGMNLDKRAVAGSSGKVIISGVNPSKGMDETV 420
 QY 330 TVNINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSDVG-DALNVGSKKDKPV 388
 Db 421 TVNINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSDVG-DALNVGSKKDKPV 480
 QY 389 PVRTNVAAGVKEGDTNVAQKGAQNLNRRIDNVGNARAGIAQAIATAGLVQAYLPDGS 448
 Db 481 PVRTNVAAGVKEGDTNVAQKGAQNLNRRIDNVGNARAGIAQAIATAGLVQAYLPDGS 540
 QY 449 KSMMAIGGTYRGEAGYAGISYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 502
 Db 541 KSMMAIGGTYRGEAGYAGISYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 594

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:05:45 ; Search time 46.3729 Seconds
(without alignments)
1848.329 Million cell updates/sec

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Perfect score: 2757
Sequence: 1 NNEQEEYLYLHPVQRTYAV.....TASGNSRGHGASASVGYQM 540

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
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18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
25: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2727	98.9	591	AAV27202	Amino acid sequenc
2	2727	98.9	591	AAV23746	A surface protein
3	2727	98.9	591	AAU06171	N. meningitidis PM
4	2720	98.7	591	AAV23741	A surface protein
5	2720	98.7	591	AAU06175	N. meningitidis Eg
6	2705	98.1	591	AAV57045	BASB029 amino acid
7	2695.5	97.8	582	AAV23737	A surface protein
8	2512	91.1	594	AAV23740	A surface protein
9	2512	91.1	594	AAV57044	BASB029 amino acid

10	2512	91.1	594	AAU06174	N. meningitidis Eg
11	2493	90.4	594	AAV23739	A surface protein
12	2493	90.4	594	AAU06179	N. meningitidis B2
13	2478	89.9	598	AAV23738	A surface protein
14	2478	89.9	598	AAV23742	A surface protein
15	2478	89.9	598	AAU06177	N. meningitidis H1
16	2478	89.9	598	AAU06178	N. meningitidis B2
17	2430.5	88.2	599	AAV23743	A surface protein
18	2430.5	88.2	599	AAU06176	N. meningitidis H3
19	2328	84.4	592	AAU06182	N. meningitidis PM
20	2321	84.2	592	AAV23744	A surface protein
21	2321	84.2	592	AAU06172	N. meningitidis H4
22	2241.5	81.3	589	AAV23745	A surface protein
23	2241.5	81.3	589	AAU06173	N. meningitidis P2
24	2236.5	81.1	502	AAU06186	N. meningitidis PM
25	2212	80.2	592	AAU06180	N. meningitidis H2
26	2206	80.0	513	AAU06183	N. meningitidis H4
27	2196	79.7	592	AAV27203	Amino acid sequenc
28	2025.5	73.5	604	AAU06181	N. meningitidis su
29	1941	70.4	433	AAU06185	N. meningitidis PM
30	1822	66.1	407	AAU06184	N. meningitidis PM
31	1153	41.8	245	AAV27201	Amino acid sequenc
32	1033.5	37.5	241	AAV23860	Haemophilus influe
33	1031.5	37.4	2353	AAV23857	Haemophilus influe
34	927	33.6	1094	AAV23858	Haemophilus influe
35	908	32.9	1098	AAV23859	Haemophilus influe
36	809.5	29.4	679	AAV23859	Haemophilus influe
37	809.5	29.4	679	AAV23855	Haemophilus influe
38	600	21.8	116	AAV23852	Haemophilus influe
39	598.5	21.7	1004	AAV23857	Haemophilus influe
40	593.5	21.5	1104	AAV23856	Haemophilus influe
41	593.5	21.5	1104	AAV23855	Haemophilus influe
42	588	21.3	1002	AAV23854	Haemophilus influe
43	451	16.4	298	AAV30477	Haemophilus influe
44	383.5	13.9	2139	ABF71294	M. catarrhalis sur
45	383	13.9	2314	AAV69136	M. catarrhalis les

ALIGNMENTS

RESULT 1	AAV27202	standard; Protein: 591 AA.
ID	AAV27202	
XX	AAV27202:	
AC	24-SEP-1999	(first entry)
XX		
DT	24-SEP-1999	
XX		
DE	Amino acid sequence of N. meningitidis protein ORF40-1.	
XX		
KW	Neisseria meningitidis protein: pharmaceutical: vaccine; diagnosis:	
KW	bacterial infection; treatment.	
XX		
OS	Neisseria meningitidis.	
XX		
PN	W09936544-A2.	
PD	22-JUL-1999.	
XX		
PF	14-JAN-1999;	99WO-IB00103.
XX		
PR	09-OCT-1998;	98GB-00022143.
PR	14-JAN-1998;	98GB-00000760.
PR	01-SEP-1998;	98GB-0019015.
XX		
PI	(CHIR-) CHIRON SPA.	
XX		
DR	Grandi G, Masignani V, Pizzari M, Rappuoli R, Scarlato V;	
DR	WPI, 1999-444400/37.	
XX	N-PSDB; AAV9124.	

	RESULT 3
ID	AAU06171
XX	AAU06171 standard; Protein; 591 AA.
AC	
XX	AAU06171;
DY	24-OCT-2001 (first entry)
XX	
DE	N. meningitidis PMC21 surface antigen Nhha polypeptide sequence.
XX	
KW	Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX	
OS	Neisseria meningitidis strain PMC21.
XX	
FH	Location/Qualifiers
FT	1..51
FT	/label= Signal_peptide
FT	1..50
FT	/label= C1
FT	/note= "Conserved region 1"
FT	51..108
FT	/label= V1
FT	/note= "Variable region 1"
FT	52..591
FT	/label= Mature_Nhha
FT	/note= "Predicted mature protein, specifically claimed in claim 12"
FT	109..120
FT	/label= C2
FT	/note= "Conserved region 2"
FT	121..124
FT	/label= V2
FT	/note= "Variable region 2"
FT	125..188
FT	/label= C3
FT	/note= "Conserved region 3"
FT	189..210
FT	/label= V3
FT	/note= "Variable region 3"
FT	211..229
FT	/label= C4
FT	/note= "Conserved region 4"
FT	230..236
FT	/label= V4
FT	/note= "Variable region 4"
FT	237..591
FT	/label= C5
FT	/note= "Conserved region 5"
XX	
PX	WO20015182-A1.
PN	
PD	02-AUG-2001.
PE	25-JAN-2001; 2001WO-AU00069.
PR	25-JAN-2000; 2000US-0177917.
PA	(UYQU) UNIV QUEENSLAND.
PQ	
PI	Peak IRA, Jennings MP;
PJ	
PK	WPI; 2001-488774/53.
PL	N-PSDB; AAS09161.
PM	
PP	New Nhba surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis .
PS	Claim 9; Fig 1; 91pp: English.
PT	
CC	The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhha (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are

CC		characterised by deletions of non-conserved amino acids, particularly
CC		the deletion of variable regions. The deletion mutants are useful in
CC		diagnostics, therapeutic and prophylactic vaccines against a broader
CC		spectrum of N. meningitidis, and in designing and/or screening of
CC		medicaments. The mutant proteins when used as a vaccine can effectively
CC		immunise against a broader spectrum of N. meningitidis strains than
CC		would be expected from a corresponding wild-type surface antigen.
CC		The present sequence representing the wild type surface antigen Nhba
CC		from N. meningitidis strain PMC21 is 1 of 10 Nhba polypeptide sequences
CC		(AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC		the present invention.
XX	Sequence	591 AA:
XX		
YY	Query Match	98.9%; Score 2727; DB 22; Length 591;
Dd	Best Local Similarity	99.3%; Pred. No. 1.6e-157;
	Matches	536; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY	1	NNEDEEYLTHHPQRTVAVLIVNSDKGAGBEKEVEENSDMAVFNENEKGLTAREITLK 60
Dd	52	NNEDEEDLTYLDPOQRTVAVLIVNSDKGEGTEKEVEENSMDAVFENEKGLTAREITLK 111
OY	61	AGDNLIKIQNGTNPFYSLSKKDLTDLTSTGTCKLSPSAHGNVNITSDFRKLFAKETGT 120
Dd	112	AGDNLIKIQNGTNPFYSLSKKDLTDLTSTGTCKLSPSAHGNVNITSDFRKLFAKETGT 171
OY	121	NGDTTVHLNIGISTLTDTLTLTGATNTNTNDNVTDDEKRRAASVKDVLNAGNNIGVRPG 180
Dd	172	NGDTTVHLNIGISTLTDTLTLTGATNTNTNDNVTDDEKRRAASVKDVLNAGNNIGVRPG 231
OY	181	TTASDNDVPFRITYDIVERFLSADFTKTTYVNVESKDNGKKTVEYIKAKTSVIKEKDKLYTG 240
Dd	232	TTASDNDVPFRITYDIVERFLSADFTKTTYVNVESKDNGKKTVEYIKAKTSVIKEKDKLYTG 291
OY	241	KDGGNGSSPTGEBGEIYTAKEVIDAVNKAGAMTKTTTANGOTGQADRETYTSGTNVTPA 300
Dd	292	KDGGNGSSPTGEBGEIYTAKEVIDAVNKAGAMTKTTTANGOTGQADRETYTSGTNVTPA 351
OY	301	SGKGTTATVSKDDQGNITVMYDVANVGDALNVNQLONSGMNLDSKRVAGSSGKVISGNVSP 360
Dd	352	SGKGTTATVSKDDQGNITVMYDVANVGDALNVNQLONSGMNLDSKRVAGSSGKVISGNVSP 411
OY	361	SKGKMETVINAGANNIEITTRNGKNIDIAFSMTPOFSSVSLGAGADPFLSYDGALNVG 420
Dd	412	SKGKMETVINAGANNIEITTRNGKNIDIAFSMTPOFSSVSLGAGADAPFLSYDGALNVG 471
OY	421	SKKOKKPVRIINVAGVKEGCVTNAOILKYAQONLNPNLIDVDNAGARAGIAQAITAGLV 480
Dd	472	SKKOKKPVRIINVAGVKEGCVTNAOILKYAQONLNPNLIDVDNAGARAGIAQAITAGLV 531
OY	481	QAYLPGRKMMAIGGCTYRGGAEGAIGAYSISIDGWNIIKIGTASGSRGHFGASASVGQM 540
Dd	532	QAYLPGRKMMAIGGCTYRGGAEGAIGAYSISIDGWNIIKIGTASGSRGHFGASASVGQM 591
RESULT 4		
AAY23741		
ID	AAY23741	standard; Protein; 591 AA.
XX		
AC	AAY23741;	
XX		
DT	08-SEP-1999	(first entry)
XX		
DE	A	surface protein of Neisseria meningitidis.
XX		
KM	Surface protein; surface glycoprotein; infection; vaccine;	
XX	Immunoreactive peptide.	
OS	Neisseria meningitidis.	
XX		
PD	W09931132-A1.	
PN		
PD	24-JUN-1999.	

XX 14-DEC-1998; 98WO-AU01031.
 PF 12-DEC-1997; 97GB-0026398.
 XX (ISIS-) ISIS INNOVATION LTD.
 PA (UYOU) UNIV QUEENSLAND.
 XX Jennings MP, Moxon ER, Peak IRA;
 PI MPI: 1999-418754/35.
 DR N-PSDB: AAX85793.
 FT Neisseria meningitidis surface proteins useful for treating N.
 PT meningitidis infections
 XX Claim 1, Page 104-106; 132pp; English.
 PS The present sequence represents a surface protein of Neisseria
 CC meningitidis which is approximately 62 kDa. The N. meningitidis
 CC surface glycoproteins, nucleic acids, the primers and optionally
 CC a thermostable polymerase, or antibodies are useful in a kit for
 CC the detection or diagnosis of N. meningitidis infection in humans.
 CC The N. meningitidis surface glycoproteins can also be used to
 CC prevent or treat N. meningitidis infection in humans, especially
 CC in the form of vaccines. The proteins and antibodies can also
 CC be used to identify immunoreactive peptides.
 XX Sequence 591 AA;

Query Match 98.7%; Score 2720; DB 20; Length 591;
 Best Local Similarity 99.1%; Pred. No. 4.3e-157;
 Matches 535; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

1 NNEOEELLYHPORFVAVLVNSDKRAGEKEKEKENSOMAYFENEKGLTAREITLK 60
 52 NNEOEELLYDPLKRYAVLVNSDKRGEKEKEKENSOMAYFENEKGLTAREITLK 111
 61 AGDLKIKQNGTNTFTYSLKDLTDLTSVTEKLSFAHKNVTISDTKGLNFAKETAGT 120
 112 AGDLKIKQNGTNTFTYSLKDLTDLTSVTEKLSFANGKNVTISDTKGLNFAKETAGT 171
 121 NGDTTTHLNGIGSTLTDLTGTATNTNNDVDEKRAAYKDYLNAGMNIKGVKPG 180
 172 NGDTTTHLNGIGSTLTDLTGTATNTNNDVDEKRAAYKDYLNAGMNIKGVKPG 231
 181 TTAADNVDFRTYDVEFLSADTKTTFYVNESKONGKTEKIGAKTSVIREKDKLVTG 240
 232 TTAADNVDFRTYDVEFLSADTKTTFYVNESKONGKTEKIGAKTSVIREKDKLVTG 291
 241 KDKGENSGSTDEGEGLVTAKEVIDAVNKAARMKTTTANGQTGAADKEFTVSGTNVFA 300
 292 KDKGENSGSTDEGEGLVTAKEVIDAVNKAARMKTTTANGQTGAADKEFTVSGTNVFA 351
 301 SGKGTATVSKDDGNTVTMDVAVGALANNOLONSGMNIDSKAVAGSSGKVISGNVSP 360
 352 SGKGTATVSKDDGNTVTMDVAVGALANNOLONSGMNIDSKAVAGSSGKVISGNVSP 411
 361 SKGAMDEFVNINAGNIEITRNKNRIDATSMTPQFSSVSLGAGADATLTVSDGALVWG 420
 412 SKGAMDEFVNINAGNIEITRNKNRIDATSMTPQFSSVSLGAGADATLTVSDGALVWG 471
 421 SKKNKPVRTINNAVGVKEDVTNVAOLKGAONLNRRIDNVGDNARAGIAQALATATLV 480
 472 SKKNKPVRTINNAVGVKEDVTNVAOLKGAONLNRRIDNVGDNARAGIAQALATATLV 531
 481 QAYLPGRSMAIIGGCTYRGEAGVAGISISIDGSMWIKGASGNSRGHFCASASVGIOW 540
 532 QAYLPGRSMAIIGGCTYRGEAGVAGISISIDGSMWIKGASGNSRGHFCASASVGIOW 591

RESULT 5
 AAU06175

ID AU06175 standard; Protein; 591 AA.
 AC AAU06175;
 XX 24-OCT-2001 (first entry)
 DE N. meningitidis EG329 surface antigen Nhha polypeptide sequence.
 XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.
 XX Neisseria meningitidis strain EG329.
 OS
 FH Key
 FT Location/Qualifiers
 FT 1..50
 FT /label= C1
 FT /note= "Conserved region 1"
 FT 51..108
 FT /label= V1
 FT /note= "Variable region 1"
 FT 109..120
 FT /label= C2
 FT /note= "Conserved region 2"
 FT 121..124
 FT /label= V2
 FT /note= "Variable region 2"
 FT 125..168
 FT /label= C3
 FT /note= "Conserved region 3"
 FT 169..210
 FT /label= V3
 FT /note= "Variable region 3"
 FT 211..229
 FT /label= C4
 FT /note= "Conserved region 4"
 FT 230..236
 FT /label= V4
 FT /note= "Variable region 4"
 FT 237..591
 FT /label= C5
 FT /note= "Conserved region 5"
 PN WO200155182-A1.
 PD 02-AUG-2001.
 XX 25-JAN-2001; 2001WO-AU00069.
 PF 25-JAN-2000; 2000US-0177917.
 PR (UYOU) UNIV QUEENSLAND.
 PA Peak IRA, Jennings MP;
 PI MPI: 2001-488774/53.
 DR N-PSDB: AAS09165.
 XX New Nhha surface antigen polypeptides and polynucleotides from
 PT Neisseria meningitidis, useful in producing vaccines for treating or
 PT preventing broad spectrum of Neisseria meningitidis -
 PS Claim 9; Fig 1; 91pp; English.
 XX The present invention relates to the isolation of novel Neisseria
 CC meningitidis mutant polypeptides of the surface antigen Nhha
 CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
 CC characterised by deletions of non-conserved amino acids, particularly
 CC the deletion of variable regions. The deletion mutants are useful in
 CC diagnostics, therapeutic and prophylactic vaccines against a broader
 CC spectrum of N. meningitidis, and in designing and/or screening of
 CC medicaments. The mutant proteins when used as a vaccine can effectively
 CC immunise against a broader spectrum of N. meningitidis strains than
 CC would be expected from a corresponding wild-type surface antigen.
 CC The present sequence representing the wild type surface antigen Nhha